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2416 GAM1191 CTGGGCGTGTGAGGCGGCTGTG A
2417 GAM337470 CTAGACTGAAGCTTTATGAGGA A
2418 GAM2350 CCTGGGGGCCACTTTGCACAGG B
2419 GAM6361 GCAGCAGGCAGGGCCAGGCAGG A
2420 GAM336553 GCAGGATGGTTGGACTGAAGGG A

2421 GAM7212 GGCCAGGACTCTTGCAGAACTG A
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2423 GAM337167 TTTGCAGCTTCCAAATTTCTGA A
2424 GAM2887 GGCCTGAGGTCAGCAGTAGAGG A
2424 GAM6083 GGCCTGAGGTCAGCAGTAGAGG A
2425 GAM3890 GGTCCACAAGGGGAGAGCAGGG A
2426 GAM4516 GGCATGATGGAGAGGGTGGAGA A
2427 GAM337581 GGCAGGATGGAGCAGGGCTAAA A
2428 GAM2868 TGGAATGGCTGAAGACTGTGAA A
2428 GAM6466 TGGAATGGCTGAAGACTGTGAA A
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2429 GAM7520 TGCCTAGGCAGGACGGAATGCA A
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2431 GAM5209 CCAGCCTGAGGTTCCTGGAGGG A
2432 GAM1650 ATTTTTCTGCATTTGTATTGGA B
2433 GAM337445 CTGGCTGCATTTAGGAACAAGG A
2434 GAM336989 CTGAGGCAGGAGGGCTCAGGAG A
2435 GAM337334 GAGAGTGCTTTGGGTGTAGGCC A
2436 GAM354 ACACAGGCCCAGAGAGGCAGTG A
2436 GAM569 ACACAGGCCCAGAGAGGCAGTG A
2436 GAM821 ACACAGGCCCAGAGAGGCAGTG A
2437 GAM337031 AATGGCAGTCCCTGGAGCAGGA A
2438 GAM7371 AGAAGGTTGGGGCTGGAGGTCT A
2439 GAM337298 AGGCTGAGTGACTGGGAGTTAG A
2440 GAM7371 AGAAGGTTGGGGCTGGAGGTCT A
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2444 GAM337591 GAGATGACTGGTGGCTGGGGGC A
2445 GAM1976 CTGGCTCCCTCTCTTCTCTCCC A
2446 GAM4382 TGACTGGAGGAAGGGAGGTAAG A
2447 GAM4142 TCTTTGATCTCTTCCGGGGCTT A
2448 GAM1653 TGGAGCAGAAAGGCAGGAGTCC A
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2448 GAM3140 TGGAGCAGAAAGGCAGGAGTCC A
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2460 GAM7845 TGAGGGCAGGTGTGAAAATGCT A
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2462 GAM337317 GAGGTGAAGGAACAAATGCTGA A
2462 GAM337318 GAGGTGAAGGAACAAATGCTGA A
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2475 GAM337256 TGGCTCAGTTTGCTCAGCAGTG A
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2477 GAM5623 GGAAGAATGTGCTTTTGTTGTT A
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2570 GAM2920 GGCTGGGCATGGTGGCTCACGC B
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2581 GAM337508 CCTTGTGTTTTCCAGATTCTGA A
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2582 GAM337171 ACTGCACTCCATCCTGGGGAGC A
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2585 GAM3271 TTCTACTAGTGGTTGATGGCCT A
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2591 GAM337512 ACTGCACTCCTGCCTGGGTGAC A
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2593 GAM269 CATTGCACTCCAGCCTGGGTGA A
2593 GAM337157 CATTGCACTCCAGCCTGGGTGA A
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2595 GAM7162 CTGGGTGGCCTTCAGTCCATGA A
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2596 GAM1770 TGGAGCAGAAAGGCAGGAGTCC A

2596 GAM3140 TGGAGCAGAAAGGCAGGAGTCC A
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2600 GAM588 TCCAGTGAAACAGGTCTCTTTG A
2600 GAM1440 TCCAGTGAAACAGGTCTCTTTG A
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2603 GAM4516 GGCATGATGGAGAGGGTGGAGA A
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2604 GAM5085 TCTGCTGTGATGGACACTTGTA A
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2605 GAM2272 TCTGCTGTGATGGACACTTGT A
2605 GAM336981 TCTGCTGTGATGGACACTTGT A
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2607 GAM8339 TGGAGCCTTGTTGTTTGTTCAC A
2608 GAM5444 TGGAGACCTGTGTGGTTTGTGG A
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2611 GAM7854 CTGTGCCCAGCCAGGGCTGTGT B
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2612 GAM6121 GAGGTAGAGGTTGCAGTGAGTC A
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2618 GAM6818 TTCTTTTTCCGCTTTCTGAGCC A
2619 GAM4975 TTCCCTCATTCTCCACCCAGTC A
2620 GAM337452 TTTGGCTGTTTGTCTTGGGCAA A
2621 GAM336455 TTGCAATAGTGAAAAAACTGAA A
2622 GAM3174 TTTGATGCATGTGACCTGGGAT A
2623 GAM336838 ATGGCCTTTTCTCTTATCCTGG A
2624 GAM291 AGATAGTTCTCTGTTGTTGGGG A
2625 GAM337066 AAGTGGCTTTTGTCTGGCAGAT A
2626 GAM336857 ACAGCTCACTACAGCCTGGATT A
2627 GAM336344 CAGGTACTTTTTGGTTTACATG A
2628 GAM336761 CAGAGAATGGCACAGCTGTCCT A
2629 GAM1650 ATTTTTCTGCATTTGTATTGGA B
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2631 GAM336888 CTCTTTAGTAGGAACTCTGGAT A

2632 GAM933 TTAGGGCAGGCATGAGAGAACT A
2632 GAM4008 TTAGGGCAGGCATGAGAGAACT A
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2634 GAM4516 GGCATGATGGAGAGGGTGGAGA A
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2636 GAM7729 GTGCTTCCATTTCCCCATCTGT A
2637 GAM4074 TACGCTGTGCTGTGACATGGTA A
2638 GAM6361 GCAGCAGGCAGGGCCAGGCAGG A
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2666 GAM5209 CCAGCCTGAGGTTCCTGGAGGG A
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2667 GAM336568 AAGGAAGTGTCTCTTGGCTGGC A
2667 GAM336569 AAGGAAGTGTCTCTTGGCTGGC A
2668 GAM337580 ACAGTCCTCTACTCCAGCTCCC A
2669 GAM336386 AGAGCTAGGAAGATACAGGGTT A
2670 GAM337217 AGGCAGTAAGGGAGAGTTTTGC A

2671 GAM2950 AGGCCAGAGAGGACTCTCTTTT A
2672 GAM7464 AGGTAGGGAGGGTAGATGCTCT B
2673 GAM3183 AGTGCAGGTTCACAGGCTGGGC A
2674 GAM337291 ATAAGCACAGGGAGGTTCTGTC A
2675 GAM336424 AGGTGGGGTTTCACCATGTTGG A
2675 GAM336448 AGGTGGGGTTTCACCATGTTGG A
2676 GAM779 TTGGTTGGTGATGAGCATTGAA A
2677 GAM6506 CAGCTATTCAGGAGCTTGAGGT B
2678 GAM337230 TTCACCAACCACTCCACCAGCT A
2679 GAM6055 TTCACCCATCTTTCCACCCAC A
2680 GAM7954 TTCACCCATCTTTCCACCCACG A
2681 GAM7966 TGTTAACATTTTGGCTAGATAG A
2682 GAM4904 TGGGGCACTGTGGAGGTGTCAT A
2683 GAM336892 GGCAGCTGTGCAGAGTGGGGGT A
2683 GAM336893 GGCAGCTGTGCAGAGTGGGGGT A
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2684 GAM6799 TCAAAGCTGCAGATTGCCTGTG A
2685 GAM336743 TATGAATGTAAGGAATGTGGGA A
2685 GAM336744 TATGAATGTAAGGAATGTGGGA A
2685 GAM336745 TATGAATGTAAGGAATGTGGGA A
2686 GAM593 ACAGCAAGTCTTTGTCAAAGCT A
2686 GAM8362 ACAGCAAGTCTTTGTCAAAGCT A

GAM NAME	PRECUR SEQ-ID	PRECURSOR SEQUENCE	GAM DESCRIPTION
GAM25	6416	GAGGCAGGAG AATTGCTTGA ACCCAGGAAG TGGAGGCTTC AGTGAGCTGA GAACACGCCA CTGCACTCCA GTCCTGGGCA ACAGAGCAAG ACTCTGTCTC	Fig. 8 further provides a conceptual description of a novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 25 (GAM25) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art. GAM25 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM25 was detected is described with additional reference to Figs. 9-15. GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome. GAM25 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM25 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM25 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM25 precursor RNA is designated SEQ ID:6416, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6416 is located from position 52222126 to position 52222224 relative to chromosome X on the `-` strand. GAM25 precursor RNA folds onto itself, forming GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof. Nucleotide sequence of GAM25 precursor RNA, designated SEQ ID NO: 6416, and a schematic representation of a predicted secondary folding of GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein. An enzyme complex designated DICER COMPLEX, `dices` the GAM25 folded precursor RNA yielding a GAM25 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM25 RNA, hereby incorporated herein. Expression of GAM25 RNA was experimentally validated in HeLa cells using the methods described with reference to

Figs.22 to 24.

GAM25 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM25 target RNA, herein designated GAM TARGET RNA. GAM25 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM25 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM25 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM25 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM25 RNA, herein designated GAM RNA, to target binding sites on GAM25 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM25 target RNA into GAM25 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM25 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM25 target genes. The mRNA of each one of this plurality of GAM25 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM25 RNA, herein designated GAM RNA, and which when bound by GAM25 RNA causes inhibition of translation of the GAM25 target mRNA into a corresponding GAM25 target protein.

The mechanism of the translational inhibition exerted by GAM25 RNA, herein designated GAM RNA, on one or more GAM25 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM25 RNA, herein designated GAM RNA, of GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM25 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM25 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM25 RNA correlate with, and may be deduced from, the identity of the GAM25 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM31 6767 GGCTGTGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGATTCAAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

AATCCAGGAT Messenger 31 (GAM31) oligonucleotides modulates expression of respective target genes

AGGCTGTTTC whose function and utility is known in the art.

CATCTGTGAG GAM31 is a novel bioinformatically detectable regulatory, non protein coding,

GCCTATTCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM31 was detected is

GATTACTTGT described with additional reference to Figs. 9-15.

TTCTGGAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCT encoded by the human genome.

GAM31 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM31 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM31

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM31 precursor RNA is designated SEQ ID:6767, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6767 is located from position 57935139 to position 57935222 relative to chromosome 12 on the `-` strand.

GAM31 precursor RNA folds onto itself, forming GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM31 precursor RNA, designated SEQ ID NO: 6767, and a schematic representation of a predicted secondary folding of GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM31 folded precursor RNA yielding a GAM31 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM31 RNA, hereby incorporated herein.

GAM31 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM31 target RNA, herein designated GAM TARGET RNA. GAM31 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM31 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM31 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM31 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM31 RNA, herein designated GAM RNA, to target binding sites on GAM31 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM31 target RNA into GAM31 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM31 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM31 target genes. The mRNA of each one of this plurality of GAM31 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM31 RNA, herein designated GAM RNA, and which when bound by GAM31 RNA causes inhibition of translation of the GAM31 target mRNA into a corresponding GAM31 target protein.

The mechanism of the translational inhibition exerted by GAM31 RNA, herein designated GAM RNA, on one or more GAM31 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM31 RNA, herein designated GAM RNA, of GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM31 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM31 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM31 RNA correlate with, and may be deduced from, the identity of the GAM31 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM44 6280 GAAAAGGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTCATGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGGGAGAAT Messenger 44 (GAM44) oligonucleotides modulates expression of respective target genes

CTTACTTCTC whose function and utility is known in the art.

AAATGGAAAT GAM44 is a novel bioinformatically detectable regulatory, non protein coding,
TGCACTTTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM44 was detected is

described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM44 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM44 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM44

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM44 precursor RNA is designated SEQ ID:6280, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6280 is located from position 48222380 to position 48222439 relative to chromosome 11 on the `+` strand.

GAM44 precursor RNA folds onto itself, forming GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM44 precursor RNA, designated SEQ ID NO: 6280, and a schematic representation of a predicted secondary folding of GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated

herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM44 folded precursor RNA yielding a GAM44 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM44 RNA, hereby incorporated herein.

GAM44 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM44 target RNA, herein designated GAM TARGET RNA. GAM44 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM44 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM44 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM44 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM44 RNA, herein designated GAM RNA, to target binding sites on GAM44 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM44 target RNA into GAM44 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM44 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM44 target genes. The mRNA of each one of this plurality of GAM44 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM44 RNA, herein designated GAM RNA, and which when bound by GAM44 RNA causes inhibition of translation of the GAM44 target mRNA into a corresponding GAM44 target protein.

The mechanism of the translational inhibition exerted by GAM44 RNA, herein designated GAM RNA, on one or more GAM44 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM44 RNA, herein designated GAM RNA, of GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM44 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM44 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM44 RNA correlate with, and may be deduced from, the identity of the GAM44 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM55 5709 ACTGGAAATC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTGCCATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAGGAGATC Messenger 55 (GAM55) oligonucleotides modulates expression of respective target genes

ACCTATCCTA whose function and utility is known in the art.

GTTTTGAGGA GAM55 is a novel bioinformatically detectable regulatory, non protein coding,
ATAGTCATTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM55 was detected is

AGGTGGGTTT described with additional reference to Figs. 9-15.

CCTTAATGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATCTCTTCTA encoded by the human genome.

GT GAM55 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM55

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM55

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM55 precursor RNA is designated SEQ ID:5709, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5709 is located from position 69071144 to position 69071235 relative to chromosome 16 on the `+` strand.

GAM55 precursor RNA folds onto itself, forming GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM55 precursor RNA, designated SEQ ID NO: 5709, and a schematic representation of a predicted secondary folding of GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM55 folded precursor RNA yielding a GAM55 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM55 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM55 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM55 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM55 target RNA, herein designated GAM TARGET RNA. GAM55 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM55 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM55 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM55 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM55 RNA, herein designated GAM RNA, to target binding sites on GAM55 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM55 target RNA into GAM55 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM55 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM55 target genes. The mRNA of each one of this plurality of GAM55 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM55 RNA, herein designated GAM RNA, and which when bound by GAM55 RNA causes inhibition of translation of the GAM55 target mRNA into a corresponding GAM55 target protein.

The mechanism of the translational inhibition exerted by GAM55 RNA, herein

designated GAM RNA, on one or more GAM55 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM55 RNA, herein designated GAM RNA, of GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM55 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM55 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM55 RNA correlate with, and may be deduced from, the identity of the GAM55 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM66 5945 AGTTTTGCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGAGACAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGCCTCACT Messenger 66 (GAM66) oligonucleotides modulates expression of respective target genes

CGCCTCACCC whose function and utility is known in the art.

TAGTCCTGGT GAM66 is a novel bioinformatically detectable regulatory, non protein coding,
GGCATTTGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM66 was detected is

TCAGGTGCAA described with additional reference to Figs. 9-15.

AATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM66 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM66 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM66

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM66 precursor RNA is designated SEQ ID:5945, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5945 is located from position 82042982 to position 82043055 relative to chromosome 10 on the `-` strand.

GAM66 precursor RNA folds onto itself, forming GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM66 precursor RNA, designated SEQ ID NO: 5945, and a schematic representation of a predicted secondary folding of GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM66 folded precursor RNA yielding a GAM66 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM66 RNA, hereby incorporated herein.

GAM66 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM66 target RNA, herein designated GAM TARGET RNA. GAM66 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM66 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM66 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM66 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM66 RNA, herein designated GAM RNA, to target binding sites on GAM66 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM66 target RNA into GAM66 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM66 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM66 target genes. The mRNA of each one of this plurality of GAM66 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM66 RNA, herein designated GAM RNA,

and which when bound by GAM66 RNA causes inhibition of translation of the GAM66 target mRNA into a corresponding GAM66 target protein.

The mechanism of the translational inhibition exerted by GAM66 RNA, herein designated GAM RNA, on one or more GAM66 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM66 RNA, herein designated GAM RNA, of GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM66 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM66 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM66 RNA correlate with, and may be deduced from, the identity of the GAM66 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM83 5649 AAAGGATGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGTGGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CATGTTTTGG Messenger 83 (GAM83) oligonucleotides modulates expression of respective target genes

GGAGAATCTT whose function and utility is known in the art.

ACTTCTCAAA GAM83 is a novel bioinformatically detectable regulatory, non protein coding,
TGGAAATTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM83 was detected is

ACTTTTTGCT described with additional reference to Figs. 9-15.

GAATCCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM83 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM83 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM83

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM83 precursor RNA is designated SEQ ID:5649, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5649 is located from position 48222373 to position 48222451 relative to chromosome 11 on the `+` strand.

GAM83 precursor RNA folds onto itself, forming GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM83 precursor RNA, designated SEQ ID NO: 5649, and a schematic representation of a predicted secondary folding of GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM83 folded precursor RNA yielding a GAM83 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM83 RNA, hereby incorporated herein.

GAM83 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM83 target RNA, herein designated GAM TARGET RNA. GAM83 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM83 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM83 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM83 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM83 RNA, herein designated GAM RNA, to target binding sites on GAM83 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM83 target RNA into GAM83 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM83 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM83 target genes. The mRNA of each one of this plurality of GAM83 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM83 RNA, herein designated GAM RNA, and which when bound by GAM83 RNA causes inhibition of translation of the GAM83 target mRNA into a corresponding GAM83 target protein.

The mechanism of the translational inhibition exerted by GAM83 RNA, herein designated GAM RNA, on one or more GAM83 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM83 RNA, herein designated GAM RNA, of GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM83 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM83 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM83 RNA correlate with, and may be deduced from, the identity of the GAM83 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM99 6127 CCTTCAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTGTAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address TATCGGGGTG Messenger 99 (GAM99) oligonucleotides modulates expression of respective target genes

GAGAGATAAG whose function and utility is known in the art.

CCAAGTATCC GAM99 is a novel bioinformatically detectable regulatory, non protein coding, AGATAACCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM99 was detected is

GGCATAAGGC described with additional reference to Figs. 9-15.

AGAATATTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGTACTATG encoded by the human genome.

AGAGGTACAA GAM99 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM99

AGGGGAGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM99 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM99 precursor RNA is designated SEQ ID:6127, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6127 is located from position 102246140 to position 102246248 relative to chromosome 10 on the `+` strand.

GAM99 precursor RNA folds onto itself, forming GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM99 precursor RNA, designated SEQ ID NO: 6127, and a schematic representation of a predicted secondary folding of GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM99 folded precursor RNA yielding a GAM99 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM99 RNA, hereby incorporated herein.

GAM99 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM99 target RNA, herein designated GAM TARGET RNA. GAM99 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM99 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM99 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM99 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM99 RNA, herein designated GAM RNA, to target binding sites on GAM99 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM99 target RNA into GAM99 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM99 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM99 target genes. The mRNA of each one of this plurality of GAM99 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM99 RNA, herein designated GAM RNA, and which when bound by GAM99 RNA causes inhibition of translation of the GAM99 target mRNA into a corresponding GAM99 target protein.

The mechanism of the translational inhibition exerted by GAM99 RNA, herein designated GAM RNA, on one or more GAM99 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM99 RNA, herein designated GAM RNA, of GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM99 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM99 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM99 RNA correlate with, and may be deduced from, the identity of the GAM99 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM106 7240 TGGGGCCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTAATATAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AAACCTTCTT Messenger 106 (GAM106) oligonucleotides modulates expression of respective target genes
GCCAATATAG whose function and utility is known in the art.

GAATATGTTG GAM106 is a novel bioinformatically detectable regulatory, non protein coding,
ACATATTAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM106 was detected is

TATAGCAAAA described with additional reference to Figs. 9-15.

GGCTTATATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCACCGAAT encoded by the human genome.

GAGGCTCTG GAM106 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM106 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM106 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM106 precursor RNA is designated SEQ ID:7240, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7240 is located from position 13445760 to position 13445858 relative to chromosome 20 on the `-` strand.

GAM106 precursor RNA folds onto itself, forming GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM106 precursor RNA, designated SEQ ID NO: 7240, and a schematic representation of a predicted secondary folding of GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM106 folded precursor RNA yielding a GAM106 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM106 RNA, hereby incorporated herein.

GAM106 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM106 target RNA, herein designated GAM TARGET RNA. GAM106 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM106 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM106 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM106 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM106 RNA, herein designated GAM RNA, to target binding sites on GAM106 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM106 target RNA into GAM106 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM106 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM106 target genes. The mRNA of each one of this plurality of GAM106 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM106 RNA, herein designated GAM RNA, and which when bound by GAM106 RNA causes inhibition of translation of the GAM106 target mRNA into a corresponding GAM106 target protein.

The mechanism of the translational inhibition exerted by GAM106 RNA, herein designated GAM RNA, on one or more GAM106 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM106 RNA, herein designated GAM RNA, of GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM106 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM106 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM106 RNA correlate with, and may be deduced from, the identity of the GAM106 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM112 6031 CAGTAAACAT AAGTTCCTCA GGAGAGTTTG ATGTGTGTCA GGTGCTTAGA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 112 (GAM112) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM112 is a novel bioinformatically detectable regulatory, non protein coding,

ACAGGGCCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM112 was detected is

ATATATAATC described with additional reference to Figs. 9-15.

AGCCCATGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCTATTAC encoded by the human genome.

TG GAM112 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM112 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM112 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM112 precursor RNA is designated SEQ ID:6031, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6031 is located from position 47490562 to position 47490653 relative to chromosome X on the `+` strand.

GAM112 precursor RNA folds onto itself, forming GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM112 precursor RNA, designated SEQ ID NO: 6031, and a schematic representation of a predicted secondary folding of GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM112 folded precursor RNA yielding a GAM112 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM112 RNA, hereby incorporated herein.

GAM112 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM112 target RNA, herein designated GAM TARGET RNA. GAM112 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM112 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM112 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM112 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM112 RNA, herein designated GAM RNA, to target binding sites on GAM112 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM112 target RNA into GAM112 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM112 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM112 target genes. The mRNA of each one of this plurality of GAM112 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM112 RNA, herein designated GAM RNA, and which when bound by GAM112 RNA causes inhibition of translation of the GAM112 target mRNA into a corresponding GAM112 target protein.

The mechanism of the translational inhibition exerted by GAM112 RNA, herein designated GAM RNA, on one or more GAM112 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM112 RNA, herein designated GAM RNA, of GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM112 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM112 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM112 RNA correlate with, and may be deduced from, the identity of the GAM112 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM144 6899 GTGATCCACA Fig. 8 further provides a conceptual description of another novel bioinformatically

CGCTGGCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGTTCGAC Messenger 144 (GAM144) oligonucleotides modulates expression of respective target
genes
ATTTACCGCG whose function and utility is known in the art.

AGGTGGGCGG GAM144 is a novel bioinformatically detectable regulatory, non protein coding,
AGAGCCTGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM144 was detected is

CCTGTGACGA described with additional reference to Figs. 9-15.

GGGATGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
encoded by the human genome.

GAM144 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM144

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM144
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM144 precursor RNA is designated SEQ ID:6899, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6899 is located from position 29007729 to position 29007806 relative to chromosome 22 on the `-` strand.

GAM144 precursor RNA folds onto itself, forming GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM144 precursor RNA, designated SEQ ID NO: 6899, and a schematic representation of a predicted secondary folding of GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM144 folded precursor RNA yielding a GAM144 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM144 RNA, hereby incorporated herein.

GAM144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM144 target RNA, herein designated GAM TARGET RNA. GAM144 target
RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM144 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM144 RNA, herein designated GAM RNA, to target binding sites on GAM144 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM144 target RNA into GAM144 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM144 target genes. The mRNA of each one of this plurality of GAM144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM144 RNA, herein designated GAM RNA, and which when bound by GAM144 RNA causes inhibition of translation of the GAM144 target mRNA into a corresponding GAM144 target protein.

The mechanism of the translational inhibition exerted by GAM144 RNA, herein designated GAM RNA, on one or more GAM144 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM144 RNA, herein designated GAM RNA, of GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM144 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM144 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM144 RNA

correlate with, and may be deduced from, the identity of the GAM144 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM175 7084 TGAACCAGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTCAGCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTGTGTTTG Messenger 175 (GAM175) oligonucleotides modulates expression of respective target genes
ACCCTGTGTT whose function and utility is known in the art.

CAAGGTTAGG GAM175 is a novel bioinformatically detectable regulatory, non protein coding,
GGAATTATAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM175 was detected is

TTTCCCAGGT described with additional reference to Figs. 9-15.

CTCCATCGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGGTAATCA encoded by the human genome.

GAGGGGCAGA GAM175 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM175
GAAGGCTTCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM175
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM175 precursor RNA is designated SEQ ID:7084, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7084 is located from position 94175190 to position 94175299 relative to chromosome X on the `+` strand.

GAM175 precursor RNA folds onto itself, forming GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM175 precursor RNA, designated SEQ ID NO: 7084, and a schematic representation of a predicted secondary folding of GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM175 folded precursor RNA yielding a GAM175 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM175 RNA, hereby incorporated herein.

GAM175 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM175 target RNA, herein designated GAM TARGET RNA. GAM175 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM175 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM175 RNA, herein designated GAM RNA, to target binding sites on GAM175 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM175 target RNA into GAM175 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM175 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM175 target genes. The mRNA of each one of this plurality of GAM175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM175 RNA, herein designated GAM RNA, and which when bound by GAM175 RNA causes inhibition of translation of the GAM175 target mRNA into a corresponding GAM175 target protein.

The mechanism of the translational inhibition exerted by GAM175 RNA, herein designated GAM RNA, on one or more GAM175 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM175 RNA, herein designated GAM RNA, of GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM175 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM175 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM175 RNA correlate with, and may be deduced from, the identity of the GAM175 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM189 6298 GAAGTTCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTGTAGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTATGATGA Messenger 189 (GAM189) oligonucleotides modulates expression of respective target genes
TCGTACGTAT whose function and utility is known in the art.

GAACAGCCAT GAM189 is a novel bioinformatically detectable regulatory, non protein coding,
TGCACTCCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM189 was detected is

CCTGGGCAAT described with additional reference to Figs. 9-15.

TC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM189 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM189

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM189
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM189 precursor RNA is designated SEQ ID:6298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6298 is located from position 95450005 to position 95450076 relative to chromosome 4 on the `+` strand.

GAM189 precursor RNA folds onto itself, forming GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM189 precursor RNA, designated SEQ ID NO: 6298, and a schematic representation of a predicted secondary folding of GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM189 folded precursor RNA yielding a GAM189 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM189 RNA, hereby incorporated herein. Expression of GAM189 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM189 target RNA, herein designated GAM TARGET RNA. GAM189 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM189 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM189 RNA, herein designated GAM RNA, to target binding sites on GAM189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM189 target RNA into GAM189 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM189 target genes. The mRNA of each one of this plurality of GAM189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM189 RNA, herein designated GAM RNA, and which when bound by GAM189 RNA causes inhibition of translation of the GAM189 target mRNA into a corresponding GAM189 target protein.

The mechanism of the translational inhibition exerted by GAM189 RNA, herein designated GAM RNA, on one or more GAM189 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM189 RNA, herein designated GAM RNA, of GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM189 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM189 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM189 RNA correlate with, and may be deduced from, the identity of the GAM189 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM193 6545 GCTGGATATT GCTAAGAATT CAGGTAGTCT CGGGATCTCC AGAGTCTCCA TACTAGGACA GGAGATCTTC AGAACCTGGA GGAATGGAAA TAGTCTAGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 193 (GAM193) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM193 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM193 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM193 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM193 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM193 precursor RNA is designated SEQ ID:6545, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6545 is located from position 150223538 to position 150223636 relative to chromosome 7 on the `-` strand.

GAM193 precursor RNA folds onto itself, forming GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM193 precursor RNA, designated SEQ ID NO: 6545, and a schematic representation of a predicted secondary folding of GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM193 folded precursor RNA yielding a GAM193 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM193 RNA, hereby incorporated herein.

GAM193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM193 target RNA, herein designated GAM TARGET RNA. GAM193 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM193 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM193 RNA, herein designated GAM RNA, to target binding sites on GAM193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM193 target RNA into GAM193 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM193 target genes. The mRNA of each one of this plurality of GAM193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM193 RNA, herein designated GAM RNA, and which when bound by GAM193 RNA causes inhibition of translation of the GAM193 target mRNA into a corresponding GAM193 target protein.

The mechanism of the translational inhibition exerted by GAM193 RNA, herein designated GAM RNA, on one or more GAM193 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM193 RNA, herein designated GAM RNA, of GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM193 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM193 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM193 RNA correlate with, and may be deduced from, the identity of the GAM193 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM205 7010 TCAGGCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCCAGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCTGGTTTC Messenger 205 (GAM205) oligonucleotides modulates expression of respective target genes

GAATTTCATG whose function and utility is known in the art.

CTTCTAACCT GAM205 is a novel bioinformatically detectable regulatory, non protein coding,

GAGCACTGTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM205 was detected is

CTGCTTGGTG described with additional reference to Figs. 9-15.

GAGTTCTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTAGTCCTAC encoded by the human genome.

CTTTCAGGCA GAM205 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM205

GA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM205

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM205 precursor RNA is designated SEQ ID:7010, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7010 is located from position 34136693 to position 34136794 relative to chromosome 19 on the `+` strand.

GAM205 precursor RNA folds onto itself, forming GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM205 precursor RNA, designated SEQ ID NO: 7010, and a schematic representation of a predicted secondary folding of GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM205 folded precursor RNA yielding a GAM205 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM205 RNA, hereby incorporated herein.

GAM205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM205 target RNA, herein designated GAM TARGET RNA. GAM205 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM205 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM205 RNA, herein designated GAM RNA, to target binding sites on GAM205 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM205 target RNA into GAM205 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM205 target genes. The mRNA of each one of this plurality of GAM205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM205 RNA, herein

designated GAM RNA, and which when bound by GAM205 RNA causes inhibition of translation of the GAM205 target mRNA into a corresponding GAM205 target protein.

The mechanism of the translational inhibition exerted by GAM205 RNA, herein designated GAM RNA, on one or more GAM205 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM205 RNA, herein designated GAM RNA, of GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM205 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM205 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM205 RNA correlate with, and may be deduced from, the identity of the GAM205 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM206 5681 ACAATAGTCT AAGAGCTAAC TAGTTGCACT TGTCTTTACC CTAGAGGCTT GCTAAATAAA GCATACTTTC TGGAGGGCAA GTGCAGGGGT CGCTTCTGTT TGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 206 (GAM206) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM206 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM206 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM206 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM206

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM206 precursor RNA is designated SEQ ID:5681, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5681 is located from position 63676328 to position 63676430 relative to chromosome 8 on the `+` strand.

GAM206 precursor RNA folds onto itself, forming GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM206 precursor RNA, designated SEQ ID NO: 5681, and a schematic representation of a predicted secondary folding of GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM206 folded precursor RNA yielding a GAM206 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM206 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM206 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM206 target RNA, herein designated GAM TARGET RNA. GAM206 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM206 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM206 RNA, herein designated GAM RNA, to target binding sites on GAM206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM206 target RNA into

GAM206 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM206 target genes. The mRNA of each one of this plurality of GAM206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM206 RNA, herein designated GAM RNA, and which when bound by GAM206 RNA causes inhibition of translation of the GAM206 target mRNA into a corresponding GAM206 target protein.

The mechanism of the translational inhibition exerted by GAM206 RNA, herein designated GAM RNA, on one or more GAM206 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM206 RNA, herein designated GAM RNA, of GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM206 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM206 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM206 RNA correlate with, and may be deduced from, the identity of the GAM206 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM240 7259 TGGTTTAGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGGAACAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCTGGCACA Messenger 240 (GAM240) oligonucleotides modulates expression of respective target genes

TAGTAAGTGT whose function and utility is known in the art.

TCAGTGAACG GAM240 is a novel bioinformatically detectable regulatory, non protein coding,

TTAGCTATTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM240 was detected is

CCATCATCAC described with additional reference to Figs. 9-15.

TATTAATGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCTAGTGAC encoded by the human genome.

TGTCCTGAGT GAM240 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM240

TACATTA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM240

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM240 precursor RNA is designated SEQ ID:7259, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7259 is located from position 73803662 to position 73803768 relative to chromosome 11 on the `-` strand.

GAM240 precursor RNA folds onto itself, forming GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM240 precursor RNA, designated SEQ ID NO: 7259, and a schematic representation of a predicted secondary folding of GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM240 folded precursor RNA yielding a GAM240 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM240 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM240 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM240 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM240 target RNA, herein designated GAM TARGET RNA. GAM240 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM240 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM240 RNA, herein designated GAM RNA, to target binding sites on GAM240 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM240 target RNA into GAM240 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM240 target genes. The mRNA of each one of this plurality of GAM240 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM240 RNA, herein designated GAM RNA, and which when bound by GAM240 RNA causes inhibition of translation of the GAM240 target mRNA into a corresponding GAM240 target protein.

The mechanism of the translational inhibition exerted by GAM240 RNA, herein designated GAM RNA, on one or more GAM240 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM240 RNA, herein designated GAM RNA, of GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM240 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM240 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM240 RNA correlate with, and may be deduced from, the identity of the GAM240 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM259 5989 CAAGTTGTGA CCTTCCCAGT CCTCTCTCCA TTTGCAGATC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 259 (GAM259) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

AGCAAGCTTC GAM259 is a novel bioinformatically detectable regulatory, non protein coding, TGTCAGCAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM259 was detected is

GAGGGGTGGA described with additional reference to Figs. 9-15.

CAATGAAACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGTTCAGCT encoded by the human genome.

TG GAM259 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM259 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM259 precursor RNA is designated SEQ ID:5989, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5989 is located from position 97689223 to position 97689314 relative to chromosome 9 on the `+` strand.

GAM259 precursor RNA folds onto itself, forming GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM259 precursor RNA, designated SEQ ID NO: 5989, and a schematic representation of a predicted secondary folding of GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM259 folded precursor RNA yielding a GAM259 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM259 RNA, hereby incorporated herein.

GAM259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM259 target RNA, herein designated GAM TARGET RNA. GAM259 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM259 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM259 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM259 RNA, herein designated GAM RNA, to target binding sites on GAM259 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM259 target RNA into GAM259 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM259 target genes. The mRNA of each one of this plurality of GAM259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM259 RNA, herein designated GAM RNA, and which when bound by GAM259 RNA causes inhibition of translation of the GAM259 target mRNA into a corresponding GAM259 target protein.

The mechanism of the translational inhibition exerted by GAM259 RNA, herein designated GAM RNA, on one or more GAM259 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM259 RNA, herein designated GAM RNA, of GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM259 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM259 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM259 RNA correlate with, and may be deduced from, the identity of the GAM259 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM269 6451 GAGGTAAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGGAGAGGT Messenger 269 (GAM269) oligonucleotides modulates expression of respective target
genes
TGTGGTGAGC whose function and utility is known in the art.

CAAGATGGCA GAM269 is a novel bioinformatically detectable regulatory, non protein coding,
CCATTGCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM269 was detected is

CCAGCCTGGG described with additional reference to Figs. 9-15.

TGACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
AGACTTC encoded by the human genome.

GAM269 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM269

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM269

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM269 precursor RNA is designated SEQ ID:6451, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6451 is located from position 75439944 to position 75440030 relative to chromosome 10 on the `+` strand.

GAM269 precursor RNA folds onto itself, forming GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM269 precursor RNA, designated SEQ ID NO: 6451, and a schematic representation of a predicted secondary folding of GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM269 folded precursor RNA yielding a GAM269 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM269 RNA, hereby incorporated herein.

GAM269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM269 target RNA, herein designated GAM TARGET RNA. GAM269 target
RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM269 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM269 RNA, herein designated GAM RNA, to target binding sites on GAM269 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM269 target RNA into GAM269 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM269 target genes. The mRNA of each one of this plurality of GAM269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM269 RNA, herein designated GAM RNA, and which when bound by GAM269 RNA causes inhibition of translation of the GAM269 target mRNA into a corresponding GAM269 target protein.

The mechanism of the translational inhibition exerted by GAM269 RNA, herein designated GAM RNA, on one or more GAM269 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM269 RNA, herein designated GAM RNA, of GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM269 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM269 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM269 RNA

correlate with, and may be deduced from, the identity of the GAM269 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM270 5974 ATGGGTAGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAACTAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGATAAAGG Messenger 270 (GAM270) oligonucleotides modulates expression of respective target genes
CTTCACGTGG whose function and utility is known in the art.

TGTTTGGCAT GAM270 is a novel bioinformatically detectable regulatory, non protein coding,
GGCGTAGGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM270 was detected is

TAGATTGGAC described with additional reference to Figs. 9-15.

CTCAGTTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCCCAT encoded by the human genome.

GAM270 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM270

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM270

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM270 precursor RNA is designated SEQ ID:5974, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5974 is located from position 46553863 to position 46553949 relative to chromosome 12 on the `+` strand.

GAM270 precursor RNA folds onto itself, forming GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM270 precursor RNA, designated SEQ ID NO: 5974, and a schematic representation of a predicted secondary folding of GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM270 folded precursor RNA yielding a GAM270 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM270 RNA, hereby incorporated herein.

GAM270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM270 target RNA, herein designated GAM TARGET RNA. GAM270 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM270 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM270 RNA, herein designated GAM RNA, to target binding sites on GAM270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM270 target RNA into GAM270 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM270 target genes. The mRNA of each one of this plurality of GAM270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM270 RNA, herein designated GAM RNA, and which when bound by GAM270 RNA causes inhibition of translation of the GAM270 target mRNA into a corresponding GAM270 target protein.

The mechanism of the translational inhibition exerted by GAM270 RNA, herein designated GAM RNA, on one or more GAM270 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM270 RNA, herein designated GAM RNA, of GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM270 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM270 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM270 RNA correlate with, and may be deduced from, the identity of the GAM270 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM281 6457 GAGGTGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATTGCTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCCCGGAGG Messenger 281 (GAM281) oligonucleotides modulates expression of respective target genes
TTGAAGCTAC whose function and utility is known in the art.

AGTGAGCCTT GAM281 is a novel bioinformatically detectable regulatory, non protein coding,
GATTGTGTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM281 was detected is

CTGCACTCCA described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGGTAAGAC encoded by the human genome.

TCTGTCTC GAM281 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM281
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM281
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM281 precursor RNA is designated SEQ ID:6457, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6457 is located from position 51464300 to position 51464397 relative to chromosome 12 on the `-` strand.

GAM281 precursor RNA folds onto itself, forming GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM281 precursor RNA, designated SEQ ID NO: 6457, and a schematic representation of a predicted secondary folding of GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM281 folded precursor RNA yielding a GAM281 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM281 RNA, hereby incorporated herein. Expression of GAM281 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM281 target RNA, herein designated GAM TARGET RNA. GAM281 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM281 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM281 RNA, herein designated GAM RNA, to target binding sites on GAM281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM281 target RNA into GAM281 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM281 target genes. The mRNA of each one of this plurality of GAM281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM281 RNA, herein designated GAM RNA, and which when bound by GAM281 RNA causes inhibition of translation of the GAM281 target mRNA into a corresponding GAM281 target protein.

The mechanism of the translational inhibition exerted by GAM281 RNA, herein designated GAM RNA, on one or more GAM281 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM281 RNA, herein designated GAM RNA, of GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM281 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM281 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM281 RNA correlate with, and may be deduced from, the identity of the GAM281 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM282 6771 GGCTTTAGGA ATCGCCTGGC TCTACCCTCT CACTTCATGG CTACAGATAC TTGTGCCCTG AGAGAGCAAG TGAATTTCCC AAAGCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 282 (GAM282) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM282 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM282 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM282 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM282 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM282 precursor RNA is designated SEQ ID:6771, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6771 is located from position 117492532 to position 117492617 relative to chromosome 9 on the `+` strand.

GAM282 precursor RNA folds onto itself, forming GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM282 precursor RNA, designated SEQ ID NO: 6771, and a schematic representation of a predicted secondary folding of GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM282 folded precursor RNA yielding a GAM282 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM282 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM282 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM282 target RNA, herein designated GAM TARGET RNA. GAM282 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM282 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM282 RNA, herein designated GAM RNA, to target binding sites on GAM282 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM282 target RNA into GAM282 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM282 target genes. The mRNA of each one of this plurality of GAM282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM282 RNA, herein designated GAM RNA, and which when bound by GAM282 RNA causes inhibition of translation of the GAM282 target mRNA into a corresponding GAM282 target protein.

The mechanism of the translational inhibition exerted by GAM282 RNA, herein designated GAM RNA, on one or more GAM282 target genes, herein collectively designated GAM

TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM282 RNA, herein designated GAM RNA, of GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM282 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM282 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM282 RNA correlate with, and may be deduced from, the identity of the GAM282 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM291 7234 TGGGCCAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTCTCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTTGGGGGA Messenger 291 (GAM291) oligonucleotides modulates expression of respective target genes
TTTCTTGTGC whose function and utility is known in the art.

ATTGTGGGAG GAM291 is a novel bioinformatically detectable regulatory, non protein coding,
ATTTCCCATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM291 was detected is

TTTCCTCACT described with additional reference to Figs. 9-15.

TCTACCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM291 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM291

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM291
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM291 precursor RNA is designated SEQ ID:7234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7234 is located from position 9780990 to position 9781067 relative to chromosome X on the `+` strand.

GAM291 precursor RNA folds onto itself, forming GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM291 precursor RNA, designated SEQ ID NO: 7234, and a schematic representation of a predicted secondary folding of GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM291 folded precursor RNA yielding a GAM291 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM291 RNA, hereby incorporated herein.

GAM291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM291 target RNA, herein designated GAM TARGET RNA. GAM291 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM291 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM291 RNA, herein designated GAM RNA, to target binding sites on GAM291 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM291 target RNA into GAM291 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM291 target genes. The mRNA of each one of this plurality of GAM291 target genes comprises one or more target binding sites, each having a

nucleotide sequence which is at least partly complementary to GAM291 RNA, herein designated GAM RNA, and which when bound by GAM291 RNA causes inhibition of translation of the GAM291 target mRNA into a corresponding GAM291 target protein.

The mechanism of the translational inhibition exerted by GAM291 RNA, herein designated GAM RNA, on one or more GAM291 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM291 RNA, herein designated GAM RNA, of GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM291 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM291 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM291 RNA correlate with, and may be deduced from, the identity of the GAM291 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM317 6729 GGCAGAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTCACTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAAAGTTCC Messenger 317 (GAM317) oligonucleotides modulates expression of respective target genes
AAATAGGGCA whose function and utility is known in the art.

AAATGTGTGT GAM317 is a novel bioinformatically detectable regulatory, non protein coding,
TTCCCTAGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM317 was detected is

AGTATTTTTT described with additional reference to Figs. 9-15.

AAAAACATTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGAGATAGA encoded by the human genome.

GTCTTGCTCT GAM317 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM317
GTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM317

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM317 precursor RNA is designated SEQ ID:6729, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6729 is located from position 4462631 to position 4462733 relative to chromosome 19 on the `+` strand.

GAM317 precursor RNA folds onto itself, forming GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM317 precursor RNA, designated SEQ ID NO: 6729, and a schematic representation of a predicted secondary folding of GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM317 folded precursor RNA yielding a GAM317 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM317 RNA, hereby incorporated herein.

GAM317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM317 target RNA, herein designated GAM TARGET RNA. GAM317 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM317 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM317 RNA, herein designated GAM RNA, to target binding sites on GAM317 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM317 target RNA into GAM317 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by

a broken line.

It is appreciated that GAM317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM317 target genes. The mRNA of each one of this plurality of GAM317 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM317 RNA, herein designated GAM RNA, and which when bound by GAM317 RNA causes inhibition of translation of the GAM317 target mRNA into a corresponding GAM317 target protein.

The mechanism of the translational inhibition exerted by GAM317 RNA, herein designated GAM RNA, on one or more GAM317 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM317 RNA, herein designated GAM RNA, of GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM317 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM317 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM317 RNA correlate with, and may be deduced from, the identity of the GAM317 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM329 6852 GGTGGTGGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAGGAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGGGCACT Messenger 329 (GAM329) oligonucleotides modulates expression of respective target genes
TTCACTGTCT whose function and utility is known in the art.

TTTCCTTCAT GAM329 is a novel bioinformatically detectable regulatory, non protein coding,
AAACTGGCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM329 was detected is

GCACTACC described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM329 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM329 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM329 precursor RNA is designated SEQ ID:6852, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6852 is located from position 37420113 to position 37420180 relative to chromosome 9 on the `+` strand.

GAM329 precursor RNA folds onto itself, forming GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM329 precursor RNA, designated SEQ ID NO: 6852, and a schematic representation of a predicted secondary folding of GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM329 folded precursor RNA yielding a GAM329 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM329 RNA, hereby incorporated herein.

GAM329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM329 target RNA, herein designated GAM TARGET RNA. GAM329 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM329 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM329 RNA, herein designated GAM RNA, to target binding sites on GAM329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM329 target RNA into GAM329 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM329 target genes. The mRNA of each one of this plurality of GAM329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM329 RNA, herein designated GAM RNA, and which when bound by GAM329 RNA causes inhibition of translation of the GAM329 target mRNA into a corresponding GAM329 target protein.

The mechanism of the translational inhibition exerted by GAM329 RNA, herein designated GAM RNA, on one or more GAM329 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM329 RNA, herein designated GAM RNA, of GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM329 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM329 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM329 RNA correlate with, and may be deduced from, the identity of the GAM329 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM330 6328 GAGAATTGCT TGAACCCAGG AGGTGGAGGT TGCAGTGAGC CGAGATCACG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 330 (GAM330) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM330 is a novel bioinformatically detectable regulatory, non protein coding,

CTACTGCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM330 was detected is

CCAGCCTGGG described with additional reference to Figs. 9-15.

TGACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTC encoded by the human genome.

GAM330 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM330

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM330

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM330 precursor RNA is designated SEQ ID:6328, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6328 is located from position 102423230 to position 102423315 relative to chromosome 7 on the `-` strand.

GAM330 precursor RNA folds onto itself, forming GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM330 precursor RNA, designated SEQ ID NO: 6328, and a schematic representation of a predicted secondary folding of GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM330 folded precursor RNA yielding a GAM330 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM330 RNA, hereby incorporated herein.

GAM330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM330 target RNA, herein designated GAM TARGET RNA. GAM330 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM330 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM330 RNA, herein designated GAM RNA, to target binding sites on GAM330 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM330 target RNA into GAM330 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM330 target genes. The mRNA of each one of this plurality of GAM330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM330 RNA, herein designated GAM RNA, and which when bound by GAM330 RNA causes inhibition of translation of the GAM330 target mRNA into a corresponding GAM330 target protein.

The mechanism of the translational inhibition exerted by GAM330 RNA, herein designated GAM RNA, on one or more GAM330 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM330 RNA, herein designated GAM RNA, of GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM330 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM330 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM330 RNA correlate with, and may be deduced from, the identity of the GAM330 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM335 5987 CAACCCAGTA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGTCCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address GTCAATGCTT Messenger 335 (GAM335) oligonucleotides modulates expression of respective target genes CTCTCCATAG whose function and utility is known in the art.

GAGACCTGTA GAM335 is a novel bioinformatically detectable regulatory, non protein coding, AATGGGCGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM335 was detected is

GGGGGGAGGA described with additional reference to Figs. 9-15.

ATTTTCTGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene CTCACACACT encoded by the human genome.

ATTATGGGTT GAM335 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM335 G precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM335

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM335 precursor RNA is designated SEQ ID:5987, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5987 is located from position 22176932 to position 22177032 relative to chromosome 22 on the `+` strand.

GAM335 precursor RNA folds onto itself, forming GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM335 precursor RNA, designated SEQ ID NO: 5987, and a schematic representation of a predicted secondary folding of GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM335 folded precursor RNA yielding a GAM335 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM335 RNA, hereby incorporated herein.

GAM335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM335 target RNA, herein designated GAM TARGET RNA. GAM335 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM335 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM335 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM335 RNA, herein designated GAM RNA, to target binding sites on GAM335 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM335 target RNA into GAM335 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM335 target genes. The mRNA of each one of this plurality of GAM335 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM335 RNA, herein designated GAM RNA, and which when bound by GAM335 RNA causes inhibition of translation of the GAM335 target mRNA into a corresponding GAM335 target protein.

The mechanism of the translational inhibition exerted by GAM335 RNA, herein designated GAM RNA, on one or more GAM335 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM335 RNA, herein designated GAM RNA, of GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM335 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM335 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM335 RNA

correlate with, and may be deduced from, the identity of the GAM335 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM347 5807 AGTCTCACTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTCTCCTAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGGAGTGC Messenger 347 (GAM347) oligonucleotides modulates expression of respective target
genes
AGTGGCGTGA whose function and utility is known in the art.

TCTCATCTCA GAM347 is a novel bioinformatically detectable regulatory, non protein coding,
TTGCAACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM347 was detected is

CACCTCCTGG described with additional reference to Figs. 9-15.

ATTCAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
TTCT encoded by the human genome.

GAM347 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM347

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM347

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM347 precursor RNA is designated SEQ ID:5807, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5807 is located from position 37269373 to position 37269456 relative to chromosome 19 on the `-` strand.

GAM347 precursor RNA folds onto itself, forming GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM347 precursor RNA, designated SEQ ID NO: 5807, and a schematic representation of a predicted secondary folding of GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM347 folded precursor RNA yielding a GAM347 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM347 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM347 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM347 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM347 target RNA, herein designated GAM TARGET RNA. GAM347 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM347 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM347 RNA, herein designated GAM RNA, to target binding sites on GAM347 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM347 target RNA into GAM347 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM347 target genes. The mRNA of each one of this plurality of GAM347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM347 RNA, herein designated GAM RNA, and which when bound by GAM347 RNA causes inhibition of translation of the GAM347 target mRNA into a corresponding GAM347 target protein.

The mechanism of the translational inhibition exerted by GAM347 RNA, herein designated GAM RNA, on one or more GAM347 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM347 RNA, herein designated GAM RNA, of GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM347 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM347 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM347 RNA correlate with, and may be deduced from, the identity of the GAM347 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM354 6728 GGCAGAGCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCCTCTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGCCGTGT Messenger 354 (GAM354) oligonucleotides modulates expression of respective target genes
GCTTTGCTCG whose function and utility is known in the art.

GTTGATCTTG GAM354 is a novel bioinformatically detectable regulatory, non protein coding,
CAGAGCCTAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM354 was detected is

GACACAGGCC described with additional reference to Figs. 9-15.

CAGAGAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGATCGCC encoded by the human genome.

GAM354 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM354

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM354

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM354 precursor RNA is designated SEQ ID:6728, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6728 is located from position 50818302 to position 50818390 relative to chromosome 19 on the `+` strand.

GAM354 precursor RNA folds onto itself, forming GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM354 precursor RNA, designated SEQ ID NO: 6728, and a schematic representation of a predicted secondary folding of GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM354 folded precursor RNA

yielding a GAM354 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM354 RNA, hereby incorporated herein.

GAM354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM354 target RNA, herein designated GAM TARGET RNA. GAM354 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM354 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM354 RNA, herein designated GAM RNA, to target binding sites on GAM354 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM354 target RNA into GAM354 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM354 target genes. The mRNA of each one of this plurality of GAM354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM354 RNA, herein designated GAM RNA, and which when bound by GAM354 RNA causes inhibition of translation of the GAM354 target mRNA into a corresponding GAM354 target protein.

The mechanism of the translational inhibition exerted by GAM354 RNA, herein designated GAM RNA, on one or more GAM354 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM354 RNA, herein designated GAM RNA, of GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM354 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM354 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM354 RNA correlate with, and may be deduced from, the identity of the GAM354 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM361 7153 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGGGAG Messenger 361 (GAM361) oligonucleotides modulates expression of respective target genes
GCGGAGGTTG whose function and utility is known in the art.

TGTTGAGCCG GAM361 is a novel bioinformatically detectable regulatory, non protein coding,
AGATCTCGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM361 was detected is

ATTGCACTCC described with additional reference to Figs. 9-15.

AGCCTAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGA encoded by the human genome.

AACTCCATCT GAM361 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM361
CA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM361

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM361 precursor RNA is designated SEQ ID:7153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7153 is located from position 94524959 to position 94525060 relative to chromosome X on the `+` strand.

GAM361 precursor RNA folds onto itself, forming GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM361 precursor RNA, designated SEQ ID NO: 7153, and a schematic representation of a predicted secondary folding of GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM361 folded precursor RNA yielding a GAM361 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM361 RNA, hereby incorporated herein.

GAM361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM361 target RNA, herein designated GAM TARGET RNA. GAM361 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM361 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM361 RNA, herein designated GAM RNA, to target binding sites on GAM361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM361 target RNA into GAM361 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM361 target genes. The mRNA of each one of this plurality of GAM361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM361 RNA, herein designated GAM RNA, and which when bound by GAM361 RNA causes inhibition of translation of the GAM361 target mRNA into a corresponding GAM361 target protein.

The mechanism of the translational inhibition exerted by GAM361 RNA, herein designated GAM RNA, on one or more GAM361 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM361 RNA, herein designated GAM RNA, of GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM361 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM361 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM361 RNA correlate with, and may be deduced from, the identity of the GAM361 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM367 7175 TGAGGTAAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGTTATTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAGGTGTGA Messenger 367 (GAM367) oligonucleotides modulates expression of respective target genes
TCTATATAGA whose function and utility is known in the art.

ACCCTGTACA GAM367 is a novel bioinformatically detectable regulatory, non protein coding,
TGAAAAGGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM367 was detected is

GAGATGCCGC described with additional reference to Figs. 9-15.

TATCTTGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGATGATCA encoded by the human genome.

TGTATTTGAA GAM367 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM367
ATAGTAACTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM367
ACAGCA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM367 precursor RNA is designated SEQ ID:7175, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7175 is located from position 121833627 to position 121833742 relative to chromosome 10 on the `+` strand.

GAM367 precursor RNA folds onto itself, forming GAM367 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM367 precursor RNA, designated SEQ ID NO: 7175, and a schematic representation of a predicted secondary folding of GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM367 folded precursor RNA yielding a GAM367 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM367 RNA, hereby incorporated herein.

GAM367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM367 target RNA, herein designated GAM TARGET RNA. GAM367 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM367 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM367 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM367 RNA, herein designated GAM RNA, to target binding sites on GAM367 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM367 target RNA into GAM367 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM367 target genes. The mRNA of each one of this plurality of GAM367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM367 RNA, herein designated GAM RNA, and which when bound by GAM367 RNA causes inhibition of translation of

the GAM367 target mRNA into a corresponding GAM367 target protein.

The mechanism of the translational inhibition exerted by GAM367 RNA, herein designated GAM RNA, on one or more GAM367 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM367 RNA, herein designated GAM RNA, of GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM367 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM367 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM367 RNA correlate with, and may be deduced from, the identity of the GAM367 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM388 5831 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 388 (GAM388) oligonucleotides modulates expression of respective target genes
GTTTGTTACA whose function and utility is known in the art.

TATGTATACA GAM388 is a novel bioinformatically detectable regulatory, non protein coding,
TGTGCCATGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM388 was detected is

TGGTGTGCTG described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM388 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM388

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM388
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM388 precursor RNA is designated SEQ ID:5831, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5831 is located from position 16098435 to position 16098516 relative to chromosome 1 on the `-` strand.

GAM388 precursor RNA folds onto itself, forming GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM388 precursor RNA, designated SEQ ID NO: 5831, and a schematic representation of a predicted secondary folding of GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM388 folded precursor RNA yielding a GAM388 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM388 RNA, hereby incorporated herein.

GAM388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM388 target RNA, herein designated GAM TARGET RNA. GAM388 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM388 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM388 RNA, herein designated GAM RNA, to target binding sites on GAM388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM388 target RNA into GAM388 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM388 target genes. The mRNA of each one of this plurality of GAM388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM388 RNA, herein designated GAM RNA, and which when bound by GAM388 RNA causes inhibition of translation of the GAM388 target mRNA into a corresponding GAM388 target protein.

The mechanism of the translational inhibition exerted by GAM388 RNA, herein designated GAM RNA, on one or more GAM388 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM388 RNA, herein designated GAM RNA, of GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM388 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM388 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM388 RNA correlate with, and may be deduced from, the identity of the GAM388 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM401 5724 AGAGAGAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCACTCTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCCAGGCTG Messenger 401 (GAM401) oligonucleotides modulates expression of respective target genes
GAGTGCAGTG whose function and utility is known in the art.

GTGTGATCTC GAM401 is a novel bioinformatically detectable regulatory, non protein coding,
GGCTCACTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM401 was detected is

AACCTCTGCC described with additional reference to Figs. 9-15.

TTCCGGATTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGTGATTCT encoded by the human genome.

CCT GAM401 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM401 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM401 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM401 precursor RNA is designated SEQ ID:5724, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5724 is located from position 14110787 to position 14110879 relative to chromosome 10 on the `+` strand.

GAM401 precursor RNA folds onto itself, forming GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM401 precursor RNA, designated SEQ ID NO: 5724, and a schematic representation of a predicted secondary folding of GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM401 folded precursor RNA yielding a GAM401 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM401 RNA, hereby incorporated herein.

GAM401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM401 target RNA, herein designated GAM TARGET RNA. GAM401 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM401 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM401 RNA, herein designated GAM RNA, to target binding sites on GAM401 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM401 target RNA into GAM401 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM401 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM401 target genes. The mRNA of each one of this plurality of GAM401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM401 RNA, herein designated GAM RNA, and which when bound by GAM401 RNA causes inhibition of translation of the GAM401 target mRNA into a corresponding GAM401 target protein.

The mechanism of the translational inhibition exerted by GAM401 RNA, herein designated GAM RNA, on one or more GAM401 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM401 RNA, herein designated GAM RNA, of GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM401 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM401 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM401 RNA correlate with, and may be deduced from, the identity of the GAM401 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM408 6597 GGACTGAAAG AGAACTGGGA TGGAGGAGAA TTAGAGGATG GTGTGGTGTT TCCCAAGACA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 408 (GAM408) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM408 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM408 was detected is

TCCCCTGATC described with additional reference to Figs. 9-15.

TTGCTATCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCATCTCCT encoded by the human genome.

AGACC GAM408 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM408 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM408 precursor RNA is designated SEQ ID:6597, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6597 is located from position 62113790 to position 62113884 relative to chromosome 14 on the `-` strand.

GAM408 precursor RNA folds onto itself, forming GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM408 precursor RNA, designated SEQ ID NO: 6597, and a schematic representation of a predicted secondary folding of GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM408 folded precursor RNA yielding a GAM408 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM408 RNA, hereby incorporated herein.

GAM408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM408 target RNA, herein designated GAM TARGET RNA. GAM408 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM408 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM408 RNA, herein designated GAM RNA, to target binding sites on GAM408 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM408 target RNA into GAM408 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM408 target genes. The mRNA of each one of this plurality of GAM408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM408 RNA, herein designated GAM RNA, and which when bound by GAM408 RNA causes inhibition of translation of the GAM408 target mRNA into a corresponding GAM408 target protein.

The mechanism of the translational inhibition exerted by GAM408 RNA, herein designated GAM RNA, on one or more GAM408 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM408 RNA, herein designated GAM RNA, of GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM408 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM408 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM408 RNA correlate with, and may be deduced from, the identity of the GAM408 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM426 6113 CCTCCTGCTG AAGCTTCTGG ATTTGAGAGG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 426 (GAM426) oligonucleotides modulates expression of respective target genes

CTTTACTCTC whose function and utility is known in the art.

CAGGAGAGTG GAM426 is a novel bioinformatically detectable regulatory, non protein coding, AAGCGAGTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM426 was detected is

GGCCAGAGCT described with additional reference to Figs. 9-15.

GAGAGTCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGG encoded by the human genome.

GAM426 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM426

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM426

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM426 precursor RNA is designated SEQ ID:6113, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6113 is located from position 6961619 to position 6961701 relative to chromosome 17 on the `-` strand.

GAM426 precursor RNA folds onto itself, forming GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM426 precursor RNA, designated SEQ ID NO: 6113, and a schematic representation of a predicted secondary folding of GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM426 folded precursor RNA yielding a GAM426 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM426 RNA, hereby incorporated herein.

GAM426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM426 target RNA, herein designated GAM TARGET RNA. GAM426 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM426 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM426 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM426 RNA, herein designated GAM RNA, to target binding sites on GAM426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM426 target RNA into GAM426 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM426 target genes. The mRNA of each one of this plurality of GAM426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM426 RNA, herein designated GAM RNA, and which when bound by GAM426 RNA causes inhibition of translation of the GAM426 target mRNA into a corresponding GAM426 target protein.

The mechanism of the translational inhibition exerted by GAM426 RNA, herein designated GAM RNA, on one or more GAM426 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM426 RNA, herein designated GAM RNA, of GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM426 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM426 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM426 RNA correlate with, and may be deduced from, the identity of the GAM426 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM492 7264 TGTCTATAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATGTGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
CATTTTCTGC Messenger 492 (GAM492) oligonucleotides modulates expression of respective target
genes
CCGTAAAATG whose function and utility is known in the art.

TTCAAATGTT GAM492 is a novel bioinformatically detectable regulatory, non protein coding,
TTCTCTCTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM492 was detected is

AAAGCTTTGT described with additional reference to Figs. 9-15.

TCATTGTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
TGGTGGAATT encoded by the human genome.

TTGGTTCTCA GAM492 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM492
GGGAGTAGAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA
genes GAM492

A precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM492 precursor RNA is designated SEQ ID:7264, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7264 is located from position 43642880 to position 43642990 relative to chromosome 17 on the `-` strand.

GAM492 precursor RNA folds onto itself, forming GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM492 precursor RNA, designated SEQ ID NO: 7264, and a schematic representation of a predicted secondary folding of GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM492 folded precursor RNA yielding a GAM492 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM492 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM492 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM492 target RNA, herein designated GAM TARGET RNA. GAM492 target
RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM492 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM492 RNA, herein designated GAM RNA, to target binding sites on GAM492 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM492 target RNA into GAM492 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM492 target genes. The mRNA of each one of this plurality of GAM492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM492 RNA, herein designated GAM RNA, and which when bound by GAM492 RNA causes inhibition of translation of the GAM492 target mRNA into a corresponding GAM492 target protein.

The mechanism of the translational inhibition exerted by GAM492 RNA, herein designated GAM RNA, on one or more GAM492 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM492 RNA, herein designated GAM RNA, of GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM492 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM492 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7,

incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM492 RNA correlate with, and may be deduced from, the identity of the GAM492 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM495 6079 CCCGACCACT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCAGCCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCAGTCACT Messenger 495 (GAM495) oligonucleotides modulates expression of respective target genes
GGAAAATGCT whose function and utility is known in the art.

TACAGGCAGT GAM495 is a novel bioinformatically detectable regulatory, non protein coding,
AGCCACCATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM495 was detected is

ATGTGGCACA described with additional reference to Figs. 9-15.

AAGTGGGCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CATCCTAGTG encoded by the human genome.

TCTAACATTT GAM495 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM495
AAGCTGTGGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM495
TCTGG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM495 precursor RNA is designated SEQ ID:6079, and is provided hereinbelow with reference to the sequence listing part.

GAM495 precursor RNA folds onto itself, forming GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM495 precursor RNA, designated SEQ ID NO: 6079, and a schematic representation of a predicted secondary folding of GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM495 folded precursor RNA yielding a GAM495 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM495 RNA, hereby incorporated herein. Expression of GAM495 RNA

was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM495 target RNA, herein designated GAM TARGET RNA. GAM495 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM495 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM495 RNA, herein designated GAM RNA, to target binding sites on GAM495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM495 target RNA into GAM495 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM495 target genes. The mRNA of each one of this plurality of GAM495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM495 RNA, herein designated GAM RNA, and which when bound by GAM495 RNA causes inhibition of translation of the GAM495 target mRNA into a corresponding GAM495 target protein.

The mechanism of the translational inhibition exerted by GAM495 RNA, herein designated GAM RNA, on one or more GAM495 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM495 RNA, herein designated GAM RNA, of GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM495 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM495 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM495 RNA correlate with, and may be deduced from, the identity of the GAM495 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM507 6783 GGGAGACCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGACCCGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGAGGTAGA Messenger 507 (GAM507) oligonucleotides modulates expression of respective target genes
GGGGAGCAGA whose function and utility is known in the art.

GACAGCCACC GAM507 is a novel bioinformatically detectable regulatory, non protein coding,
AGCTTCTATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM507 was detected is

TTCTGCTCTA described with additional reference to Figs. 9-15.

AGCACATTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCACGAGTT encoded by the human genome.

TAAGTTTCCT GAM507 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM507
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM507
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM507 precursor RNA is designated SEQ ID:6783, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6783 is located from position 40608766 to position 40608865 relative to chromosome 15 on the `+` strand.

GAM507 precursor RNA folds onto itself, forming GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM507 precursor RNA, designated SEQ ID NO: 6783, and a schematic representation of a predicted secondary folding of GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM507 folded precursor RNA yielding a GAM507 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM507 RNA, hereby incorporated herein.

GAM507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM507 target RNA, herein designated GAM TARGET RNA. GAM507 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM507 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM507 RNA, herein designated GAM RNA, to target binding sites on GAM507 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM507 target RNA into GAM507 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM507 target genes. The mRNA of each one of this plurality of GAM507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM507 RNA, herein designated GAM RNA, and which when bound by GAM507 RNA causes inhibition of translation of the GAM507 target mRNA into a corresponding GAM507 target protein.

The mechanism of the translational inhibition exerted by GAM507 RNA, herein designated GAM RNA, on one or more GAM507 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM507 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM507 RNA, herein designated GAM RNA, of GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM507 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM507 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM507 RNA correlate with, and may be deduced from, the identity of the GAM507 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM519 5696 ACCTATTCCC TGTGGCTTAG GTGAGCATGT GACCAGGCCT GGCCTCCTGA GTCCCACAGC TTCCTAGCCA CAGTGATAAA AGAATGGGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 519 (GAM519) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM519 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM519 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM519 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM519 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM519 precursor RNA is designated SEQ ID:5696, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5696 is located from position 32800605 to position 32800693 relative to chromosome 18 on the `-` strand.

GAM519 precursor RNA folds onto itself, forming GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM519 precursor RNA, designated SEQ ID NO: 5696, and a schematic representation of a predicted secondary folding of GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM519 folded precursor RNA yielding a GAM519 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM519 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM519 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM519 target RNA, herein designated GAM TARGET RNA. GAM519 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM519 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM519 RNA, herein designated GAM RNA, to target binding sites on GAM519 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM519 target RNA into GAM519 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM519 target genes. The mRNA of each one of this plurality of GAM519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM519 RNA, herein designated GAM RNA, and which when bound by GAM519 RNA causes inhibition of translation of the GAM519 target mRNA into a corresponding GAM519 target protein.

The mechanism of the translational inhibition exerted by GAM519 RNA, herein

designated GAM RNA, on one or more GAM519 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM519 RNA, herein designated GAM RNA, of GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM519 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM519 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM519 RNA correlate with, and may be deduced from, the identity of the GAM519 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM520 6864 GTAGGAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCAGGGATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGGTTTGA Messenger 520 (GAM520) oligonucleotides modulates expression of respective target genes
GAGACAATGA whose function and utility is known in the art.

CACACACCCC GAM520 is a novel bioinformatically detectable regulatory, non protein coding,
TAAGTTCACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM520 was detected is

TTCTCTCGAA described with additional reference to Figs. 9-15.

TAGTAGGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCTCTTAC encoded by the human genome.

GAM520 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM520

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM520

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM520 precursor RNA is designated SEQ ID:6864, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6864 is located from position 43020516 to position 43020604 relative to chromosome 17

on the `+` strand.

GAM520 precursor RNA folds onto itself, forming GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM520 precursor RNA, designated SEQ ID NO: 6864, and a schematic representation of a predicted secondary folding of GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM520 folded precursor RNA yielding a GAM520 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM520 RNA, hereby incorporated herein.

GAM520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM520 target RNA, herein designated GAM TARGET RNA. GAM520 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM520 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM520 RNA, herein designated GAM RNA, to target binding sites on GAM520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM520 target RNA into GAM520 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM520 target genes. The mRNA of each one of this plurality

of GAM520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM520 RNA, herein designated GAM RNA, and which when bound by GAM520 RNA causes inhibition of translation of the GAM520 target mRNA into a corresponding GAM520 target protein.

The mechanism of the translational inhibition exerted by GAM520 RNA, herein designated GAM RNA, on one or more GAM520 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM520 RNA, herein designated GAM RNA, of GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM520 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM520 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM520 RNA correlate with, and may be deduced from, the identity of the GAM520 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM550 6952 TAAATCTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGAGGGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCATGTCCAC Messenger 550 (GAM550) oligonucleotides modulates expression of respective target genes

ACCAGGTGCC whose function and utility is known in the art.

CAGACATCTG GAM550 is a novel bioinformatically detectable regulatory, non protein coding,

GTTGGCTTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM550 was detected is

GCTGATTTGT described with additional reference to Figs. 9-15.

CCTGCAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGCCTTGT encoded by the human genome.

CTGGATTTGC GAM550 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM550

ACACTTTCCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM550

AGTTGCCCAT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar TA to the nucleotide sequence of GAM550 precursor RNA is designated SEQ ID:6952, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6952 is located from position 28205837 to position 28205958 relative to chromosome 15 on the `-` strand.

GAM550 precursor RNA folds onto itself, forming GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM550 precursor RNA, designated SEQ ID NO: 6952, and a schematic representation of a predicted secondary folding of GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM550 folded precursor RNA yielding a GAM550 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM550 RNA, hereby incorporated herein.

GAM550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM550 target RNA, herein designated GAM TARGET RNA. GAM550 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM550 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM550 RNA, herein designated GAM RNA, to target binding sites on GAM550 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM550 target RNA into GAM550 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM550 target genes. The mRNA of each one of this plurality of GAM550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM550 RNA, herein designated GAM RNA, and which when bound by GAM550 RNA causes inhibition of translation of the GAM550 target mRNA into a corresponding GAM550 target protein.

The mechanism of the translational inhibition exerted by GAM550 RNA, herein designated GAM RNA, on one or more GAM550 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM550 RNA, herein designated GAM RNA, of GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM550 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM550 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM550 RNA correlate with, and may be deduced from, the identity of the GAM550 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM569 6459 GAGTAAGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGAGCGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTCTCTGCA Messenger 569 (GAM569) oligonucleotides modulates expression of respective target genes

GGCCGTGTGC whose function and utility is known in the art.

TTTGCTCGGT GAM569 is a novel bioinformatically detectable regulatory, non protein coding,

TGATCTTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM569 was detected is

GAGCCTAAGA described with additional reference to Figs. 9-15.

CACAGGCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGAGGCAGT encoded by the human genome.

GATCGCCAAA GAM569 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM569

GATC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM569

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM569 precursor RNA is designated SEQ ID:6459, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6459 is located from position 50818294 to position 50818397 relative to chromosome 19 on the `+` strand.

GAM569 precursor RNA folds onto itself, forming GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM569 precursor RNA, designated SEQ ID NO: 6459, and a schematic representation of a predicted secondary folding of GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM569 folded precursor RNA yielding a GAM569 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM569 RNA, hereby incorporated herein.

GAM569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM569 target RNA, herein designated GAM TARGET RNA. GAM569 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM569 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM569 RNA, herein designated GAM RNA, to target binding sites on GAM569 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM569 target RNA into GAM569 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM569 target genes. The mRNA of each one of this plurality of GAM569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM569 RNA, herein designated GAM RNA, and which when bound by GAM569 RNA causes inhibition of translation of the GAM569 target mRNA into a corresponding GAM569 target protein.

The mechanism of the translational inhibition exerted by GAM569 RNA, herein designated GAM RNA, on one or more GAM569 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM569 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM569 RNA, herein designated GAM RNA, of GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM569 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM569 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM569 RNA correlate with, and may be deduced from, the identity of the GAM569 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM572 5713 AGAACAAGGG CTAAATTCAA ATCAAATTTT CCCTGTACCC Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 572 (GAM572) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

TAAGAAAAAT GAM572 is a novel bioinformatically detectable regulatory, non protein coding, AATTAGGCCG micro RNA (miRNA)-like oligonucleotide. The method by which GAM572 was detected is

GGAGATGTTT described with additional reference to Figs. 9-15.

GACTAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTAGGCATTG encoded by the human genome.

TTCT GAM572 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM572

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM572

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM572 precursor RNA is designated SEQ ID:5713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5713 is located from position 14718325 to position 14718418 relative to chromosome 10 on the `-` strand.

GAM572 precursor RNA folds onto itself, forming GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM572 precursor RNA, designated SEQ ID NO: 5713, and a schematic representation of a predicted secondary folding of GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM572 folded precursor RNA yielding a GAM572 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM572 RNA, hereby incorporated herein.

GAM572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM572 target RNA, herein designated GAM TARGET RNA. GAM572 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM572 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM572 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM572 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM572 RNA, herein designated GAM RNA, to target binding sites on GAM572 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM572 target RNA into GAM572 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM572 target genes. The mRNA of each one of this plurality of GAM572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM572 RNA, herein designated GAM RNA, and which when bound by GAM572 RNA causes inhibition of translation of the GAM572 target mRNA into a corresponding GAM572 target protein.

The mechanism of the translational inhibition exerted by GAM572 RNA, herein designated GAM RNA, on one or more GAM572 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM572 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM572 RNA, herein designated GAM RNA, of GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM572 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM572 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM572 RNA correlate with, and may be deduced from, the identity of the GAM572 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM584 6201 CTGAGGCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCACTGGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTTTGTGAG Messenger 584 (GAM584) oligonucleotides modulates expression of respective target genes
GCACGCTTGA whose function and utility is known in the art.

CCTGGGTTTC GAM584 is a novel bioinformatically detectable regulatory, non protein coding,
ATGGAAAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM584 was detected is

TGTGCCCTCA described with additional reference to Figs. 9-15.

CCAAAGGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAAACAAGG encoded by the human genome.

CCCCAG GAM584 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM584
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM584
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM584 precursor RNA is designated SEQ ID:6201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6201 is located from position 67800165 to position 67800260 relative to chromosome 11 on the `+` strand.

GAM584 precursor RNA folds onto itself, forming GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM584 precursor RNA, designated SEQ ID NO: 6201, and a schematic representation of a predicted secondary folding of GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM584 folded precursor RNA yielding a GAM584 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM584 RNA, hereby incorporated herein.

GAM584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM584 target RNA, herein designated GAM TARGET RNA. GAM584 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM584 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM584 RNA, herein designated GAM RNA, to target binding sites on GAM584 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM584 target RNA into GAM584 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM584 target genes. The mRNA of each one of this plurality of GAM584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM584 RNA, herein designated GAM RNA, and which when bound by GAM584 RNA causes inhibition of translation of the GAM584 target mRNA into a corresponding GAM584 target protein.

The mechanism of the translational inhibition exerted by GAM584 RNA, herein designated GAM RNA, on one or more GAM584 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM584 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM584 RNA, herein designated GAM RNA, of GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM584 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM584 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM584 RNA correlate with, and may be deduced from, the identity of the GAM584 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM588 5983 CAAAGAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TAGAATCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTGGTCCTT Messenger 588 (GAM588) oligonucleotides modulates expression of respective target genes
CAAGGCAGCT whose function and utility is known in the art.

CATTGCAGCT GAM588 is a novel bioinformatically detectable regulatory, non protein coding,
ACTGGCCTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM588 was detected is

AGTGAAACAG described with additional reference to Figs. 9-15.

GTCTCTTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM588 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM588

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM588
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM588 precursor RNA is designated SEQ ID:5983, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5983 is located from position 45420375 to position 45420453 relative to chromosome 11 on the `-` strand.

GAM588 precursor RNA folds onto itself, forming GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM588 precursor RNA, designated SEQ ID NO: 5983, and a schematic representation of a predicted secondary folding of GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM588 folded precursor RNA yielding a GAM588 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM588 RNA, hereby incorporated herein.

GAM588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM588 target RNA, herein designated GAM TARGET RNA. GAM588 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM588 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM588 RNA, herein designated GAM RNA, to target binding sites on GAM588 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM588 target RNA into GAM588 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM588 target genes. The mRNA of each one of this plurality of GAM588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM588 RNA, herein designated GAM RNA, and which when bound by GAM588 RNA causes inhibition of translation of the GAM588 target mRNA into a corresponding GAM588 target protein.

The mechanism of the translational inhibition exerted by GAM588 RNA, herein designated GAM RNA, on one or more GAM588 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM588 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM588 RNA, herein designated GAM RNA, of GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM588 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM588 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM588 RNA correlate with, and may be deduced from, the identity of the GAM588 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM593 5778 AGGCTCACAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCAAGTCTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTCAAAGCT Messenger 593 (GAM593) oligonucleotides modulates expression of respective target genes
TAGGAATGGA whose function and utility is known in the art.

AGTAGGTTGT GAM593 is a novel bioinformatically detectable regulatory, non protein coding,
CCCCTCCTAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM593 was detected is

TCATGGGATC described with additional reference to Figs. 9-15.

TCTCCAACTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACTAGACAAT encoded by the human genome.

CTTGCTTTAC GAM593 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM593
GTGCTGATGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM593
ACATGCTCTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
TGAGCAGCCT to the nucleotide sequence of GAM593 precursor RNA is designated SEQ ID:5778, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5778 is located from position 43562097 to position 43562226 relative to chromosome 15 on the `+` strand.

GAM593 precursor RNA folds onto itself, forming GAM593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM593 precursor RNA, designated SEQ ID NO: 5778, and a schematic representation of a predicted secondary folding of GAM593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM593 folded precursor RNA yielding a GAM593 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM593 RNA, hereby incorporated herein.

GAM593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM593 target RNA, herein designated GAM TARGET RNA. GAM593 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM593 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM593 RNA, herein designated GAM RNA, to target binding sites on GAM593 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM593 target RNA into GAM593 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM593 target genes. The mRNA of each one of this plurality of GAM593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM593 RNA, herein designated GAM RNA, and which when bound by GAM593 RNA causes inhibition of translation of the GAM593 target mRNA into a corresponding GAM593 target protein.

The mechanism of the translational inhibition exerted by GAM593 RNA, herein designated GAM RNA, on one or more GAM593 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM593 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM593 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM593 RNA, herein designated GAM RNA, of GAM593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM593 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM593 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM593 RNA correlate with, and may be deduced from, the identity of the GAM593 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM604 6153 CTAGCTGCTG CCAGCCAAGC TGCTACCAGA CCAGCTCCTG CGGAACTGGC TGTGGCATTG GTGGTGGCAT TGG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 604 (GAM604) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM604 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM604 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM604 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM604 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM604 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM604 precursor RNA is designated SEQ ID:6153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6153 is located from position 39106109 to position 39106181 relative to chromosome 17 on the `-` strand.

GAM604 precursor RNA folds onto itself, forming GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM604 precursor RNA, designated SEQ ID NO: 6153, and a schematic representation of a predicted secondary folding of GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM604 folded precursor RNA yielding a GAM604 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM604 RNA, hereby incorporated herein.

GAM604 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM604 target RNA, herein designated GAM TARGET RNA. GAM604 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM604 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM604 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM604 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM604 RNA, herein designated GAM RNA, to target binding sites on GAM604 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM604 target RNA into GAM604 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM604 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM604 target genes. The mRNA of each one of this plurality of GAM604 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM604 RNA, herein designated GAM RNA, and which when bound by GAM604 RNA causes inhibition of translation of the GAM604 target mRNA into a corresponding GAM604 target protein.

The mechanism of the translational inhibition exerted by GAM604 RNA, herein designated GAM RNA, on one or more GAM604 target genes, herein collectively designated GAM

TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM604 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM604 RNA, herein designated GAM RNA, of GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM604 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM604 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM604 RNA correlate with, and may be deduced from, the identity of the GAM604 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM640 6536 GCTCGTTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGCTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCAATGGCG Messenger 640 (GAM640) oligonucleotides modulates expression of respective target genes
TGATCTTGGC whose function and utility is known in the art.

TCACCACAAC GAM640 is a novel bioinformatically detectable regulatory, non protein coding,
CTCCACTTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM640 was detected is

CAGGTTCAAG described with additional reference to Figs. 9-15.

CGATTCTCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCTTAGCCT encoded by the human genome.

CCCAAGTAGC GAM640 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM640
TGGGATTACA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM640
GGC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM640 precursor RNA is designated SEQ ID:6536, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6536 is located from position 74052253 to position 74052365 relative to chromosome 2 on the `-` strand.

GAM640 precursor RNA folds onto itself, forming GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM640 precursor RNA, designated SEQ ID NO: 6536, and a schematic representation of a predicted secondary folding of GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM640 folded precursor RNA yielding a GAM640 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM640 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM640 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM640 target RNA, herein designated GAM TARGET RNA. GAM640 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM640 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM640 RNA, herein designated GAM RNA, to target binding sites on GAM640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM640 target RNA into GAM640 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM640 target genes. The mRNA of each one of this plurality

of GAM640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM640 RNA, herein designated GAM RNA, and which when bound by GAM640 RNA causes inhibition of translation of the GAM640 target mRNA into a corresponding GAM640 target protein.

The mechanism of the translational inhibition exerted by GAM640 RNA, herein designated GAM RNA, on one or more GAM640 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM640 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM640 RNA, herein designated GAM RNA, of GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM640 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM640 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM640 RNA correlate with, and may be deduced from, the identity of the GAM640 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM667 6906 GTGCCTCATC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTAGGTGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAGAGAATG Messenger 667 (GAM667) oligonucleotides modulates expression of respective target genes
AAAGGAGGTA whose function and utility is known in the art.

GCATGAGCAG GAM667 is a novel bioinformatically detectable regulatory, non protein coding,
GGCACTCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM667 was detected is

TCGGAGGCAG described with additional reference to Figs. 9-15.

TGCCTAGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACATTGCTTA encoded by the human genome.

TCTTCACTGT GAM667 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM667

GAATTTGGCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM667
TTTTTCCTAC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar TCTTGAATCT to the nucleotide sequence of GAM667 precursor RNA is designated SEQ ID:6906, and is

T provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6906 is located from position 44371974 to position 44372104 relative to chromosome 7 on the `+` strand.

GAM667 precursor RNA folds onto itself, forming GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM667 precursor RNA, designated SEQ ID NO: 6906, and a schematic representation of a predicted secondary folding of GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM667 folded precursor RNA yielding a GAM667 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM667 RNA, hereby incorporated herein.

GAM667 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM667 target RNA, herein designated GAM TARGET RNA. GAM667 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM667 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM667 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM667 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM667 RNA, herein designated GAM RNA, to target binding sites on GAM667 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM667 target RNA into GAM667 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM667 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM667 target genes. The mRNA of each one of this plurality of GAM667 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM667 RNA, herein designated GAM RNA, and which when bound by GAM667 RNA causes inhibition of translation of the GAM667 target mRNA into a corresponding GAM667 target protein.

The mechanism of the translational inhibition exerted by GAM667 RNA, herein designated GAM RNA, on one or more GAM667 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM667 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM667 RNA, herein designated GAM RNA, of GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM667 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM667 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM667 RNA correlate with, and may be deduced from, the identity of the GAM667 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM674 5993 CACAGCCAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCTTTGATG detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTCAAAACG Messenger 674 (GAM674) oligonucleotides modulates expression of respective target genes

TACTTTGTGA whose function and utility is known in the art.

TCTTGCCAAG GAM674 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTGAGATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM674 was detected is

ATCGTTACAA described with additional reference to Figs. 9-15.

GCAGCATTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTTGTG encoded by the human genome.

GAM674 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM674 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM674 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM674 precursor RNA is designated SEQ ID:5993, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5993 is located from position 43395844 to position 43395930 relative to chromosome 17 on the `+` strand.

GAM674 precursor RNA folds onto itself, forming GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM674 precursor RNA, designated SEQ ID NO: 5993, and a schematic representation of a predicted secondary folding of GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM674 folded precursor RNA yielding a GAM674 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM674 RNA, hereby incorporated herein.

GAM674 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM674 target RNA, herein designated GAM TARGET RNA. GAM674 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM674 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM674 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM674 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM674 RNA, herein designated GAM RNA, to target binding sites on GAM674 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM674 target RNA into GAM674 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM674 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM674 target genes. The mRNA of each one of this plurality of GAM674 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM674 RNA, herein designated GAM RNA, and which when bound by GAM674 RNA causes inhibition of translation of the GAM674 target mRNA into a corresponding GAM674 target protein.

The mechanism of the translational inhibition exerted by GAM674 RNA, herein designated GAM RNA, on one or more GAM674 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM674 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM674 RNA, herein designated GAM RNA, of GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM674 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM674 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM674 RNA correlate with, and may be deduced from, the identity of the GAM674 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM689 6376 GAGGCAGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAAGGCA Messenger 689 (GAM689) oligonucleotides modulates expression of respective target genes
GAGGTTGCAG whose function and utility is known in the art.

TCAGCAGATA GAM689 is a novel bioinformatically detectable regulatory, non protein coding, TTGCACCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM689 was detected is

GCACTCCAGC described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGCAAGACT encoded by the human genome.

CTGCCTC GAM689 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM689

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM689

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM689 precursor RNA is designated SEQ ID:6376, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6376 is located from position 69076605 to position 69076701 relative to chromosome 5 on the `-` strand.

GAM689 precursor RNA folds onto itself, forming GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM689 precursor RNA, designated SEQ ID NO: 6376, and a schematic representation of a predicted secondary folding of GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM689 folded precursor RNA yielding a GAM689 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM689 RNA, hereby incorporated herein. Expression of GAM689 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM689 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM689 target RNA, herein designated GAM TARGET RNA. GAM689 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM689 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM689 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM689 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM689 RNA, herein designated GAM RNA, to target binding sites on GAM689 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM689 target RNA into GAM689 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM689 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM689 target genes. The mRNA of each one of this plurality of GAM689 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM689 RNA, herein designated GAM RNA, and which when bound by GAM689 RNA causes inhibition of translation of the GAM689 target mRNA into a corresponding GAM689 target protein.

The mechanism of the translational inhibition exerted by GAM689 RNA, herein designated GAM RNA, on one or more GAM689 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM689 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM689 RNA, herein designated GAM RNA, of GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM689 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM689 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM689 RNA correlate with, and may be deduced from, the identity of the GAM689 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM744 5804 AGTCACTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAATGCTTAC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGTAGC Messenger 744 (GAM744) oligonucleotides modulates expression of respective target genes
CACCATCATG whose function and utility is known in the art.

TGGCACAAAG GAM744 is a novel bioinformatically detectable regulatory, non protein coding,
TGGGCATCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM744 was detected is

CCTAGTGTCT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM744 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM744

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM744
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM744 precursor RNA is designated SEQ ID:5804, and is provided hereinbelow with reference to the sequence listing part.

GAM744 precursor RNA folds onto itself, forming GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM744 precursor RNA, designated SEQ ID NO: 5804, and a schematic representation of a predicted secondary folding of GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM744 folded precursor RNA yielding a GAM744 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM744 RNA, hereby incorporated herein. Expression of GAM744 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM744 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM744 target RNA, herein designated GAM TARGET RNA. GAM744 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM744 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM744 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM744 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM744 RNA, herein designated GAM RNA, to target binding sites on GAM744 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM744 target RNA into GAM744 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM744 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM744 target genes. The mRNA of each one of this plurality of GAM744 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM744 RNA, herein designated GAM RNA, and which when bound by GAM744 RNA causes inhibition of translation of the GAM744 target mRNA into a corresponding GAM744 target protein.

The mechanism of the translational inhibition exerted by GAM744 RNA, herein designated GAM RNA, on one or more GAM744 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM744 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM744 RNA, herein designated GAM RNA, of GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM744 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM744 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7,

incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM744 RNA correlate with, and may be deduced from, the identity of the GAM744 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM750 5683 ACACCTCCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTCCCTGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTGAACCCT Messenger 750 (GAM750) oligonucleotides modulates expression of respective target genes
GTGTTAACAA whose function and utility is known in the art.

TGAGAAGCTT GAM750 is a novel bioinformatically detectable regulatory, non protein coding,
GTTTATTTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM750 was detected is

AGGCTGGGTT described with additional reference to Figs. 9-15.

CTCATTGGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CACAGGGGTA encoded by the human genome.

GGTTGTAATT GAM750 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM750
GTGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM750

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM750 precursor RNA is designated SEQ ID:5683, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5683 is located from position 46615364 to position 46615467 relative to chromosome 20 on the `-` strand.

GAM750 precursor RNA folds onto itself, forming GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM750 precursor RNA, designated SEQ ID NO: 5683, and a schematic representation of a predicted secondary folding of GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM750 folded precursor RNA yielding a GAM750 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a

nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM750 RNA, hereby incorporated herein.

GAM750 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM750 target RNA, herein designated GAM TARGET RNA. GAM750 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM750 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM750 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM750 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM750 RNA, herein designated GAM RNA, to target binding sites on GAM750 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM750 target RNA into GAM750 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM750 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM750 target genes. The mRNA of each one of this plurality of GAM750 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM750 RNA, herein designated GAM RNA, and which when bound by GAM750 RNA causes inhibition of translation of the GAM750 target mRNA into a corresponding GAM750 target protein.

The mechanism of the translational inhibition exerted by GAM750 RNA, herein designated GAM RNA, on one or more GAM750 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM750 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM750 RNA, herein designated GAM RNA, of GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM750 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM750 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM750 RNA correlate with, and may be deduced from, the identity of the GAM750 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM760 7046 TCGCAGTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACGTTTGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAGCAGTGG Messenger 760 (GAM760) oligonucleotides modulates expression of respective target genes

AAGAGGCAAC whose function and utility is known in the art.

TGGTGCTTTT GAM760 is a novel bioinformatically detectable regulatory, non protein coding,

CAGCTAGGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM760 was detected is

TTGAAAAATT described with additional reference to Figs. 9-15.

GCTTCAGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGATTTCGA encoded by the human genome.

GAM760 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM760

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM760

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM760 precursor RNA is designated SEQ ID:7046, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7046 is located from position 15036029 to position 15036118 relative to chromosome 10 on the `+` strand.

GAM760 precursor RNA folds onto itself, forming GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM760 precursor RNA, designated SEQ ID NO: 7046, and a schematic representation of a predicted secondary folding of GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM760 folded precursor RNA yielding a GAM760 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM760 RNA, hereby incorporated herein.

GAM760 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM760 target RNA, herein designated GAM TARGET RNA. GAM760 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM760 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM760 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM760 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM760 RNA, herein designated GAM RNA, to target binding sites on GAM760 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM760 target RNA into GAM760 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM760 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM760 target genes. The mRNA of each one of this plurality of GAM760 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM760 RNA, herein designated GAM RNA, and which when bound by GAM760 RNA causes inhibition of translation of the GAM760 target mRNA into a corresponding GAM760 target protein.

The mechanism of the translational inhibition exerted by GAM760 RNA, herein designated GAM RNA, on one or more GAM760 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM760 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM760 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM760 RNA, herein designated GAM RNA, of GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM760 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM760 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM760 RNA correlate with, and may be deduced from, the identity of the GAM760 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM772 7223 TGGCACCAGC TTCCAAAGCC AGGATGAAGA GGAGGAGAAA GGATGGGGTC CACACCTTGT TTTCTCCACC ATCATCCAGG GGCTCTGCTG CTGCTA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 772 (GAM772) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM772 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM772 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM772 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM772 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM772 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM772 precursor RNA is designated SEQ ID:7223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7223 is located from position 26891775 to position 26891870 relative to chromosome 17 on the `+` strand.

GAM772 precursor RNA folds onto itself, forming GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM772 precursor RNA, designated SEQ ID NO: 7223, and a schematic representation of a predicted secondary folding of GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM772 folded precursor RNA yielding a GAM772 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM772 RNA, hereby incorporated herein.

GAM772 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM772 target RNA, herein designated GAM TARGET RNA. GAM772 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM772 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM772 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM772 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM772 RNA, herein designated GAM RNA, to target binding sites on GAM772 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM772 target RNA into GAM772 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM772 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM772 target genes. The mRNA of each one of this plurality of GAM772 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM772 RNA, herein designated GAM RNA, and which when bound by GAM772 RNA causes inhibition of translation of the GAM772 target mRNA into a corresponding GAM772 target protein.

The mechanism of the translational inhibition exerted by GAM772 RNA, herein designated GAM RNA, on one or more GAM772 target genes, herein collectively designated GAM

TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM772 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM772 RNA, herein designated GAM RNA, of GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM772 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM772 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM772 RNA correlate with, and may be deduced from, the identity of the GAM772 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM779 6097 CCGATGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGGCCGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCTTCATAC Messenger 779 (GAM779) oligonucleotides modulates expression of respective target genes

CCTTTCATTA whose function and utility is known in the art.

GTAGCTCTAA GAM779 is a novel bioinformatically detectable regulatory, non protein coding,

GATGTTTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM779 was detected is

TAAGGTGTAC described with additional reference to Figs. 9-15.

GTTTACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGTTGGTTG encoded by the human genome.

GTGATGAGCA GAM779 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM779

TTGAACATTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM779

GGGTTCTTCG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

G to the nucleotide sequence of GAM779 precursor RNA is designated SEQ ID:6097, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6097 is located from position 131264455 to position 131264575 relative to chromosome 10 on the `+` strand.

GAM779 precursor RNA folds onto itself, forming GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM779 precursor RNA, designated SEQ ID NO: 6097, and a schematic representation of a predicted secondary folding of GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM779 folded precursor RNA yielding a GAM779 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM779 RNA, hereby incorporated herein.

GAM779 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM779 target RNA, herein designated GAM TARGET RNA. GAM779 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM779 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM779 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM779 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM779 RNA, herein designated GAM RNA, to target binding sites on GAM779 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM779 target RNA into GAM779 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM779 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM779 target genes. The mRNA of each one of this plurality of GAM779 target genes comprises one or more target binding sites, each having a

nucleotide sequence which is at least partly complementary to GAM779 RNA, herein designated GAM RNA, and which when bound by GAM779 RNA causes inhibition of translation of the GAM779 target mRNA into a corresponding GAM779 target protein.

The mechanism of the translational inhibition exerted by GAM779 RNA, herein designated GAM RNA, on one or more GAM779 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM779 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM779 RNA, herein designated GAM RNA, of GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM779 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM779 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM779 RNA correlate with, and may be deduced from, the identity of the GAM779 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM785 6082 CCCGGAGTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGGTCTGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGAAGATCC Messenger 785 (GAM785) oligonucleotides modulates expression of respective target genes
CTGCTCTGAG whose function and utility is known in the art.

TCACTGCCAA GAM785 is a novel bioinformatically detectable regulatory, non protein coding,
GCTCTAGCTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM785 was detected is

TGTGACTTTG described with additional reference to Figs. 9-15.

AACAGGGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCTGTCCCT encoded by the human genome.

ATCTATAAAA GAM785 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM785
TAAACGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM785

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM785 precursor RNA is designated SEQ ID:6082, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6082 is located from position 30319064 to position 30319171 relative to chromosome 17 on the `+` strand.

GAM785 precursor RNA folds onto itself, forming GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM785 precursor RNA, designated SEQ ID NO: 6082, and a schematic representation of a predicted secondary folding of GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM785 folded precursor RNA yielding a GAM785 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM785 RNA, hereby incorporated herein.

GAM785 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM785 target RNA, herein designated GAM TARGET RNA. GAM785 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM785 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM785 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM785 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM785 RNA, herein designated GAM RNA, to target binding sites on GAM785 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM785 target RNA into GAM785 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by

a broken line.

It is appreciated that GAM785 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM785 target genes. The mRNA of each one of this plurality of GAM785 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM785 RNA, herein designated GAM RNA, and which when bound by GAM785 RNA causes inhibition of translation of the GAM785 target mRNA into a corresponding GAM785 target protein.

The mechanism of the translational inhibition exerted by GAM785 RNA, herein designated GAM RNA, on one or more GAM785 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM785 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM785 RNA, herein designated GAM RNA, of GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM785 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM785 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM785 RNA correlate with, and may be deduced from, the identity of the GAM785 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM801 6307 GAATTCCTAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATGTGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTATTGTGC Messenger 801 (GAM801) oligonucleotides modulates expression of respective target genes

TTGTACTGAC whose function and utility is known in the art.

CATGTATATA GAM801 is a novel bioinformatically detectable regulatory, non protein coding,

TGCTATGGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM801 was detected is

ATTTAGTGCT described with additional reference to Figs. 9-15.

AGCTAAGAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATACCATTTC encoded by the human genome.

CCCAGTAGCA GAM801 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM801

GTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM801

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM801 precursor RNA is designated SEQ ID:6307, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6307 is located from position 53583235 to position 53583337 relative to chromosome 12 on the `+` strand.

GAM801 precursor RNA folds onto itself, forming GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM801 precursor RNA, designated SEQ ID NO: 6307, and a schematic representation of a predicted secondary folding of GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM801 folded precursor RNA yielding a GAM801 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM801 RNA, hereby incorporated herein.

GAM801 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM801 target RNA, herein designated GAM TARGET RNA. GAM801 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM801 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM801 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM801 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM801 RNA, herein designated GAM RNA, to target binding sites on GAM801 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM801 target RNA into GAM801 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM801 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM801 target genes. The mRNA of each one of this plurality of GAM801 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM801 RNA, herein designated GAM RNA, and which when bound by GAM801 RNA causes inhibition of translation of the GAM801 target mRNA into a corresponding GAM801 target protein.

The mechanism of the translational inhibition exerted by GAM801 RNA, herein designated GAM RNA, on one or more GAM801 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM801 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM801 RNA, herein designated GAM RNA, of GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM801 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM801 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM801 RNA correlate with, and may be deduced from, the identity of the GAM801 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM807 7089 TGACAATCTT GGTTACCATC CATTAAGTGC TGCTGATTTT GGAAAGATCA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 807 (GAM807) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM807 is a novel bioinformatically detectable regulatory, non protein coding,

TGAAAAACGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM807 was detected is

CTTTCCAAAC described with additional reference to Figs. 9-15.

ATGAAGGCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCGTTTGGG encoded by the human genome.

CACAAGAGGC GAM807 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM807

A precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM807

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM807 precursor RNA is designated SEQ ID:7089, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7089 is located from position 53974897 to position 53974997 relative to chromosome 15 on the `-` strand.

GAM807 precursor RNA folds onto itself, forming GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM807 precursor RNA, designated SEQ ID NO: 7089, and a schematic representation of a predicted secondary folding of GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM807 folded precursor RNA yielding a GAM807 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM807 RNA, hereby incorporated herein.

GAM807 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM807 target RNA, herein designated GAM TARGET RNA. GAM807 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM807 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM807 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM807 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM807 RNA, herein designated GAM RNA, to target binding sites on GAM807 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM807 target RNA into GAM807 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM807 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM807 target genes. The mRNA of each one of this plurality of GAM807 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM807 RNA, herein designated GAM RNA, and which when bound by GAM807 RNA causes inhibition of translation of the GAM807 target mRNA into a corresponding GAM807 target protein.

The mechanism of the translational inhibition exerted by GAM807 RNA, herein designated GAM RNA, on one or more GAM807 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM807 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM807 RNA, herein designated GAM RNA, of GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM807 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM807 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM807 RNA correlate with, and may be deduced from, the identity of the GAM807 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM821 6140 CGCTGCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGCAGGCCG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGCTTTGC Messenger 821 (GAM821) oligonucleotides modulates expression of respective target genes
TCGGTTGATC whose function and utility is known in the art.

TTGCAGAGCC GAM821 is a novel bioinformatically detectable regulatory, non protein coding,
TAAGACACAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM821 was detected is

GCCCAGAGAG described with additional reference to Figs. 9-15.

GCAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM821 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM821

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM821
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM821 precursor RNA is designated SEQ ID:6140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6140 is located from position 50818309 to position 50818384 relative to chromosome 19 on the `+` strand.

GAM821 precursor RNA folds onto itself, forming GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM821 precursor RNA, designated SEQ ID NO: 6140, and a schematic representation of a predicted secondary folding of GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM821 folded precursor RNA yielding a GAM821 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM821 RNA, hereby incorporated herein.

GAM821 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM821 target RNA, herein designated GAM TARGET RNA. GAM821 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM821 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM821 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM821 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM821 RNA, herein designated GAM RNA, to target binding sites on GAM821 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM821 target RNA into GAM821 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM821 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM821 target genes. The mRNA of each one of this plurality of GAM821 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM821 RNA, herein designated GAM RNA, and which when bound by GAM821 RNA causes inhibition of translation of the GAM821 target mRNA into a corresponding GAM821 target protein.

The mechanism of the translational inhibition exerted by GAM821 RNA, herein designated GAM RNA, on one or more GAM821 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM821 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM821 RNA, herein designated GAM RNA, of GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM821 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM821 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM821 RNA

correlate with, and may be deduced from, the identity of the GAM821 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM828 5710 ACTGGAGACA Fig. 8 further provides a conceptual description of another novel bioinformatically
CATCTAATGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGTGCTGAT Messenger 828 (GAM828) oligonucleotides modulates expression of respective target genes
GTCAAGGGAC whose function and utility is known in the art.

TTTCTAATCA GAM828 is a novel bioinformatically detectable regulatory, non protein coding,
TGTTCATCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM828 was detected is

TTGATAGCAG described with additional reference to Figs. 9-15.

ATGCTGTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGT encoded by the human genome.

GAM828 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM828

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM828

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM828 precursor RNA is designated SEQ ID:5710, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5710 is located from position 14758025 to position 14758108 relative to chromosome Y on the `-` strand.

GAM828 precursor RNA folds onto itself, forming GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM828 precursor RNA, designated SEQ ID NO: 5710, and a schematic representation of a predicted secondary folding of GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM828 folded precursor RNA yielding a GAM828 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM828 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM828 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM828 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM828 target RNA, herein designated GAM TARGET RNA. GAM828 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM828 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM828 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM828 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM828 RNA, herein designated GAM RNA, to target binding sites on GAM828 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM828 target RNA into GAM828 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM828 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM828 target genes. The mRNA of each one of this plurality of GAM828 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM828 RNA, herein designated GAM RNA, and which when bound by GAM828 RNA causes inhibition of translation of the GAM828 target mRNA into a corresponding GAM828 target protein.

The mechanism of the translational inhibition exerted by GAM828 RNA, herein designated GAM RNA, on one or more GAM828 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM828 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM828 RNA, herein designated GAM RNA, of GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM828 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM828 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM828 RNA correlate with, and may be deduced from, the identity of the GAM828 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM834 6503 GCCCAGGCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTCAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCAGGATCAT Messenger 834 (GAM834) oligonucleotides modulates expression of respective target genes
AGCTCACTGC whose function and utility is known in the art.

AGCCTCGAAC GAM834 is a novel bioinformatically detectable regulatory, non protein coding,
TCCTAGGCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM834 was detected is

AAGCAATCCT described with additional reference to Figs. 9-15.

CCTGCTTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTCCTGGGT encoded by the human genome.

GAM834 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM834

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM834

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM834 precursor RNA is designated SEQ ID:6503, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6503 is located from position 90514756 to position 90514845 relative to chromosome 14 on the `+` strand.

GAM834 precursor RNA folds onto itself, forming GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM834 precursor RNA, designated SEQ ID NO: 6503, and a schematic representation of a predicted secondary folding of GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM834 folded precursor RNA

yielding a GAM834 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM834 RNA, hereby incorporated herein.

GAM834 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM834 target RNA, herein designated GAM TARGET RNA. GAM834 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM834 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM834 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM834 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM834 RNA, herein designated GAM RNA, to target binding sites on GAM834 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM834 target RNA into GAM834 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM834 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM834 target genes. The mRNA of each one of this plurality of GAM834 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM834 RNA, herein designated GAM RNA, and which when bound by GAM834 RNA causes inhibition of translation of the GAM834 target mRNA into a corresponding GAM834 target protein.

The mechanism of the translational inhibition exerted by GAM834 RNA, herein designated GAM RNA, on one or more GAM834 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM834 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM834 RNA, herein designated GAM RNA, of GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM834 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM834 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM834 RNA correlate with, and may be deduced from, the identity of the GAM834 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM840 6623 GGAGAATCAT TTGAACCCAG GAGGTGGAAG TTGCAGTGAG CTCAGATCGC ACCATTGCAC TCCAGCCTGG GTAACAAGAA TGAAACTCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 840 (GAM840) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM840 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM840 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM840 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM840 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM840 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM840 precursor RNA is designated SEQ ID:6623, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6623 is located from position 100281294 to position 100281382 relative to chromosome 7 on the `+` strand.

GAM840 precursor RNA folds onto itself, forming GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM840 precursor RNA, designated SEQ ID NO: 6623, and a schematic representation of a predicted secondary folding of GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM840 folded precursor RNA yielding a GAM840 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM840 RNA, hereby incorporated herein.

GAM840 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM840 target RNA, herein designated GAM TARGET RNA. GAM840 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM840 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM840 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM840 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM840 RNA, herein designated GAM RNA, to target binding sites on GAM840 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM840 target RNA into GAM840 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM840 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM840 target genes. The mRNA of each one of this plurality of GAM840 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM840 RNA, herein designated GAM RNA, and which when bound by GAM840 RNA causes inhibition of translation of the GAM840 target mRNA into a corresponding GAM840 target protein.

The mechanism of the translational inhibition exerted by GAM840 RNA, herein designated GAM RNA, on one or more GAM840 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM840 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM840 RNA, herein designated GAM RNA, of GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM840 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM840 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM840 RNA correlate with, and may be deduced from, the identity of the GAM840 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM842 6233 CTGGGGGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGACCACCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCCTGCCCC Messenger 842 (GAM842) oligonucleotides modulates expression of respective target genes

CTTCTTTCTG whose function and utility is known in the art.

CCTTAAGAAT GAM842 is a novel bioinformatically detectable regulatory, non protein coding,

GTCCTTTTAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM842 was detected is

GCTGGGCATG described with additional reference to Figs. 9-15.

GTGGCTCACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGTAACCC encoded by the human genome.

CAG GAM842 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM842

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM842

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM842 precursor RNA is designated SEQ ID:6233, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6233 is located from position 1319182 to position 1319274 relative to chromosome 17 on the `-` strand.

GAM842 precursor RNA folds onto itself, forming GAM842 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM842 precursor RNA, designated SEQ ID NO: 6233, and a schematic representation of a predicted secondary folding of GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM842 folded precursor RNA yielding a GAM842 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM842 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM842 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM842 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM842 target RNA, herein designated GAM TARGET RNA. GAM842 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM842 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM842 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM842 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM842 RNA, herein designated GAM RNA, to target binding sites on GAM842 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM842 target RNA into GAM842 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM842 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM842 target genes. The mRNA of each one of this plurality of GAM842 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM842 RNA, herein

designated GAM RNA, and which when bound by GAM842 RNA causes inhibition of translation of the GAM842 target mRNA into a corresponding GAM842 target protein.

The mechanism of the translational inhibition exerted by GAM842 RNA, herein designated GAM RNA, on one or more GAM842 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM842 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM842 RNA, herein designated GAM RNA, of GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM842 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM842 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM842 RNA correlate with, and may be deduced from, the identity of the GAM842 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM846 7044 TCCTGTGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGTAGAAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGAGCATGT Messenger 846 (GAM846) oligonucleotides modulates expression of respective target genes
CCTGCTTTAT whose function and utility is known in the art.

GCAGGCTTTG GAM846 is a novel bioinformatically detectable regulatory, non protein coding,
CTTTAGTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM846 was detected is

TCTGAAGTGT described with additional reference to Figs. 9-15.

ATGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM846 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM846

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM846

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM846 precursor RNA is designated SEQ ID:7044, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7044 is located from position 127720318 to position 127720391 relative to chromosome 9 on the `+` strand.

GAM846 precursor RNA folds onto itself, forming GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM846 precursor RNA, designated SEQ ID NO: 7044, and a schematic representation of a predicted secondary folding of GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM846 folded precursor RNA yielding a GAM846 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM846 RNA, hereby incorporated herein.

GAM846 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM846 target RNA, herein designated GAM TARGET RNA. GAM846 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM846 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM846 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM846 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM846 RNA, herein designated GAM RNA, to target binding sites on GAM846 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE

I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM846 target RNA into GAM846 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by

a broken line.

It is appreciated that GAM846 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM846 target genes. The mRNA of each one of this plurality of GAM846 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM846 RNA, herein designated GAM RNA, and which when bound by GAM846 RNA causes inhibition of translation of the GAM846 target mRNA into a corresponding GAM846 target protein.

The mechanism of the translational inhibition exerted by GAM846 RNA, herein designated GAM RNA, on one or more GAM846 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM846 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM846 RNA, herein designated GAM RNA, of GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM846 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM846 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM846 RNA correlate with, and may be deduced from, the identity of the GAM846 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM869 6574 GGAAAGAATA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGCTTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCAGCCTAG Messenger 869 (GAM869) oligonucleotides modulates expression of respective target genes
GTTCAAGTAC whose function and utility is known in the art.

TGCATCTTGA GAM869 is a novel bioinformatically detectable regulatory, non protein coding,
CCTGGCCTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM869 was detected is

AGGCAAGTCT described with additional reference to Figs. 9-15.

TTTCACTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

C encoded by the human genome.

GAM869 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM869 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM869 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM869 precursor RNA is designated SEQ ID:6574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6574 is located from position 43962141 to position 43962221 relative to chromosome 20 on the `-` strand.

GAM869 precursor RNA folds onto itself, forming GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM869 precursor RNA, designated SEQ ID NO: 6574, and a schematic representation of a predicted secondary folding of GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM869 folded precursor RNA yielding a GAM869 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM869 RNA, hereby incorporated herein.

GAM869 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM869 target RNA, herein designated GAM TARGET RNA. GAM869 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM869 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM869 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM869 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM869 RNA, herein designated GAM RNA, to target binding sites on GAM869 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM869 target RNA into GAM869 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM869 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM869 target genes. The mRNA of each one of this plurality of GAM869 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM869 RNA, herein designated GAM RNA, and which when bound by GAM869 RNA causes inhibition of translation of the GAM869 target mRNA into a corresponding GAM869 target protein.

The mechanism of the translational inhibition exerted by GAM869 RNA, herein designated GAM RNA, on one or more GAM869 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM869 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM869 RNA, herein designated GAM RNA, of GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM869 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM869 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM869 RNA correlate with, and may be deduced from, the identity of the GAM869 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM892 7230 TGGCTTTATC TCTTGCCTTG ACCTCCTACA TTATCAACAA AGTGAGAGTT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 892 (GAM892) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM892 is a novel bioinformatically detectable regulatory, non protein coding,

TAAGATCTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM892 was detected is

TGGGCAGGAG described with additional reference to Figs. 9-15.

ATTTCAGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCA encoded by the human genome.

GAM892 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM892

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM892

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM892 precursor RNA is designated SEQ ID:7230, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7230 is located from position 101743922 to position 101744004 relative to chromosome 10 on the `+` strand.

GAM892 precursor RNA folds onto itself, forming GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM892 precursor RNA, designated SEQ ID NO: 7230, and a schematic representation of a predicted secondary folding of GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM892 folded precursor RNA yielding a GAM892 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM892 RNA, hereby incorporated herein.

GAM892 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM892 target RNA, herein designated GAM TARGET RNA. GAM892 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM892 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM892 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM892 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM892 RNA, herein designated GAM RNA, to target binding sites on GAM892 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM892 target RNA into GAM892 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM892 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM892 target genes. The mRNA of each one of this plurality of GAM892 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM892 RNA, herein designated GAM RNA, and which when bound by GAM892 RNA causes inhibition of translation of the GAM892 target mRNA into a corresponding GAM892 target protein.

The mechanism of the translational inhibition exerted by GAM892 RNA, herein designated GAM RNA, on one or more GAM892 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM892 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM892 RNA, herein designated GAM RNA, of GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM892 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM892 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM892 RNA correlate with, and may be deduced from, the identity of the GAM892 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM933 5698 ACCTCTCATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTCCTCAAT detected oligonucleotides of the present invention, referred to here as Genomic Address GCCACTGCAC Messenger 933 (GAM933) oligonucleotides modulates expression of respective target genes

TGATGTCAAC whose function and utility is known in the art.

TGACTTAGGG GAM933 is a novel bioinformatically detectable regulatory, non protein coding, CAGGCATGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM933 was detected is

AGAACTGAGG described with additional reference to Figs. 9-15.

T GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM933 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM933

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM933

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM933 precursor RNA is designated SEQ ID:5698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5698 is located from position 86637069 to position 86637139 relative to chromosome 14 on the `+` strand.

GAM933 precursor RNA folds onto itself, forming GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM933 precursor RNA, designated SEQ ID NO: 5698, and a schematic representation of a predicted secondary folding of GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM933 folded precursor RNA yielding a GAM933 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM933 RNA, hereby incorporated herein.

GAM933 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM933 target RNA, herein designated GAM TARGET RNA. GAM933 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM933 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM933 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM933 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM933 RNA, herein designated GAM RNA, to target binding sites on GAM933 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM933 target RNA into GAM933 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM933 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM933 target genes. The mRNA of each one of this plurality of GAM933 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM933 RNA, herein designated GAM RNA, and which when bound by GAM933 RNA causes inhibition of translation of the GAM933 target mRNA into a corresponding GAM933 target protein.

The mechanism of the translational inhibition exerted by GAM933 RNA, herein designated GAM RNA, on one or more GAM933 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM933 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM933 RNA, herein designated GAM RNA, of GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM933 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM933 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM933 RNA

correlate with, and may be deduced from, the identity of the GAM933 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM965 7245 TGGGTAGCAT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAACTAAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATAAAGGC Messenger 965 (GAM965) oligonucleotides modulates expression of respective target genes
TTCACGTGGT whose function and utility is known in the art.

GTTTGGCATG GAM965 is a novel bioinformatically detectable regulatory, non protein coding,
GCGTAGGTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM965 was detected is

AGATTGGACC described with additional reference to Figs. 9-15.

TCAGTTTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCCA encoded by the human genome.

GAM965 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM965

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM965

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM965 precursor RNA is designated SEQ ID:7245, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7245 is located from position 46553864 to position 46553948 relative to chromosome 12 on the `+` strand.

GAM965 precursor RNA folds onto itself, forming GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM965 precursor RNA, designated SEQ ID NO: 7245, and a schematic representation of a predicted secondary folding of GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM965 folded precursor RNA yielding a GAM965 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM965 RNA, hereby incorporated herein.

GAM965 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM965 target RNA, herein designated GAM TARGET RNA. GAM965 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM965 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM965 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM965 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM965 RNA, herein designated GAM RNA, to target binding sites on GAM965 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM965 target RNA into GAM965 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM965 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM965 target genes. The mRNA of each one of this plurality of GAM965 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM965 RNA, herein designated GAM RNA, and which when bound by GAM965 RNA causes inhibition of translation of the GAM965 target mRNA into a corresponding GAM965 target protein.

The mechanism of the translational inhibition exerted by GAM965 RNA, herein designated GAM RNA, on one or more GAM965 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM965 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM965 RNA, herein designated GAM RNA, of GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM965 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM965 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM965 RNA correlate with, and may be deduced from, the identity of the GAM965 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM973 5671 AAGTGCTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TATTGCTAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AATTCAGGTA Messenger 973 (GAM973) oligonucleotides modulates expression of respective target genes
GTCTCGGGAT whose function and utility is known in the art.

CTCCAGAGTC GAM973 is a novel bioinformatically detectable regulatory, non protein coding,
TCCATACTAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM973 was detected is

GACAGGAGAT described with additional reference to Figs. 9-15.

CTTCAGAACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGAGGAATG encoded by the human genome.

GAAATAGTCT GAM973 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM973
AGTCAGCTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM973
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM973 precursor RNA is designated SEQ ID:5671, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5671 is located from position 150223532 to position 150223640 relative to chromosome 7 on the `-` strand.

GAM973 precursor RNA folds onto itself, forming GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM973 precursor RNA, designated SEQ ID NO: 5671, and a schematic representation of a predicted secondary folding of GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM973 folded precursor RNA yielding a GAM973 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM973 RNA, hereby incorporated herein.

GAM973 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM973 target RNA, herein designated GAM TARGET RNA. GAM973 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM973 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM973 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM973 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM973 RNA, herein designated GAM RNA, to target binding sites on GAM973 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM973 target RNA into GAM973 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM973 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM973 target genes. The mRNA of each one of this plurality of GAM973 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM973 RNA, herein designated GAM RNA, and which when bound by GAM973 RNA causes inhibition of translation of the GAM973 target mRNA into a corresponding GAM973 target protein.

The mechanism of the translational inhibition exerted by GAM973 RNA, herein designated GAM RNA, on one or more GAM973 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM973 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM973 RNA, herein designated GAM RNA, of GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM973 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM973 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM973 RNA correlate with, and may be deduced from, the identity of the GAM973 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM999 5722 AGACCACCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCTTTTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TATGGGTATG Messenger 999 (GAM999) oligonucleotides modulates expression of respective target genes
TGGCATGAAT whose function and utility is known in the art.

GCCATCATTT GAM999 is a novel bioinformatically detectable regulatory, non protein coding,
ATTTACCCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM999 was detected is

CTGCCAGTTG described with additional reference to Figs. 9-15.

AAGAACATTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGTCT encoded by the human genome.

GAM999 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM999

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM999

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM999 precursor RNA is designated SEQ ID:5722, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5722 is located from position 93949150 to position 93949235 relative to chromosome 11 on the `+` strand.

GAM999 precursor RNA folds onto itself, forming GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM999 precursor RNA, designated SEQ ID NO: 5722, and a

schematic representation of a predicted secondary folding of GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM999 folded precursor RNA yielding a GAM999 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM999 RNA, hereby incorporated herein.

GAM999 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM999 target RNA, herein designated GAM TARGET RNA. GAM999 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM999 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM999 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM999 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM999 RNA, herein designated GAM RNA, to target binding sites on GAM999 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM999 target RNA into GAM999 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM999 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM999 target genes. The mRNA of each one of this plurality of GAM999 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM999 RNA, herein designated GAM RNA, and which when bound by GAM999 RNA causes inhibition of translation of the GAM999 target mRNA into a corresponding GAM999 target protein.

The mechanism of the translational inhibition exerted by GAM999 RNA, herein designated GAM RNA, on one or more GAM999 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM999 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM999 RNA, herein designated GAM RNA, of GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM999 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM999 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM999 RNA correlate with, and may be deduced from, the identity of the GAM999 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1017 6666 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAATCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 1017 (GAM1017) oligonucleotides modulates expression of respective target genes

TTGCAGTGAG whose function and utility is known in the art.

CTGAGATCGC GAM1017 is a novel bioinformatically detectable regulatory, non protein coding,

ACCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1017 was detected is

TCCAGCCTGT described with additional reference to Figs. 9-15.

TGACAGCGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTCC encoded by the human genome.

GAM1017 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1017

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1017

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1017 precursor RNA is designated SEQ ID:6666, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6666 is located from position 18499225 to position 18499309 relative to chromosome 20 on the `+` strand.

GAM1017 precursor RNA folds onto itself, forming GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1017 precursor RNA, designated SEQ ID NO: 6666, and a schematic representation of a predicted secondary folding of GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1017 folded precursor RNA yielding a GAM1017 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1017 RNA, hereby incorporated herein.

GAM1017 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1017 target RNA, herein designated GAM TARGET RNA. GAM1017 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1017 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1017 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1017 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1017 RNA, herein designated GAM RNA, to target binding sites on GAM1017 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1017 target RNA into GAM1017 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1017 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1017 target genes. The mRNA of each one of this plurality of GAM1017 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1017 RNA, herein designated GAM RNA, and which when bound by GAM1017 RNA causes inhibition of translation of the GAM1017 target mRNA into a corresponding GAM1017 target protein.

The mechanism of the translational inhibition exerted by GAM1017 RNA, herein designated GAM RNA, on one or more GAM1017 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1017 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1017 RNA, herein designated GAM RNA, of GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1017 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1017 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1017 RNA correlate with, and may be deduced from, the identity of the GAM1017 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1032 6527 GCTAGTCACT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGGCAAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGACTAAAAC Messenger 1032 (GAM1032) oligonucleotides modulates expression of respective target genes
ACTTTTCCTG whose function and utility is known in the art.

CCCTCGAGGA GAM1032 is a novel bioinformatically detectable regulatory, non protein coding,
GCTCACAGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1032 was detected is

TAGTATGTCT described with additional reference to Figs. 9-15.

CATCCCCTAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGACTGAAG encoded by the human genome.

CTCCTTGAGG GAM1032 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1032
ACAGGGATGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1032
TCATACTCAC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CTCGGTGTTG to the nucleotide sequence of GAM1032 precursor RNA is designated SEQ ID:6527, and is

C provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6527 is located from position 141427052 to position 141427182 relative to chromosome 8 on the `-` strand.

GAM1032 precursor RNA folds onto itself, forming GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1032 precursor RNA, designated SEQ ID NO: 6527, and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1032 folded precursor RNA yielding a GAM1032 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1032 RNA, hereby incorporated herein. Expression of GAM1032 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM1032 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1032 target RNA, herein designated GAM TARGET RNA. GAM1032 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1032 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1032 RNA, herein designated GAM RNA, to target binding sites on GAM1032 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1032 target RNA into GAM1032 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1032 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1032 target genes. The mRNA of each one of this plurality of GAM1032 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1032 RNA, herein designated GAM RNA, and which when bound by GAM1032 RNA causes inhibition of translation of the GAM1032 target mRNA into a corresponding GAM1032 target protein.

The mechanism of the translational inhibition exerted by GAM1032 RNA, herein designated GAM RNA, on one or more GAM1032 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1032 RNA, herein designated GAM RNA, of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1032 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1032 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1032 RNA correlate with, and may be deduced from, the identity of the GAM1032 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1033 6449 GAGGGGAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TAAAGAATCA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGTTCCCAG Messenger 1033 (GAM1033) oligonucleotides modulates expression of respective target genes
GGGAAAAGGG whose function and utility is known in the art.

CCTTAAATTG GAM1033 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGGTCTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1033 was detected is

TCAATGGCTG described with additional reference to Figs. 9-15.

ACACTGTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAACTCTCCC encoded by the human genome.

CTT GAM1033 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1033 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1033 precursor RNA is designated SEQ ID:6449, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6449 is located from position 126882804 to position 126882896 relative to chromosome X on the `-` strand.

GAM1033 precursor RNA folds onto itself, forming GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1033 precursor RNA, designated SEQ ID NO: 6449, and a schematic representation of a predicted secondary folding of GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1033 folded precursor RNA yielding a GAM1033 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1033 RNA, hereby incorporated herein.

GAM1033 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1033 target RNA, herein designated GAM TARGET RNA. GAM1033 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1033 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1033 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1033 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1033 RNA, herein designated GAM RNA, to target binding sites on GAM1033 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1033 target RNA into GAM1033 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1033 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1033 target genes. The mRNA of each one of this plurality of GAM1033 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1033 RNA, herein designated GAM RNA, and which when bound by GAM1033 RNA causes inhibition of translation of the GAM1033 target mRNA into a corresponding GAM1033 target protein.

The mechanism of the translational inhibition exerted by GAM1033 RNA, herein designated GAM RNA, on one or more GAM1033 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1033 RNA, herein designated GAM RNA, of GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1033 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1033 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1033 RNA correlate with, and may be deduced from, the identity of the GAM1033 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1087 5796 AGGTGGCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGCAATAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CAATCCTTCT Messenger 1087 (GAM1087) oligonucleotides modulates expression of respective target genes
GCATCACACA whose function and utility is known in the art.

GTGGGAAAAG GAM1087 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGTCTCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1087 was detected is

TGCAGTTCTC described with additional reference to Figs. 9-15.

TTCCAAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM1087 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1087 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1087 precursor RNA is designated SEQ ID:5796, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5796 is located from position 105533378 to position 105533457 relative to chromosome 10 on the `-` strand.

GAM1087 precursor RNA folds onto itself, forming GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1087 precursor RNA, designated SEQ ID NO: 5796, and a schematic representation of a predicted secondary folding of GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1087 folded precursor RNA yielding a GAM1087 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1087 RNA, hereby incorporated herein.

GAM1087 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1087 target RNA, herein designated GAM TARGET RNA. GAM1087 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1087 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1087 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1087 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1087 RNA, herein designated GAM RNA, to target binding sites on GAM1087 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1087 target RNA into GAM1087 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1087 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1087 target genes. The mRNA of each one of this plurality of GAM1087 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1087 RNA, herein designated GAM RNA, and which when bound by GAM1087 RNA causes inhibition of translation of the GAM1087 target mRNA into a corresponding GAM1087 target protein.

The mechanism of the translational inhibition exerted by GAM1087 RNA, herein designated GAM RNA, on one or more GAM1087 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1087 RNA, herein designated GAM RNA, of GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1087 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1087 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1087 RNA correlate with, and may be deduced from, the identity of the GAM1087 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1088 6098 CCGCAGGGAG AAGAGCTGTG TGCTGTGATG Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1088 (GAM1088) oligonucleotides modulates expression of respective target genes

TGGTTTATAA whose function and utility is known in the art.

ATTACCATTT GAM1088 is a novel bioinformatically detectable regulatory, non protein coding, GGAAGGAGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1088 was detected is

GCACAGCACA described with additional reference to Figs. 9-15.

GCAGCCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACTACTCTTC encoded by the human genome.

CTGAGG GAM1088 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1088 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1088 precursor RNA is designated SEQ ID:6098, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6098 is located from position 82179625 to position 82179720 relative to chromosome 7 on the `-` strand.

GAM1088 precursor RNA folds onto itself, forming GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1088 precursor RNA, designated SEQ ID NO: 6098, and a schematic representation of a predicted secondary folding of GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1088 folded precursor RNA yielding a GAM1088 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1088 RNA, hereby incorporated herein.

GAM1088 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1088 target RNA, herein designated GAM TARGET RNA. GAM1088 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1088 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1088 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1088 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1088 RNA, herein designated GAM RNA, to target binding sites on GAM1088 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1088 target RNA into GAM1088 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1088 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1088 target genes. The mRNA of each one of this plurality of GAM1088 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1088 RNA, herein designated GAM RNA, and which when bound by GAM1088 RNA causes inhibition of translation of the GAM1088 target mRNA into a corresponding GAM1088 target protein.

The mechanism of the translational inhibition exerted by GAM1088 RNA, herein designated GAM RNA, on one or more GAM1088 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1088 RNA, herein designated GAM RNA, of GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1088 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1088 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1088 RNA correlate with, and may be deduced from, the identity of the GAM1088 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1089 6889 GTCTGAAATC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGTGTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGGGCCGTG Messenger 1089 (GAM1089) oligonucleotides modulates expression of respective target genes

CTCCCTCCGA whose function and utility is known in the art.

AGGCTCTAGG GAM1089 is a novel bioinformatically detectable regulatory, non protein coding,

GGAGGATCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1089 was detected is

TGCTCAACTT described with additional reference to Figs. 9-15.

ATTTTTGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

C encoded by the human genome.

GAM1089 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1089

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1089

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1089 precursor RNA is designated SEQ ID:6889, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6889 is located from position 114030793 to position 114030873 relative to chromosome 12 on the `-` strand.

GAM1089 precursor RNA folds onto itself, forming GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1089 precursor RNA, designated SEQ ID NO: 6889, and a schematic representation of a predicted secondary folding of GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1089 folded precursor RNA yielding a GAM1089 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1089 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1089 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1089 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1089 target RNA, herein designated GAM TARGET RNA. GAM1089 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1089 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1089 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1089 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1089 RNA, herein designated GAM RNA, to target binding sites on GAM1089 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1089 target RNA into GAM1089 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1089 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1089 target genes. The mRNA of each one of this plurality of GAM1089 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1089 RNA, herein designated GAM RNA, and which when bound by GAM1089 RNA causes inhibition of translation of the GAM1089 target mRNA into a corresponding GAM1089 target protein.

The mechanism of the translational inhibition exerted by GAM1089 RNA, herein designated GAM RNA, on one or more GAM1089 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1089 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1089 RNA, herein designated GAM RNA, of GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1089 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1089 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1089 RNA correlate with, and may be deduced from, the identity of the GAM1089 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1099 6974 TAGTATGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCATCTTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTAAGTGTA Messenger 1099 (GAM1099) oligonucleotides modulates expression of respective target genes
CTTGCCATCT whose function and utility is known in the art.

GTAGATCTTC GAM1099 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGGTGAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1099 was detected is

TGTCTGTTCA described with additional reference to Figs. 9-15.

GATCTGTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CATTTTTAAT encoded by the human genome.

TGGGTTGTTT GAM1099 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1099
AACTTATTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1099
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1099 precursor RNA is designated SEQ ID:6974, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6974 is located from position 46973081 to position 46973189 relative to chromosome 21 on the `+` strand.

GAM1099 precursor RNA folds onto itself, forming GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1099 precursor RNA, designated SEQ ID NO: 6974, and a schematic representation of a predicted secondary folding of GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1099 folded precursor RNA yielding a GAM1099 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM1099 RNA, hereby incorporated herein.

GAM1099 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1099 target RNA, herein designated GAM TARGET RNA. GAM1099 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1099 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1099 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1099 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1099 RNA, herein designated GAM RNA, to target binding sites on GAM1099 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1099 target RNA into GAM1099 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1099 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1099 target genes. The mRNA of each one of this plurality of GAM1099 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1099 RNA, herein designated GAM RNA, and which when bound by GAM1099 RNA causes inhibition of translation of the GAM1099 target mRNA into a corresponding GAM1099 target protein.

The mechanism of the translational inhibition exerted by GAM1099 RNA, herein designated GAM RNA, on one or more GAM1099 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1099 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1099 RNA, herein designated GAM RNA, of GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1099 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1099 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1099 RNA correlate with, and may be deduced from, the identity of the GAM1099 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1144 6173 CTCTCATCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATTAATCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTAGTTGCA Messenger 1144 (GAM1144) oligonucleotides modulates expression of respective target genes

AGGGACCAGT whose function and utility is known in the art.

AAATTAACAG GAM1144 is a novel bioinformatically detectable regulatory, non protein coding,

AATGGTGAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1144 was detected is

ATTTTCCTTT described with additional reference to Figs. 9-15.

TCTTGGTGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGCTGGAT encoded by the human genome.

GACTAGTGGT GAM1144 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1144

TTCTGCTGGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1144

ACAGAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1144 precursor RNA is designated SEQ ID:6173, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6173 is located from position 26088289 to position 26088404 relative to chromosome 13 on the `+` strand.

GAM1144 precursor RNA folds onto itself, forming GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1144 precursor RNA, designated SEQ ID NO: 6173, and a schematic representation of a predicted secondary folding of GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1144 folded precursor RNA

yielding a GAM1144 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1144 RNA, hereby incorporated herein.

GAM1144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1144 target RNA, herein designated GAM TARGET RNA. GAM1144 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1144 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1144 RNA, herein designated GAM RNA, to target binding sites on GAM1144 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1144 target RNA into GAM1144 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1144 target genes. The mRNA of each one of this plurality of GAM1144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1144 RNA, herein designated GAM RNA, and which when bound by GAM1144 RNA causes inhibition of translation of the GAM1144 target mRNA into a corresponding GAM1144 target protein.

The mechanism of the translational inhibition exerted by GAM1144 RNA, herein designated GAM RNA, on one or more GAM1144 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1144 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1144 RNA, herein designated GAM RNA, of GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1144 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1144 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1144 RNA correlate with, and may be deduced from, the identity of the GAM1144 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1163 6920 GTGGTGTATG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGATCTGCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGGTGGTC Messenger 1163 (GAM1163) oligonucleotides modulates expression of respective target genes

TATGAGAAAG whose function and utility is known in the art.

CAAACCCCAG GAM1163 is a novel bioinformatically detectable regulatory, non protein coding,

TGAGTGCTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1163 was detected is

TTCGGGATTC described with additional reference to Figs. 9-15.

TCTCCAACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAACCATGCC encoded by the human genome.

TAC GAM1163 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1163

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1163

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1163 precursor RNA is designated SEQ ID:6920, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6920 is located from position 92946370 to position 92946462 relative to chromosome 9 on the `+` strand.

GAM1163 precursor RNA folds onto itself, forming GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1163 precursor RNA, designated SEQ ID NO: 6920, and a

schematic representation of a predicted secondary folding of GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1163 folded precursor RNA yielding a GAM1163 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1163 RNA, hereby incorporated herein.

GAM1163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1163 target RNA, herein designated GAM TARGET RNA. GAM1163 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1163 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1163 RNA, herein designated GAM RNA, to target binding sites on GAM1163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1163 target RNA into GAM1163 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1163 target genes. The mRNA of each one of this plurality of GAM1163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1163 RNA, herein designated GAM RNA, and which when bound by GAM1163 RNA causes inhibition of translation of the GAM1163 target mRNA into a corresponding GAM1163 target protein.

The mechanism of the translational inhibition exerted by GAM1163 RNA, herein designated GAM RNA, on one or more GAM1163 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1163 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1163 RNA, herein designated GAM RNA, of GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1163 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1163 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1163 RNA correlate with, and may be deduced from, the identity of the GAM1163 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1191 7206 TGCTGGGCGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGAGGCGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTGCTGTGC Messenger 1191 (GAM1191) oligonucleotides modulates expression of respective target genes

CTGTGAGACA whose function and utility is known in the art.

GGAATGGTTC GAM1191 is a novel bioinformatically detectable regulatory, non protein coding,

CATTACACCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1191 was detected is

TGGGAAATCA described with additional reference to Figs. 9-15.

CTGATTTATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTCCCAAAC encoded by the human genome.

TGCCACACAT GAM1191 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1191

CAGCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1191

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1191 precursor RNA is designated SEQ ID:7206, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7206 is located from position 24390494 to position 24390598 relative to chromosome 13 on the `+` strand.

GAM1191 precursor RNA folds onto itself, forming GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1191 precursor RNA, designated SEQ ID NO: 7206, and a schematic representation of a predicted secondary folding of GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1191 folded precursor RNA yielding a GAM1191 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1191 RNA, hereby incorporated herein.

GAM1191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1191 target RNA, herein designated GAM TARGET RNA. GAM1191 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1191 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1191 RNA, herein designated GAM RNA, to target binding sites on GAM1191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1191 target RNA into GAM1191 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1191 target genes. The mRNA of each one of this plurality of GAM1191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1191 RNA, herein designated GAM RNA, and which when bound by GAM1191 RNA causes inhibition of translation of the GAM1191 target mRNA into a corresponding GAM1191 target protein.

The mechanism of the translational inhibition exerted by GAM1191 RNA, herein

designated GAM RNA, on one or more GAM1191 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1191 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1191 RNA, herein designated GAM RNA, of GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1191 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1191 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1191 RNA correlate with, and may be deduced from, the identity of the GAM1191 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1193 6364 GAGCTGGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCGCTCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACCCAGGCT Messenger 1193 (GAM1193) oligonucleotides modulates expression of respective target genes
GGAGTGCAGT whose function and utility is known in the art.

GGTGCGATCT GAM1193 is a novel bioinformatically detectable regulatory, non protein coding,
TGGCTCACTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1193 was detected is

CAACCTCCAC described with additional reference to Figs. 9-15.

CTTTGTGTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGCAATTCT encoded by the human genome.

CCTTCCTC GAM1193 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1193
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1193
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1193 precursor RNA is designated SEQ ID:6364, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6364 is located from position 138504313 to position 138504410 relative to chromosome 7

on the `-` strand.

GAM1193 precursor RNA folds onto itself, forming GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1193 precursor RNA, designated SEQ ID NO: 6364, and a schematic representation of a predicted secondary folding of GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1193 folded precursor RNA yielding a GAM1193 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1193 RNA, hereby incorporated herein.

GAM1193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1193 target RNA, herein designated GAM TARGET RNA. GAM1193 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1193 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1193 RNA, herein designated GAM RNA, to target binding sites on GAM1193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1193 target RNA into GAM1193 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1193 target genes. The mRNA of each one of this plurality of GAM1193 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM1193 RNA, herein designated GAM RNA, and which when bound by GAM1193 RNA causes inhibition of translation of the GAM1193 target mRNA into a corresponding GAM1193 target protein.

The mechanism of the translational inhibition exerted by GAM1193 RNA, herein designated GAM RNA, on one or more GAM1193 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1193 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1193 RNA, herein designated GAM RNA, of GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1193 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1193 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1193 RNA correlate with, and may be deduced from, the identity of the GAM1193 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1197 5740 AGATTTTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGATACTACA detected oligonucleotides of the present invention, referred to here as Genomic Address
TATTGTCAGT Messenger 1197 (GAM1197) oligonucleotides modulates expression of respective target genes
TTTTTAAATA whose function and utility is known in the art.

CTCAGTTTGT GAM1197 is a novel bioinformatically detectable regulatory, non protein coding,
GCTAAAAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1197 was detected is

AACATTCGGC described with additional reference to Figs. 9-15.

AACTGATATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCTGTTCTG encoded by the human genome.

TATGTATCTG GAM1197 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1197
TCAGTCCAGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1197

TTT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1197 precursor RNA is designated SEQ ID:5740, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5740 is located from position 62494484 to position 62494596 relative to chromosome 19 on the `+` strand.

GAM1197 precursor RNA folds onto itself, forming GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1197 precursor RNA, designated SEQ ID NO: 5740, and a schematic representation of a predicted secondary folding of GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1197 folded precursor RNA yielding a GAM1197 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1197 RNA, hereby incorporated herein.

GAM1197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1197 target RNA, herein designated GAM TARGET RNA. GAM1197 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1197 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1197 RNA, herein designated GAM RNA, to target binding sites on GAM1197 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1197 target RNA into GAM1197 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1197 target genes. The mRNA of each one of this plurality of GAM1197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1197 RNA, herein designated GAM RNA, and which when bound by GAM1197 RNA causes inhibition of translation of the GAM1197 target mRNA into a corresponding GAM1197 target protein.

The mechanism of the translational inhibition exerted by GAM1197 RNA, herein designated GAM RNA, on one or more GAM1197 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1197 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1197 RNA, herein designated GAM RNA, of GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1197 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1197 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1197 RNA correlate with, and may be deduced from, the identity of the GAM1197 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1216 7296 TTCAGTGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGGGCCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGGGATGC Messenger 1216 (GAM1216) oligonucleotides modulates expression of respective target genes

TGAGTTATCC whose function and utility is known in the art.

ACTGGAGCAT GAM1216 is a novel bioinformatically detectable regulatory, non protein coding,

CGGCAGTACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1216 was detected is

GGCAGGCACA described with additional reference to Figs. 9-15.

GAGGCAGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

A encoded by the human genome.

GAM1216 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1216 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1216 precursor RNA is designated SEQ ID:7296, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7296 is located from position 69762458 to position 69762538 relative to chromosome 16 on the `+` strand.

GAM1216 precursor RNA folds onto itself, forming GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1216 precursor RNA, designated SEQ ID NO: 7296, and a schematic representation of a predicted secondary folding of GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1216 folded precursor RNA yielding a GAM1216 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1216 RNA, hereby incorporated herein.

GAM1216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1216 target RNA, herein designated GAM TARGET RNA. GAM1216 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1216 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1216 RNA, herein designated GAM RNA, to target binding sites on GAM1216 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1216 target RNA into GAM1216 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1216 target genes. The mRNA of each one of this plurality of GAM1216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1216 RNA, herein designated GAM RNA, and which when bound by GAM1216 RNA causes inhibition of translation of the GAM1216 target mRNA into a corresponding GAM1216 target protein.

The mechanism of the translational inhibition exerted by GAM1216 RNA, herein designated GAM RNA, on one or more GAM1216 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1216 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1216 RNA, herein designated GAM RNA, of GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1216 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1216 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1216 RNA correlate with, and may be deduced from, the identity of the GAM1216 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1217 5699 ACCTGCCTAT ATTACATTCA TTTTGATGGT TTGTATCTCA AAGGAGTACA GTGAACGAAA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1217 (GAM1217) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM1217 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM1217 was detected is

CTTGTTTAAA described with additional reference to Figs. 9-15.

GATACACCGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGAAAAAG encoded by the human genome.

AGAAGAGGCA GAM1217 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1217

GAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1217

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1217 precursor RNA is designated SEQ ID:5699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5699 is located from position 88520253 to position 88520356 relative to chromosome 9 on the `+` strand.

GAM1217 precursor RNA folds onto itself, forming GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1217 precursor RNA, designated SEQ ID NO: 5699, and a schematic representation of a predicted secondary folding of GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1217 folded precursor RNA yielding a GAM1217 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1217 RNA, hereby incorporated herein.

GAM1217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1217 target RNA, herein designated GAM TARGET RNA. GAM1217 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1217 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1217 RNA, herein designated GAM RNA, to target binding sites on GAM1217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1217 target RNA into GAM1217 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1217 target genes. The mRNA of each one of this plurality of GAM1217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1217 RNA, herein designated GAM RNA, and which when bound by GAM1217 RNA causes inhibition of translation of the GAM1217 target mRNA into a corresponding GAM1217 target protein.

The mechanism of the translational inhibition exerted by GAM1217 RNA, herein designated GAM RNA, on one or more GAM1217 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1217 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1217 RNA, herein designated GAM RNA, of GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1217 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1217 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1217 RNA correlate with, and may be deduced from, the identity of the GAM1217 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1221 7086 TGAAGACTCC ATCACAGTTC CAGATGGGTA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1221 (GAM1221) oligonucleotides modulates expression of respective target genes

GGAATACCTT whose function and utility is known in the art.

GCAGGGCTGG GAM1221 is a novel bioinformatically detectable regulatory, non protein coding, GGCAAGGTAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1221 was detected is

TGCCTTCTCT described with additional reference to Figs. 9-15.

GGAAGGCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCATTCTCTT encoded by the human genome.

CA GAM1221 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1221

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1221

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1221 precursor RNA is designated SEQ ID:7086, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7086 is located from position 26323250 to position 26323341 relative to chromosome 10 on the `+` strand.

GAM1221 precursor RNA folds onto itself, forming GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1221 precursor RNA, designated SEQ ID NO: 7086, and a schematic representation of a predicted secondary folding of GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1221 folded precursor RNA yielding a GAM1221 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1221 RNA, hereby incorporated herein.

GAM1221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1221 target RNA, herein designated GAM TARGET RNA. GAM1221 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1221 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1221 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1221 RNA, herein designated GAM RNA, to target binding sites on GAM1221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1221 target RNA into GAM1221 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1221 target genes. The mRNA of each one of this plurality of GAM1221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1221 RNA, herein designated GAM RNA, and which when bound by GAM1221 RNA causes inhibition of translation of the GAM1221 target mRNA into a corresponding GAM1221 target protein.

The mechanism of the translational inhibition exerted by GAM1221 RNA, herein designated GAM RNA, on one or more GAM1221 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1221 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1221 RNA, herein designated GAM RNA, of GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1221 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1221 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1221 RNA correlate with, and may be deduced from, the identity of the GAM1221 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1234 7276 TGTGGGGATC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGTGCTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTCTGCATG Messenger 1234 (GAM1234) oligonucleotides modulates expression of respective target genes

AAGACAGTAA whose function and utility is known in the art.

CGGTGTCTTC GAM1234 is a novel bioinformatically detectable regulatory, non protein coding,

ATCCAGGAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1234 was detected is

CACATTGTCT described with additional reference to Figs. 9-15.

GGACCTACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1234 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1234

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1234

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1234 precursor RNA is designated SEQ ID:7276, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7276 is located from position 138312903 to position 138312981 relative to chromosome 7 on the `-` strand.

GAM1234 precursor RNA folds onto itself, forming GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1234 precursor RNA, designated SEQ ID NO: 7276, and a schematic representation of a predicted secondary folding of GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1234 folded precursor RNA yielding a GAM1234 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1234 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1234 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1234 target RNA, herein designated GAM TARGET RNA. GAM1234 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1234 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1234 RNA, herein designated GAM RNA, to target binding sites on GAM1234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1234 target RNA into GAM1234 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1234 target genes. The mRNA of each one of this plurality of GAM1234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1234 RNA, herein designated GAM RNA, and which when bound by GAM1234 RNA causes inhibition of translation of the GAM1234 target mRNA into a corresponding GAM1234 target protein.

The mechanism of the translational inhibition exerted by GAM1234 RNA, herein designated GAM RNA, on one or more GAM1234 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1234 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1234 RNA, herein designated GAM RNA, of GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1234 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1234 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1234 RNA correlate with, and may be deduced from, the identity of the GAM1234 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1238 6615 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAGG Messenger 1238 (GAM1238) oligonucleotides modulates expression of respective target genes

TTGTTGCAGT whose function and utility is known in the art.

GAGCCGAGAT GAM1238 is a novel bioinformatically detectable regulatory, non protein coding,

TGCACCACTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1238 was detected is

CACTCCAGCC described with additional reference to Figs. 9-15.

TGGGTGACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTGAGACTC encoded by the human genome.

C GAM1238 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1238

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1238

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1238 precursor RNA is designated SEQ ID:6615, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6615 is located from position 56600621 to position 56600711 relative to chromosome 20 on the `-` strand.

GAM1238 precursor RNA folds onto itself, forming GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1238 precursor RNA, designated SEQ ID NO: 6615, and a schematic representation of a predicted secondary folding of GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1238 folded precursor RNA yielding a GAM1238 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM1238 RNA, hereby incorporated herein.

GAM1238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1238 target RNA, herein designated GAM TARGET RNA. GAM1238 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1238 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1238 RNA, herein designated GAM RNA, to target binding sites on GAM1238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1238 target RNA into GAM1238 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1238 target genes. The mRNA of each one of this plurality of GAM1238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1238 RNA, herein designated GAM RNA, and which when bound by GAM1238 RNA causes inhibition of translation of the GAM1238 target mRNA into a corresponding GAM1238 target protein.

The mechanism of the translational inhibition exerted by GAM1238 RNA, herein designated GAM RNA, on one or more GAM1238 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1238 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1238 RNA, herein designated GAM RNA, of GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1238 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1238 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1238 RNA correlate with, and may be deduced from, the identity of the GAM1238 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1293 6923 GTGTCCCTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAGCTGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAACTGTTCA Messenger 1293 (GAM1293) oligonucleotides modulates expression of respective target genes
AACTCAGGCC whose function and utility is known in the art.

TGTGTGACTC GAM1293 is a novel bioinformatically detectable regulatory, non protein coding,
CATTGGGGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1293 was detected is

AGAGGTGAAA described with additional reference to Figs. 9-15.

GCATAACATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGTACAGAGG encoded by the human genome.

GGACAAC GAM1293 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1293
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1293
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1293 precursor RNA is designated SEQ ID:6923, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6923 is located from position 56453734 to position 56453830 relative to chromosome 12 on the `-` strand.

GAM1293 precursor RNA folds onto itself, forming GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1293 precursor RNA, designated SEQ ID NO: 6923, and a schematic representation of a predicted secondary folding of GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1293 folded precursor RNA

yielding a GAM1293 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1293 RNA, hereby incorporated herein.

GAM1293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1293 target RNA, herein designated GAM TARGET RNA. GAM1293 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1293 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1293 RNA, herein designated GAM RNA, to target binding sites on GAM1293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1293 target RNA into GAM1293 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1293 target genes. The mRNA of each one of this plurality of GAM1293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1293 RNA, herein designated GAM RNA, and which when bound by GAM1293 RNA causes inhibition of translation of the GAM1293 target mRNA into a corresponding GAM1293 target protein.

The mechanism of the translational inhibition exerted by GAM1293 RNA, herein designated GAM RNA, on one or more GAM1293 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1293 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1293 RNA, herein designated GAM RNA, of GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1293 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1293 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1293 RNA correlate with, and may be deduced from, the identity of the GAM1293 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1294 6234 CTGGGTTCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATTCTCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTGTTCTG Messenger 1294 (GAM1294) oligonucleotides modulates expression of respective target genes

CATCATTGTC whose function and utility is known in the art.

TAGATGGATT GAM1294 is a novel bioinformatically detectable regulatory, non protein coding,

AGTAAAGAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1294 was detected is

AATGAAAACT described with additional reference to Figs. 9-15.

CCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1294 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1294

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1294

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1294 precursor RNA is designated SEQ ID:6234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6234 is located from position 74684805 to position 74684878 relative to chromosome 16 on the `-` strand.

GAM1294 precursor RNA folds onto itself, forming GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1294 precursor RNA, designated SEQ ID NO: 6234, and a

schematic representation of a predicted secondary folding of GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1294 folded precursor RNA yielding a GAM1294 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1294 RNA, hereby incorporated herein.

GAM1294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1294 target RNA, herein designated GAM TARGET RNA. GAM1294 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1294 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1294 RNA, herein designated GAM RNA, to target binding sites on GAM1294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1294 target RNA into GAM1294 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1294 target genes. The mRNA of each one of this plurality of GAM1294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1294 RNA, herein designated GAM RNA, and which when bound by GAM1294 RNA causes inhibition of translation of the GAM1294 target mRNA into a corresponding GAM1294 target protein.

The mechanism of the translational inhibition exerted by GAM1294 RNA, herein designated GAM RNA, on one or more GAM1294 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1294 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1294 RNA, herein designated GAM RNA, of GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1294 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1294 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1294 RNA correlate with, and may be deduced from, the identity of the GAM1294 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1295 7061 TCTAGGGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCAGGACCC detected oligonucleotides of the present invention, referred to here as Genomic Address
GGGAGAGAGG Messenger 1295 (GAM1295) oligonucleotides modulates expression of respective target genes
TAGAGGGGAG whose function and utility is known in the art.

CAGAGACAGC GAM1295 is a novel bioinformatically detectable regulatory, non protein coding,
CACCAGCTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1295 was detected is

TATCTTCTGC described with additional reference to Figs. 9-15.

TCTAAGCACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCTTTCACG encoded by the human genome.

AGTTTAAGTT GAM1295 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1295
TCCTAGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1295
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1295 precursor RNA is designated SEQ ID:7061, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7061 is located from position 40608762 to position 40608868 relative to chromosome 15 on the `+` strand.

GAM1295 precursor RNA folds onto itself, forming GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1295 precursor RNA, designated SEQ ID NO: 7061, and a schematic representation of a predicted secondary folding of GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1295 folded precursor RNA yielding a GAM1295 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1295 RNA, hereby incorporated herein.

GAM1295 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1295 target RNA, herein designated GAM TARGET RNA. GAM1295 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1295 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1295 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1295 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1295 RNA, herein designated GAM RNA, to target binding sites on GAM1295 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1295 target RNA into GAM1295 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1295 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1295 target genes. The mRNA of each one of this plurality of GAM1295 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1295 RNA, herein designated GAM RNA, and which when bound by GAM1295 RNA causes inhibition of translation of the GAM1295 target mRNA into a corresponding GAM1295 target protein.

The mechanism of the translational inhibition exerted by GAM1295 RNA, herein

designated GAM RNA, on one or more GAM1295 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1295 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1295 RNA, herein designated GAM RNA, of GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1295 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1295 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1295 RNA correlate with, and may be deduced from, the identity of the GAM1295 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1300 7203 TGCTAGGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCTCTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCATTCAGTC Messenger 1300 (GAM1300) oligonucleotides modulates expression of respective target genes
TCTCAATCAA whose function and utility is known in the art.

TCAATACTTA GAM1300 is a novel bioinformatically detectable regulatory, non protein coding,
CTGAGTACTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1300 was detected is

GTCATTGCAA described with additional reference to Figs. 9-15.

GACCTGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAGAGGGGC encoded by the human genome.

TAGCA GAM1300 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1300
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1300
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1300 precursor RNA is designated SEQ ID:7203, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7203 is located from position 82918189 to position 82918283 relative to chromosome 16

on the `+` strand.

GAM1300 precursor RNA folds onto itself, forming GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1300 precursor RNA, designated SEQ ID NO: 7203, and a schematic representation of a predicted secondary folding of GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1300 folded precursor RNA yielding a GAM1300 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1300 RNA, hereby incorporated herein.

GAM1300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1300 target RNA, herein designated GAM TARGET RNA. GAM1300 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1300 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1300 RNA, herein designated GAM RNA, to target binding sites on GAM1300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1300 target RNA into GAM1300 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1300 target genes. The mRNA of each one of this plurality of GAM1300 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM1300 RNA, herein designated GAM RNA, and which when bound by GAM1300 RNA causes inhibition of translation of the GAM1300 target mRNA into a corresponding GAM1300 target protein.

The mechanism of the translational inhibition exerted by GAM1300 RNA, herein designated GAM RNA, on one or more GAM1300 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1300 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1300 RNA, herein designated GAM RNA, of GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1300 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1300 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1300 RNA correlate with, and may be deduced from, the identity of the GAM1300 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1310 6756 GGCGTCTTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTATTGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTGGAGTG Messenger 1310 (GAM1310) oligonucleotides modulates expression of respective target genes
CAGTGGTGCG whose function and utility is known in the art.

ATCTCAGCTC GAM1310 is a novel bioinformatically detectable regulatory, non protein coding,
ACTGCAACCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1310 was detected is

CCGCCTCCCA described with additional reference to Figs. 9-15.

GATTCAAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTCTCCTGC encoded by the human genome.

C GAM1310 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1310
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1310

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1310 precursor RNA is designated SEQ ID:6756, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6756 is located from position 51215356 to position 51215446 relative to chromosome 14 on the `+` strand.

GAM1310 precursor RNA folds onto itself, forming GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1310 precursor RNA, designated SEQ ID NO: 6756, and a schematic representation of a predicted secondary folding of GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1310 folded precursor RNA yielding a GAM1310 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1310 RNA, hereby incorporated herein.

GAM1310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1310 target RNA, herein designated GAM TARGET RNA. GAM1310 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1310 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1310 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1310 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1310 RNA, herein designated GAM RNA, to target binding sites on GAM1310 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1310 target RNA into GAM1310 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1310 target genes. The mRNA of each one of this plurality of GAM1310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1310 RNA, herein designated GAM RNA, and which when bound by GAM1310 RNA causes inhibition of translation of the GAM1310 target mRNA into a corresponding GAM1310 target protein.

The mechanism of the translational inhibition exerted by GAM1310 RNA, herein designated GAM RNA, on one or more GAM1310 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1310 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1310 RNA, herein designated GAM RNA, of GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1310 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1310 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1310 RNA correlate with, and may be deduced from, the identity of the GAM1310 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1332 6486 GCACCCTGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGTAGGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTAACTGTG Messenger 1332 (GAM1332) oligonucleotides modulates expression of respective target genes

TGCACCCTGT whose function and utility is known in the art.

GAGGTAGGTG GAM1332 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTAACTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1332 was detected is

GTGCACATTG described with additional reference to Figs. 9-15.

TGAGGTAGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTGAAACTG encoded by the human genome.

C GAM1332 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1332 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1332 precursor RNA is designated SEQ ID:6486, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6486 is located from position 93614973 to position 93615063 relative to chromosome 14 on the `+` strand.

GAM1332 precursor RNA folds onto itself, forming GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1332 precursor RNA, designated SEQ ID NO: 6486, and a schematic representation of a predicted secondary folding of GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1332 folded precursor RNA yielding a GAM1332 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1332 RNA, hereby incorporated herein.

GAM1332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1332 target RNA, herein designated GAM TARGET RNA. GAM1332 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1332 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1332 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1332 RNA, herein designated GAM RNA, to target binding sites on GAM1332 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1332 target RNA into GAM1332 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1332 target genes. The mRNA of each one of this plurality of GAM1332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1332 RNA, herein designated GAM RNA, and which when bound by GAM1332 RNA causes inhibition of translation of the GAM1332 target mRNA into a corresponding GAM1332 target protein.

The mechanism of the translational inhibition exerted by GAM1332 RNA, herein designated GAM RNA, on one or more GAM1332 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1332 RNA, herein designated GAM RNA, of GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1332 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1332 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1332 RNA correlate with, and may be deduced from, the identity of the GAM1332 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1338 6668 GGAGAATGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGC Messenger 1338 (GAM1338) oligonucleotides modulates expression of respective target genes
TTGCAGTGAG whose function and utility is known in the art.

CAGAGATCAC GAM1338 is a novel bioinformatically detectable regulatory, non protein coding,
GCCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1338 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM1338 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1338 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1338 precursor RNA is designated SEQ ID:6668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6668 is located from position 62757693 to position 62757780 relative to chromosome 11 on the `+` strand.

GAM1338 precursor RNA folds onto itself, forming GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1338 precursor RNA, designated SEQ ID NO: 6668, and a schematic representation of a predicted secondary folding of GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1338 folded precursor RNA yielding a GAM1338 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1338 RNA, hereby incorporated herein. Expression of GAM1338 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM1338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1338 target RNA, herein designated GAM TARGET RNA. GAM1338 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1338 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1338 RNA, herein designated GAM RNA, to target binding sites on GAM1338 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1338 target RNA into GAM1338 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1338 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1338 target genes. The mRNA of each one of this plurality of GAM1338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1338 RNA, herein designated GAM RNA, and which when bound by GAM1338 RNA causes inhibition of translation of the GAM1338 target mRNA into a corresponding GAM1338 target protein.

The mechanism of the translational inhibition exerted by GAM1338 RNA, herein designated GAM RNA, on one or more GAM1338 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1338 RNA, herein designated GAM RNA, of GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1338 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1338 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1338 RNA correlate with, and may be deduced from, the identity of the GAM1338 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1361 6009 CAGAAGGGGT TTTTATCAAA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

AATATGTAGA Messenger 1361 (GAM1361) oligonucleotides modulates expression of respective target genes

TTCTACTACA whose function and utility is known in the art.

ATATTTTAGC GAM1361 is a novel bioinformatically detectable regulatory, non protein coding, TAAAGAAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1361 was detected is

GAAGTAGTAG described with additional reference to Figs. 9-15.

TAGCAGTAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTCAGTATT encoded by the human genome.

TTTGACCCTG GAM1361 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1361

ACCCAACTCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1361

G precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1361 precursor RNA is designated SEQ ID:6009, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6009 is located from position 40576956 to position 40577066 relative to chromosome X on the `+` strand.

GAM1361 precursor RNA folds onto itself, forming GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1361 precursor RNA, designated SEQ ID NO: 6009, and a schematic representation of a predicted secondary folding of GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1361 folded precursor RNA yielding a GAM1361 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1361 RNA, hereby incorporated herein.

GAM1361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1361 target RNA, herein designated GAM TARGET RNA. GAM1361 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1361 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1361 RNA, herein designated GAM RNA, to target binding sites on GAM1361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1361 target RNA into GAM1361 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1361 target genes. The mRNA of each one of this plurality of GAM1361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1361 RNA, herein designated GAM RNA, and which when bound by GAM1361 RNA causes inhibition of translation of the GAM1361 target mRNA into a corresponding GAM1361 target protein.

The mechanism of the translational inhibition exerted by GAM1361 RNA, herein designated GAM RNA, on one or more GAM1361 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1361 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1361 RNA, herein designated GAM RNA, of GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1361 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1361 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1361 RNA correlate with, and may be deduced from, the identity of the GAM1361 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1363 5727 AGAGCTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTAGCGGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTTCTGTC Messenger 1363 (GAM1363) oligonucleotides modulates expression of respective target genes

TGCTGGCACT whose function and utility is known in the art.

AGGTATTTTA GAM1363 is a novel bioinformatically detectable regulatory, non protein coding,

CACATTAAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1363 was detected is

CAGCTCGTTC described with additional reference to Figs. 9-15.

TCACATCAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCT encoded by the human genome.

GAM1363 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1363

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1363

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1363 precursor RNA is designated SEQ ID:5727, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5727 is located from position 54861174 to position 54861256 relative to chromosome 7 on the `+` strand.

GAM1363 precursor RNA folds onto itself, forming GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1363 precursor RNA, designated SEQ ID NO: 5727, and a schematic representation of a predicted secondary folding of GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1363 folded precursor RNA yielding a GAM1363 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1363 RNA, hereby incorporated herein.

GAM1363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1363 target RNA, herein designated GAM TARGET RNA. GAM1363 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1363 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1363 RNA, herein designated GAM RNA, to target binding sites on GAM1363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1363 target RNA into GAM1363 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1363 target genes. The mRNA of each one of this plurality of GAM1363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1363 RNA, herein designated GAM RNA, and which when bound by GAM1363 RNA causes inhibition of translation of the GAM1363 target mRNA into a corresponding GAM1363 target protein.

The mechanism of the translational inhibition exerted by GAM1363 RNA, herein designated GAM RNA, on one or more GAM1363 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1363 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1363 RNA, herein designated GAM RNA, of GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1363 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1363 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1363 RNA correlate with, and may be deduced from, the identity of the GAM1363 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1372 6523 GCTAGGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACCACTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCCAACCTG Messenger 1372 (GAM1372) oligonucleotides modulates expression of respective target genes
GACAACAGAG whose function and utility is known in the art.

CAAGACCCTG GAM1372 is a novel bioinformatically detectable regulatory, non protein coding,
TCTCTAGGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1372 was detected is

AGGTGCAGTG described with additional reference to Figs. 9-15.

GCTCACACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTAATCCCAG encoded by the human genome.

C GAM1372 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1372
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1372
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1372 precursor RNA is designated SEQ ID:6523, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6523 is located from position 71938248 to position 71938338 relative to chromosome 7 on the `+` strand.

GAM1372 precursor RNA folds onto itself, forming GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1372 precursor RNA, designated SEQ ID NO: 6523, and a schematic representation of a predicted secondary folding of GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1372 folded precursor RNA yielding a GAM1372 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM1372 RNA, hereby incorporated herein.

GAM1372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1372 target RNA, herein designated GAM TARGET RNA. GAM1372 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1372 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1372 RNA, herein designated GAM RNA, to target binding sites on GAM1372 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1372 target RNA into GAM1372 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1372 target genes. The mRNA of each one of this plurality of GAM1372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1372 RNA, herein designated GAM RNA, and which when bound by GAM1372 RNA causes inhibition of translation of the GAM1372 target mRNA into a corresponding GAM1372 target protein.

The mechanism of the translational inhibition exerted by GAM1372 RNA, herein designated GAM RNA, on one or more GAM1372 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1372 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1372 RNA, herein designated GAM RNA, of GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1372 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1372 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1372 RNA correlate with, and may be deduced from, the identity of the GAM1372 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1423 6359 GAGCAAGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGTTGTGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTCCCAGTC Messenger 1423 (GAM1423) oligonucleotides modulates expression of respective target genes
CTCTCTCCAT whose function and utility is known in the art.

TTGCAGATCA GAM1423 is a novel bioinformatically detectable regulatory, non protein coding,
GCAAGCTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1423 was detected is

GTCAGCAAGG described with additional reference to Figs. 9-15.

AGGGGTGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATGAAACTG encoded by the human genome.

GGTTCAGCTT GAM1423 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1423
GATTTGTTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1423
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1423 precursor RNA is designated SEQ ID:6359, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6359 is located from position 97689214 to position 97689322 relative to chromosome 9 on the `+` strand.

GAM1423 precursor RNA folds onto itself, forming GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1423 precursor RNA, designated SEQ ID NO: 6359, and a schematic representation of a predicted secondary folding of GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1423 folded precursor RNA

yielding a GAM1423 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1423 RNA, hereby incorporated herein.

GAM1423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1423 target RNA, herein designated GAM TARGET RNA. GAM1423 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1423 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1423 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1423 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1423 RNA, herein designated GAM RNA, to target binding sites on GAM1423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1423 target RNA into GAM1423 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1423 target genes. The mRNA of each one of this plurality of GAM1423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1423 RNA, herein designated GAM RNA, and which when bound by GAM1423 RNA causes inhibition of translation of the GAM1423 target mRNA into a corresponding GAM1423 target protein.

The mechanism of the translational inhibition exerted by GAM1423 RNA, herein designated GAM RNA, on one or more GAM1423 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1423 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1423 RNA, herein designated GAM RNA, of GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1423 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1423 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1423 RNA correlate with, and may be deduced from, the identity of the GAM1423 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1431 6316 GAGAACTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGAGGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTAGAGGAT Messenger 1431 (GAM1431) oligonucleotides modulates expression of respective target genes

GGTGTGGTGT whose function and utility is known in the art.

TTCCCAAGAC GAM1431 is a novel bioinformatically detectable regulatory, non protein coding,

ATCCCCTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1431 was detected is

CTTGCTATCC described with additional reference to Figs. 9-15.

CAGCATCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1431 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1431

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1431

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1431 precursor RNA is designated SEQ ID:6316, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6316 is located from position 62113797 to position 62113875 relative to chromosome 14 on the `-` strand.

GAM1431 precursor RNA folds onto itself, forming GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1431 precursor RNA, designated SEQ ID NO: 6316, and a

schematic representation of a predicted secondary folding of GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1431 folded precursor RNA yielding a GAM1431 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1431 RNA, hereby incorporated herein.

GAM1431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1431 target RNA, herein designated GAM TARGET RNA. GAM1431 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1431 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1431 RNA, herein designated GAM RNA, to target binding sites on GAM1431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1431 target RNA into GAM1431 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1431 target genes. The mRNA of each one of this plurality of GAM1431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1431 RNA, herein designated GAM RNA, and which when bound by GAM1431 RNA causes inhibition of translation of the GAM1431 target mRNA into a corresponding GAM1431 target protein.

The mechanism of the translational inhibition exerted by GAM1431 RNA, herein designated GAM RNA, on one or more GAM1431 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1431 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1431 RNA, herein designated GAM RNA, of GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1431 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1431 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1431 RNA correlate with, and may be deduced from, the identity of the GAM1431 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1440 6286 GAACACAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGTGTAGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGGGTTGG Messenger 1440 (GAM1440) oligonucleotides modulates expression of respective target genes
TCCTTCAAGG whose function and utility is known in the art.

CAGCTCATTG GAM1440 is a novel bioinformatically detectable regulatory, non protein coding,
CAGCTACTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1440 was detected is

CCTCCAGTGA described with additional reference to Figs. 9-15.

AACAGGTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTGAGCTAT encoded by the human genome.

TTGTTC GAM1440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1440
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1440
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1440 precursor RNA is designated SEQ ID:6286, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6286 is located from position 45420363 to position 45420458 relative to chromosome 11 on the `-` strand.

GAM1440 precursor RNA folds onto itself, forming GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1440 precursor RNA, designated SEQ ID NO: 6286, and a schematic representation of a predicted secondary folding of GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1440 folded precursor RNA yielding a GAM1440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1440 RNA, hereby incorporated herein.

GAM1440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1440 target RNA, herein designated GAM TARGET RNA. GAM1440 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1440 RNA, herein designated GAM RNA, to target binding sites on GAM1440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1440 target RNA into GAM1440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1440 target genes. The mRNA of each one of this plurality of GAM1440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1440 RNA, herein designated GAM RNA, and which when bound by GAM1440 RNA causes inhibition of translation of the GAM1440 target mRNA into a corresponding GAM1440 target protein.

The mechanism of the translational inhibition exerted by GAM1440 RNA, herein

designated GAM RNA, on one or more GAM1440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1440 RNA, herein designated GAM RNA, of GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1440 RNA correlate with, and may be deduced from, the identity of the GAM1440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1443 6192 CTGAAGGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGAGGGCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCATGCAGG Messenger 1443 (GAM1443) oligonucleotides modulates expression of respective target genes
CATGTGTGAG whose function and utility is known in the art.

CAGCTGCAGG GAM1443 is a novel bioinformatically detectable regulatory, non protein coding,
TGTGTGAGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1443 was detected is

AATGTGCATC described with additional reference to Figs. 9-15.

ACTGGGGAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGTGTCTGT encoded by the human genome.

GGATGAGGGA GAM1443 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1443
GGAAGTGAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1443
GTGAGG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1443 precursor RNA is designated SEQ ID:6192, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6192 is located from position 79169031 to position 79169146 relative to chromosome 10

on the `+` strand.

GAM1443 precursor RNA folds onto itself, forming GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1443 precursor RNA, designated SEQ ID NO: 6192, and a schematic representation of a predicted secondary folding of GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1443 folded precursor RNA yielding a GAM1443 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1443 RNA, hereby incorporated herein.

GAM1443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1443 target RNA, herein designated GAM TARGET RNA. GAM1443 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1443 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1443 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1443 RNA, herein designated GAM RNA, to target binding sites on GAM1443 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1443 target RNA into GAM1443 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1443 target genes. The mRNA of each one of this plurality of GAM1443 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM1443 RNA, herein designated GAM RNA, and which when bound by GAM1443 RNA causes inhibition of translation of the GAM1443 target mRNA into a corresponding GAM1443 target protein.

The mechanism of the translational inhibition exerted by GAM1443 RNA, herein designated GAM RNA, on one or more GAM1443 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1443 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1443 RNA, herein designated GAM RNA, of GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1443 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1443 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1443 RNA correlate with, and may be deduced from, the identity of the GAM1443 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1447 6873 GTCCACACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCTTCTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCATGGCATA Messenger 1447 (GAM1447) oligonucleotides modulates expression of respective target genes

TGCCCATGTC whose function and utility is known in the art.

AGGCAGTGCT GAM1447 is a novel bioinformatically detectable regulatory, non protein coding,

GTGCTAAAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1447 was detected is

AAGGATTACA described with additional reference to Figs. 9-15.

TGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1447 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1447

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1447

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1447 precursor RNA is designated SEQ ID:6873, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6873 is located from position 84120401 to position 84120475 relative to chromosome X on the `+` strand.

GAM1447 precursor RNA folds onto itself, forming GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1447 precursor RNA, designated SEQ ID NO: 6873, and a schematic representation of a predicted secondary folding of GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1447 folded precursor RNA yielding a GAM1447 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1447 RNA, hereby incorporated herein.

GAM1447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1447 target RNA, herein designated GAM TARGET RNA. GAM1447 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1447 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1447 RNA, herein designated GAM RNA, to target binding sites on GAM1447 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1447 target RNA into GAM1447 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1447 target genes. The mRNA of each one of this plurality of GAM1447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1447 RNA, herein designated GAM RNA, and which when bound by GAM1447 RNA causes inhibition of translation of the GAM1447 target mRNA into a corresponding GAM1447 target protein.

The mechanism of the translational inhibition exerted by GAM1447 RNA, herein designated GAM RNA, on one or more GAM1447 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1447 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1447 RNA, herein designated GAM RNA, of GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1447 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1447 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1447 RNA correlate with, and may be deduced from, the identity of the GAM1447 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1456 6957 TAAGATGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGATATTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATATCCAGTT Messenger 1456 (GAM1456) oligonucleotides modulates expression of respective target genes

AGTAATGAAA whose function and utility is known in the art.

ACAATACAAT GAM1456 is a novel bioinformatically detectable regulatory, non protein coding,

ACTGAGAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1456 was detected is

AAAGCTTGTC described with additional reference to Figs. 9-15.

TTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1456 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1456 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1456 precursor RNA is designated SEQ ID:6957, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6957 is located from position 27561775 to position 27561847 relative to chromosome 10 on the `+` strand.

GAM1456 precursor RNA folds onto itself, forming GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1456 precursor RNA, designated SEQ ID NO: 6957, and a schematic representation of a predicted secondary folding of GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1456 folded precursor RNA yielding a GAM1456 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1456 RNA, hereby incorporated herein.

GAM1456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1456 target RNA, herein designated GAM TARGET RNA. GAM1456 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1456 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1456 RNA, herein designated GAM RNA, to target binding sites on GAM1456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1456 target RNA into GAM1456 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1456 target genes. The mRNA of each one of this plurality of GAM1456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1456 RNA, herein designated GAM RNA, and which when bound by GAM1456 RNA causes inhibition of translation of the GAM1456 target mRNA into a corresponding GAM1456 target protein.

The mechanism of the translational inhibition exerted by GAM1456 RNA, herein designated GAM RNA, on one or more GAM1456 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1456 RNA, herein designated GAM RNA, of GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1456 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1456 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1456 RNA correlate with, and may be deduced from, the identity of the GAM1456 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1461 7268 TGTGAAACCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTATGCAGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGAAGATG Messenger 1461 (GAM1461) oligonucleotides modulates expression of respective target genes
AAGCCCGAGA whose function and utility is known in the art.

GGTTATGAAA GAM1461 is a novel bioinformatically detectable regulatory, non protein coding,
CAGACCCAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1461 was detected is

TGGGCTCGCT described with additional reference to Figs. 9-15.

CTTCAGTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCATAAGGA encoded by the human genome.

ATCCG GAM1461 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1461 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1461 precursor RNA is designated SEQ ID:7268, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7268 is located from position 11377024 to position 11377118 relative to chromosome 16 on the `+` strand.

GAM1461 precursor RNA folds onto itself, forming GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1461 precursor RNA, designated SEQ ID NO: 7268, and a schematic representation of a predicted secondary folding of GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1461 folded precursor RNA yielding a GAM1461 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1461 RNA, hereby incorporated herein.

GAM1461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1461 target RNA, herein designated GAM TARGET RNA. GAM1461 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1461 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1461 RNA, herein designated GAM RNA, to target binding sites on GAM1461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1461 target RNA into GAM1461 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1461 target genes. The mRNA of each one of this plurality of GAM1461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1461 RNA, herein designated GAM RNA, and which when bound by GAM1461 RNA causes inhibition of translation of the GAM1461 target mRNA into a corresponding GAM1461 target protein.

The mechanism of the translational inhibition exerted by GAM1461 RNA, herein designated GAM RNA, on one or more GAM1461 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1461 RNA, herein designated GAM RNA, of GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1461 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1461 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1461 RNA correlate with, and may be deduced from, the identity of the GAM1461 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1469 6871 GTCAGGACTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGCTAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAATGTCTGC Messenger 1469 (GAM1469) oligonucleotides modulates expression of respective target genes

TTGGACTGAT whose function and utility is known in the art.

CATTGAACAA GAM1469 is a novel bioinformatically detectable regulatory, non protein coding,
TCTTTCCAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1469 was detected is

TAAAAGCTTC described with additional reference to Figs. 9-15.

TATGATTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAAGTAGCAA encoded by the human genome.

TCAGCACCGA GAM1469 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1469
CAGTTATGAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1469

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1469 precursor RNA is designated SEQ ID:6871, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6871 is located from position 51978690 to position 51978799 relative to chromosome 14 on the `-` strand.

GAM1469 precursor RNA folds onto itself, forming GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1469 precursor RNA, designated SEQ ID NO: 6871, and a schematic representation of a predicted secondary folding of GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1469 folded precursor RNA yielding a GAM1469 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1469 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1469 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1469 target RNA, herein designated GAM TARGET RNA. GAM1469 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1469 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM1469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1469 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1469 RNA, herein designated GAM RNA, to target binding sites on GAM1469 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1469 target RNA into GAM1469 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1469 target genes. The mRNA of each one of this plurality of GAM1469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1469 RNA, herein designated GAM RNA, and which when bound by GAM1469 RNA causes inhibition of translation of the GAM1469 target mRNA into a corresponding GAM1469 target protein.

The mechanism of the translational inhibition exerted by GAM1469 RNA, herein designated GAM RNA, on one or more GAM1469 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1469 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1469 RNA, herein designated GAM RNA, of GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1469 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1469 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1469 RNA correlate with, and may be deduced from, the identity of the GAM1469 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1479 6776 GGGAAGGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TAGGTTGTAT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTTATCTTC Messenger 1479 (GAM1479) oligonucleotides modulates expression of respective target genes
CGAGGGGCAA whose function and utility is known in the art.

CATCACTGCC GAM1479 is a novel bioinformatically detectable regulatory, non protein coding,
CTGAAACCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1479 was detected is

ACAACCTACT described with additional reference to Figs. 9-15.

ACCTCACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM1479 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1479

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1479
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1479 precursor RNA is designated SEQ ID:6776, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6776 is located from position 44721810 to position 44721887 relative to chromosome 22 on the `-` strand.

GAM1479 precursor RNA folds onto itself, forming GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1479 precursor RNA, designated SEQ ID NO: 6776, and a schematic representation of a predicted secondary folding of GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1479 folded precursor RNA yielding a GAM1479 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1479 RNA, hereby incorporated herein. Expression of GAM1479 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM1479 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM1479 target RNA, herein designated GAM TARGET RNA. GAM1479 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1479 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1479 RNA, herein designated GAM RNA, to target binding sites on GAM1479 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1479 target RNA into GAM1479 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1479 target genes. The mRNA of each one of this plurality of GAM1479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1479 RNA, herein designated GAM RNA, and which when bound by GAM1479 RNA causes inhibition of translation of the GAM1479 target mRNA into a corresponding GAM1479 target protein.

The mechanism of the translational inhibition exerted by GAM1479 RNA, herein designated GAM RNA, on one or more GAM1479 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1479 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1479 RNA, herein designated GAM RNA, of GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1479 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM1479 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1479 RNA correlate with, and may be deduced from, the identity of the GAM1479 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1484 7257 TGGTTGCAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCAGGAAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGGTGAAAT Messenger 1484 (GAM1484) oligonucleotides modulates expression of respective target genes
GCTAGCAAAG whose function and utility is known in the art.

TCACAATTTC GAM1484 is a novel bioinformatically detectable regulatory, non protein coding,
TACTCTGAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1484 was detected is

ATGATTTGCA described with additional reference to Figs. 9-15.

GTGTTCATCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTATTTTTCT encoded by the human genome.

GAACCCTGCT GAM1484 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1484
TTACCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1484
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1484 precursor RNA is designated SEQ ID:7257, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7257 is located from position 63061687 to position 63061792 relative to chromosome 10 on the `-` strand.

GAM1484 precursor RNA folds onto itself, forming GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1484 precursor RNA, designated SEQ ID NO: 7257, and a schematic representation of a predicted secondary folding of GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1484 folded precursor RNA yielding a GAM1484 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1484 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1484 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1484 target RNA, herein designated GAM TARGET RNA. GAM1484 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1484 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1484 RNA, herein designated GAM RNA, to target binding sites on GAM1484 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1484 target RNA into GAM1484 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1484 target genes. The mRNA of each one of this plurality of GAM1484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1484 RNA, herein designated GAM RNA, and which when bound by GAM1484 RNA causes inhibition of translation of the GAM1484 target mRNA into a corresponding GAM1484 target protein.

The mechanism of the translational inhibition exerted by GAM1484 RNA, herein designated GAM RNA, on one or more GAM1484 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1484 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1484 RNA, herein designated GAM RNA, of GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1484 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1484 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1484 RNA correlate with, and may be deduced from, the identity of the GAM1484 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1490 6362 GAGCTCCCAC GGCTTTTCTA GAAATTGGCA CACAAACTCC AAAGCGTGTG TGGAAATGCA GATGACCTGG GAGACCCAAA ACAACCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1490 (GAM1490) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM1490 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM1490 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM1490 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1490 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1490 precursor RNA is designated SEQ ID:6362, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6362 is located from position 132157864 to position 132157951 relative to chromosome 12 on the `+` strand.

GAM1490 precursor RNA folds onto itself, forming GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1490 precursor RNA, designated SEQ ID NO: 6362, and a schematic representation of a predicted secondary folding of GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1490 folded precursor RNA yielding a GAM1490 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1490 RNA, hereby incorporated herein.

GAM1490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1490 target RNA, herein designated GAM TARGET RNA. GAM1490 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1490 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1490 RNA, herein designated GAM RNA, to target binding sites on GAM1490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1490 target RNA into GAM1490 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1490 target genes. The mRNA of each one of this plurality of GAM1490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1490 RNA, herein designated GAM RNA, and which when bound by GAM1490 RNA causes inhibition of translation of the GAM1490 target mRNA into a corresponding GAM1490 target protein.

The mechanism of the translational inhibition exerted by GAM1490 RNA, herein designated GAM RNA, on one or more GAM1490 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1490 RNA, herein designated GAM RNA, of GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1490 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1490 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1490 RNA correlate with, and may be deduced from, the identity of the GAM1490 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1500 6505 GCCCGGTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CGGTTTGTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGTGTCAT Messenger 1500 (GAM1500) oligonucleotides modulates expression of respective target genes

TAGCTGATTG whose function and utility is known in the art.

TACTGTGGTG GAM1500 is a novel bioinformatically detectable regulatory, non protein coding,

GTTACAATCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1500 was detected is

CTAACTCCAC described with additional reference to Figs. 9-15.

TGCCATCAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGGCACA encoded by the human genome.

GC GAM1500 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1500

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1500

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1500 precursor RNA is designated SEQ ID:6505, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6505 is located from position 111417608 to position 111417699 relative to chromosome 11 on the `+` strand.

GAM1500 precursor RNA folds onto itself, forming GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1500 precursor RNA, designated SEQ ID NO: 6505, and a schematic representation of a predicted secondary folding of GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1500 folded precursor RNA yielding a GAM1500 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1500 RNA, hereby incorporated herein.

GAM1500 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1500 target RNA, herein designated GAM TARGET RNA. GAM1500 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1500 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1500 RNA, herein designated GAM RNA, to target binding sites on GAM1500 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1500 target RNA into GAM1500 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1500 target genes. The mRNA of each one of this plurality of GAM1500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1500 RNA, herein designated GAM RNA, and which when bound by GAM1500 RNA causes inhibition of translation of the GAM1500 target mRNA into a corresponding GAM1500 target protein.

The mechanism of the translational inhibition exerted by GAM1500 RNA, herein designated GAM RNA, on one or more GAM1500 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1500 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1500 RNA, herein designated GAM RNA, of GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1500 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1500 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1500 RNA correlate with, and may be deduced from, the identity of the GAM1500 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1502 6035 CATATATGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGTATTCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGTCTAGT Messenger 1502 (GAM1502) oligonucleotides modulates expression of respective target genes

AGTCTAGTAT whose function and utility is known in the art.

AATACACATA GAM1502 is a novel bioinformatically detectable regulatory, non protein coding,

GCCTAGGACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1502 was detected is

TGTATG described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1502 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1502

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1502

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1502 precursor RNA is designated SEQ ID:6035, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6035 is located from position 37916875 to position 37916940 relative to chromosome 13 on the `-` strand.

GAM1502 precursor RNA folds onto itself, forming GAM1502 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1502 precursor RNA, designated SEQ ID NO: 6035, and a schematic representation of a predicted secondary folding of GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1502 folded precursor RNA yielding a GAM1502 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1502 RNA, hereby incorporated herein.

GAM1502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1502 target RNA, herein designated GAM TARGET RNA. GAM1502 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1502 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1502 RNA, herein designated GAM RNA, to target binding sites on GAM1502 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1502 target RNA into GAM1502 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1502 target genes. The mRNA of each one of this plurality of GAM1502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1502 RNA, herein designated GAM RNA, and which when bound by GAM1502 RNA causes inhibition of translation of the GAM1502 target mRNA into a corresponding GAM1502 target protein.

The mechanism of the translational inhibition exerted by GAM1502 RNA, herein designated GAM RNA, on one or more GAM1502 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1502 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1502 RNA, herein designated GAM RNA, of GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1502 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1502 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1502 RNA correlate with, and may be deduced from, the identity of the GAM1502 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1523 6065 CCCAAAGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACAGTTTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTGAATCAT Messenger 1523 (GAM1523) oligonucleotides modulates expression of respective target genes

ATACAATCTC whose function and utility is known in the art.

GTAGTTTGGA GAM1523 is a novel bioinformatically detectable regulatory, non protein coding,

TGGCTGTGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1523 was detected is

TGACTGCAGA described with additional reference to Figs. 9-15.

CTGCTAGACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAGGG encoded by the human genome.

GAM1523 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1523

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1523

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1523 precursor RNA is designated SEQ ID:6065, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6065 is located from position 102859224 to position 102859309 relative to chromosome 10 on the `-` strand.

GAM1523 precursor RNA folds onto itself, forming GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1523 precursor RNA, designated SEQ ID NO: 6065, and a schematic representation of a predicted secondary folding of GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1523 folded precursor RNA yielding a GAM1523 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1523 RNA, hereby incorporated herein.

GAM1523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1523 target RNA, herein designated GAM TARGET RNA. GAM1523 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1523 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1523 RNA, herein designated GAM RNA, to target binding sites on GAM1523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1523 target RNA into GAM1523 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1523 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM1523 target genes. The mRNA of each one of this plurality of GAM1523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1523 RNA, herein designated GAM RNA, and which when bound by GAM1523 RNA causes inhibition of translation of the GAM1523 target mRNA into a corresponding GAM1523 target protein.

The mechanism of the translational inhibition exerted by GAM1523 RNA, herein designated GAM RNA, on one or more GAM1523 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1523 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1523 RNA, herein designated GAM RNA, of GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1523 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1523 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1523 RNA correlate with, and may be deduced from, the identity of the GAM1523 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1543 6677 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 1543 (GAM1543) oligonucleotides modulates expression of respective target genes

TTGCAGTGAG whose function and utility is known in the art.

CCACGATTGT GAM1543 is a novel bioinformatically detectable regulatory, non protein coding,

GCCATTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1543 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM1543 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1543

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1543 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1543 precursor RNA is designated SEQ ID:6677, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6677 is located from position 28383578 to position 28383665 relative to chromosome 16 on the `-` strand.

GAM1543 precursor RNA folds onto itself, forming GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1543 precursor RNA, designated SEQ ID NO: 6677, and a schematic representation of a predicted secondary folding of GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1543 folded precursor RNA yielding a GAM1543 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1543 RNA, hereby incorporated herein.

GAM1543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1543 target RNA, herein designated GAM TARGET RNA. GAM1543 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1543 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1543 RNA, herein designated GAM RNA, to target binding sites on GAM1543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1543 target RNA

into GAM1543 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1543 target genes. The mRNA of each one of this plurality of GAM1543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1543 RNA, herein designated GAM RNA, and which when bound by GAM1543 RNA causes inhibition of translation of the GAM1543 target mRNA into a corresponding GAM1543 target protein.

The mechanism of the translational inhibition exerted by GAM1543 RNA, herein designated GAM RNA, on one or more GAM1543 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1543 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1543 RNA, herein designated GAM RNA, of GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1543 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1543 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1543 RNA correlate with, and may be deduced from, the identity of the GAM1543 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1550 7284 TTACTGAGTA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCACCAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGGGTGGA Messenger 1550 (GAM1550) oligonucleotides modulates expression of respective target genes

GAAAGAAGAC whose function and utility is known in the art.

TTAAAGATTC GAM1550 is a novel bioinformatically detectable regulatory, non protein coding,

CCTAGACATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1550 was detected is

TCCTCTCCCC described with additional reference to Figs. 9-15.

TAGACTCAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACCATGGCAC encoded by the human genome.

TTATTTTCTA GAM1550 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1550 G precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1550 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1550 precursor RNA is designated SEQ ID:7284, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7284 is located from position 35798284 to position 35798384 relative to chromosome 9 on the `+` strand.

GAM1550 precursor RNA folds onto itself, forming GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1550 precursor RNA, designated SEQ ID NO: 7284, and a schematic representation of a predicted secondary folding of GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1550 folded precursor RNA yielding a GAM1550 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1550 RNA, hereby incorporated herein.

GAM1550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1550 target RNA, herein designated GAM TARGET RNA. GAM1550 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1550 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1550 RNA, herein designated GAM RNA, to target binding sites on GAM1550 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1550 target RNA into GAM1550 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1550 target genes. The mRNA of each one of this plurality of GAM1550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1550 RNA, herein designated GAM RNA, and which when bound by GAM1550 RNA causes inhibition of translation of the GAM1550 target mRNA into a corresponding GAM1550 target protein.

The mechanism of the translational inhibition exerted by GAM1550 RNA, herein designated GAM RNA, on one or more GAM1550 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1550 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1550 RNA, herein designated GAM RNA, of GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1550 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1550 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1550 RNA correlate with, and may be deduced from, the identity of the GAM1550 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1602 6292 GAAGAAGTAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGGGCTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

AATCACACAA Messenger 1602 (GAM1602) oligonucleotides modulates expression of respective target genes

TGGGTGCATC whose function and utility is known in the art.

ACCAGTGCGG GAM1602 is a novel bioinformatically detectable regulatory, non protein coding,

ACACCTAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1602 was detected is

GTACAGGGAA described with additional reference to Figs. 9-15.

CCATGGCTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGAGTGTAA encoded by the human genome.

AGAAGGATGT GAM1602 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1602

TACCCCAGGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1602

TGCAGTTCAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar ACAATTTTAT to the nucleotide sequence of GAM1602 precursor RNA is designated SEQ ID:6292, and is

C provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6292 is located from position 33016836 to position 33016966 relative to chromosome 19 on the `-` strand.

GAM1602 precursor RNA folds onto itself, forming GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1602 precursor RNA, designated SEQ ID NO: 6292, and a schematic representation of a predicted secondary folding of GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1602 folded precursor RNA yielding a GAM1602 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1602 RNA, hereby incorporated herein.

GAM1602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1602 target RNA, herein designated GAM TARGET RNA. GAM1602 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1602 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1602 RNA, herein designated GAM RNA, to target binding sites on GAM1602 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1602 target RNA into GAM1602 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1602 target genes. The mRNA of each one of this plurality of GAM1602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1602 RNA, herein designated GAM RNA, and which when bound by GAM1602 RNA causes inhibition of translation of the GAM1602 target mRNA into a corresponding GAM1602 target protein.

The mechanism of the translational inhibition exerted by GAM1602 RNA, herein designated GAM RNA, on one or more GAM1602 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1602 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1602 RNA, herein designated GAM RNA, of GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1602 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1602 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1602 RNA correlate with, and may be deduced from, the identity of the GAM1602 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1607 6972 TAGGCTGTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGTTAATG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTAATCGTGA Messenger 1607 (GAM1607) oligonucleotides modulates expression of respective target genes

TAGGGGTTTT whose function and utility is known in the art.

TGCCTCCAAC GAM1607 is a novel bioinformatically detectable regulatory, non protein coding,
TGACTCCTAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1607 was detected is

ATATTAGCAT described with additional reference to Figs. 9-15.

TAACAGTGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGATGCCTG encoded by the human genome.

GAM1607 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1607

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1607

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1607 precursor RNA is designated SEQ ID:6972, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6972 is located from position 25868151 to position 25868239 relative to chromosome 21 on the `+` strand.

GAM1607 precursor RNA folds onto itself, forming GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1607 precursor RNA, designated SEQ ID NO: 6972, and a schematic representation of a predicted secondary folding of GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1607 folded precursor RNA yielding a GAM1607 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1607 RNA, hereby incorporated herein.

GAM1607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1607 target RNA, herein designated GAM TARGET RNA. GAM1607 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1607 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1607 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1607 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1607 RNA, herein designated GAM RNA, to target binding sites on GAM1607 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1607 target RNA into GAM1607 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1607 target genes. The mRNA of each one of this plurality of GAM1607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1607 RNA, herein designated GAM RNA, and which when bound by GAM1607 RNA causes inhibition of translation of the GAM1607 target mRNA into a corresponding GAM1607 target protein.

The mechanism of the translational inhibition exerted by GAM1607 RNA, herein designated GAM RNA, on one or more GAM1607 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1607 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1607 RNA, herein designated GAM RNA, of GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1607 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1607 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1607 RNA correlate with, and may be deduced from, the identity of the GAM1607 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1617 5952 ATAGACAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCACTCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCCCAGGCT Messenger 1617 (GAM1617) oligonucleotides modulates expression of respective target genes

GGAGTGCAGT whose function and utility is known in the art.

GGTGTGACTG GAM1617 is a novel bioinformatically detectable regulatory, non protein coding,

TAGCTCACTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1617 was detected is

TAGCCACCAA described with additional reference to Figs. 9-15.

GTCCTGGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGCGATCC encoded by the human genome.

TCCTGTCTAT GAM1617 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1617

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1617

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1617 precursor RNA is designated SEQ ID:5952, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5952 is located from position 48119610 to position 48119709 relative to chromosome 16 on the `+` strand.

GAM1617 precursor RNA folds onto itself, forming GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1617 precursor RNA, designated SEQ ID NO: 5952, and a schematic representation of a predicted secondary folding of GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1617 folded precursor RNA yielding a GAM1617 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1617 RNA, hereby incorporated herein.

GAM1617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1617 target RNA, herein designated GAM TARGET RNA. GAM1617 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1617 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1617 RNA, herein designated GAM RNA, to target binding sites on GAM1617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1617 target RNA into GAM1617 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1617 target genes. The mRNA of each one of this plurality of GAM1617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1617 RNA, herein designated GAM RNA, and which when bound by GAM1617 RNA causes inhibition of translation of the GAM1617 target mRNA into a corresponding GAM1617 target protein.

The mechanism of the translational inhibition exerted by GAM1617 RNA, herein designated GAM RNA, on one or more GAM1617 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1617 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1617 RNA, herein designated GAM RNA, of GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1617 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1617 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1617 RNA correlate with, and may be deduced from, the identity of the GAM1617 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1650 7253 TGGTGGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTGTGTAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTATTTTTCT Messenger 1650 (GAM1650) oligonucleotides modulates expression of respective target genes

GCATTTGTAT whose function and utility is known in the art.

TGGAAAAGGT GAM1650 is a novel bioinformatically detectable regulatory, non protein coding,

TTCTTTTAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1650 was detected is

ACATTTTCCA described with additional reference to Figs. 9-15.

AAAGTGGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGAATATGTG encoded by the human genome.

TGTTCAGGAA GAM1650 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1650

GGGCTTTCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1650

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1650 precursor RNA is designated SEQ ID:7253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7253 is located from position 108489391 to position 108489499 relative to chromosome X on the `+` strand.

GAM1650 precursor RNA folds onto itself, forming GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1650 precursor RNA, designated SEQ ID NO: 7253, and a schematic representation of a predicted secondary folding of GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1650 folded precursor RNA yielding a GAM1650 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1650 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1650 RNA and an

alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1650 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1650 target RNA, herein designated GAM TARGET RNA. GAM1650 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1650 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1650 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1650 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1650 RNA, herein designated GAM RNA, to target binding sites on GAM1650 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1650 target RNA into GAM1650 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1650 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1650 target genes. The mRNA of each one of this plurality of GAM1650 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1650 RNA, herein designated GAM RNA, and which when bound by GAM1650 RNA causes inhibition of translation of the GAM1650 target mRNA into a corresponding GAM1650 target protein.

The mechanism of the translational inhibition exerted by GAM1650 RNA, herein designated GAM RNA, on one or more GAM1650 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1650 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1650 RNA, herein designated GAM RNA, of GAM1650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1650 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1650 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1650 RNA correlate with, and may be deduced from, the identity of the GAM1650 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1653 6846 GGTGGAGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGGCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTCCTGCTCC Messenger 1653 (GAM1653) oligonucleotides modulates expression of respective target genes
CTGGCACCAT whose function and utility is known in the art.

CATGGAGCAT GAM1653 is a novel bioinformatically detectable regulatory, non protein coding,
GCCCAGCCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1653 was detected is

GATCTGCCCC described with additional reference to Figs. 9-15.

CC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM1653 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1653

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1653
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1653 precursor RNA is designated SEQ ID:6846, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6846 is located from position 38591310 to position 38591381 relative to chromosome 17 on the `+` strand.

GAM1653 precursor RNA folds onto itself, forming GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1653 precursor RNA, designated SEQ ID NO: 6846, and a schematic representation of a predicted secondary folding of GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1653 folded precursor RNA

yielding a GAM1653 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1653 RNA, hereby incorporated herein.

GAM1653 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1653 target RNA, herein designated GAM TARGET RNA. GAM1653 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1653 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1653 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1653 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1653 RNA, herein designated GAM RNA, to target binding sites on GAM1653 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1653 target RNA into GAM1653 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1653 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1653 target genes. The mRNA of each one of this plurality of GAM1653 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1653 RNA, herein designated GAM RNA, and which when bound by GAM1653 RNA causes inhibition of translation of the GAM1653 target mRNA into a corresponding GAM1653 target protein.

The mechanism of the translational inhibition exerted by GAM1653 RNA, herein designated GAM RNA, on one or more GAM1653 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1653 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1653 RNA, herein designated GAM RNA, of GAM1653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1653 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1653 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1653 RNA correlate with, and may be deduced from, the identity of the GAM1653 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1698 6925 GTGTGACCTT GGCCCTGTGA GGCTTCACCT CTTGAGCCTG AGAAGCAGAG GTGACAGTAC TGGCCCTGGT TCTTAGCAGG GGGGTGGCGG GCAGGGTAGG GGGTGGCGC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1698 (GAM1698) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM1698 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM1698 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM1698 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1698 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1698 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1698 precursor RNA is designated SEQ ID:6925, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6925 is located from position 30012807 to position 30012915 relative to chromosome 16 on the `+` strand.

GAM1698 precursor RNA folds onto itself, forming GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1698 precursor RNA, designated SEQ ID NO: 6925, and a

schematic representation of a predicted secondary folding of GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1698 folded precursor RNA yielding a GAM1698 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1698 RNA, hereby incorporated herein.

GAM1698 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1698 target RNA, herein designated GAM TARGET RNA. GAM1698 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1698 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1698 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1698 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1698 RNA, herein designated GAM RNA, to target binding sites on GAM1698 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1698 target RNA into GAM1698 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1698 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1698 target genes. The mRNA of each one of this plurality of GAM1698 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1698 RNA, herein designated GAM RNA, and which when bound by GAM1698 RNA causes inhibition of translation of the GAM1698 target mRNA into a corresponding GAM1698 target protein.

The mechanism of the translational inhibition exerted by GAM1698 RNA, herein designated GAM RNA, on one or more GAM1698 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1698 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1698 RNA, herein designated GAM RNA, of GAM1698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1698 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1698 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1698 RNA correlate with, and may be deduced from, the identity of the GAM1698 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1735 6884 GTCTAACCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCCAGTGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGAACCAGG Messenger 1735 (GAM1735) oligonucleotides modulates expression of respective target genes

TATCTCAGCT whose function and utility is known in the art.

GGAAATGCAG GAM1735 is a novel bioinformatically detectable regulatory, non protein coding,

AAATCACCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1735 was detected is

CCTTCTCTGT described with additional reference to Figs. 9-15.

TGGTCTCCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGAGCTGCA encoded by the human genome.

GAC GAM1735 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1735

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1735

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1735 precursor RNA is designated SEQ ID:6884, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6884 is located from position 16961669 to position 16961761 relative to chromosome 8 on the `+` strand.

GAM1735 precursor RNA folds onto itself, forming GAM1735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1735 precursor RNA, designated SEQ ID NO: 6884, and a schematic representation of a predicted secondary folding of GAM1735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1735 folded precursor RNA yielding a GAM1735 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1735 RNA, hereby incorporated herein.

GAM1735 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1735 target RNA, herein designated GAM TARGET RNA. GAM1735 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1735 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1735 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1735 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1735 RNA, herein designated GAM RNA, to target binding sites on GAM1735 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1735 target RNA into GAM1735 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1735 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1735 target genes. The mRNA of each one of this plurality of GAM1735 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1735 RNA, herein designated GAM RNA, and which when bound by GAM1735 RNA causes inhibition of translation of the GAM1735 target mRNA into a corresponding GAM1735 target protein.

The mechanism of the translational inhibition exerted by GAM1735 RNA, herein

designated GAM RNA, on one or more GAM1735 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1735 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1735 RNA, herein designated GAM RNA, of GAM1735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1735 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1735 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1735 RNA correlate with, and may be deduced from, the identity of the GAM1735 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1748 7053 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 1748 (GAM1748) oligonucleotides modulates expression of respective target genes

TGAGCTGAGA whose function and utility is known in the art.

TCGTAGCCAC GAM1748 is a novel bioinformatically detectable regulatory, non protein coding,

TGCACTCCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1748 was detected is

TCTGGGTGAC described with additional reference to Figs. 9-15.

AGAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1748 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1748

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1748

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1748 precursor RNA is designated SEQ ID:7053, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7053 is located from position 17342458 to position 17342534 relative to chromosome 19

on the `-` strand.

GAM1748 precursor RNA folds onto itself, forming GAM1748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1748 precursor RNA, designated SEQ ID NO: 7053, and a schematic representation of a predicted secondary folding of GAM1748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1748 folded precursor RNA yielding a GAM1748 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1748 RNA, hereby incorporated herein.

GAM1748 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1748 target RNA, herein designated GAM TARGET RNA. GAM1748 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1748 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1748 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1748 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1748 RNA, herein designated GAM RNA, to target binding sites on GAM1748 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1748 target RNA into GAM1748 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1748 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1748 target genes. The mRNA of each one of this plurality of GAM1748 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM1748 RNA, herein designated GAM RNA, and which when bound by GAM1748 RNA causes inhibition of translation of the GAM1748 target mRNA into a corresponding GAM1748 target protein.

The mechanism of the translational inhibition exerted by GAM1748 RNA, herein designated GAM RNA, on one or more GAM1748 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1748 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1748 RNA, herein designated GAM RNA, of GAM1748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1748 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1748 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1748 RNA correlate with, and may be deduced from, the identity of the GAM1748 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1770 6845 GGTGGAGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGGCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCCTGCTCC Messenger 1770 (GAM1770) oligonucleotides modulates expression of respective target genes

CTGGCACCAT whose function and utility is known in the art.

CATGGAGCAT GAM1770 is a novel bioinformatically detectable regulatory, non protein coding,

GCCCAGCCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1770 was detected is

GATCTGCCCC described with additional reference to Figs. 9-15.

C GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1770 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1770

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1770

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1770 precursor RNA is designated SEQ ID:6845, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6845 is located from position 38591310 to position 38591380 relative to chromosome 17 on the `+` strand.

GAM1770 precursor RNA folds onto itself, forming GAM1770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1770 precursor RNA, designated SEQ ID NO: 6845, and a schematic representation of a predicted secondary folding of GAM1770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1770 folded precursor RNA yielding a GAM1770 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1770 RNA, hereby incorporated herein.

GAM1770 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1770 target RNA, herein designated GAM TARGET RNA. GAM1770 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1770 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1770 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1770 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1770 RNA, herein designated GAM RNA, to target binding sites on GAM1770 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1770 target RNA into GAM1770 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1770 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1770 target genes. The mRNA of each one of this plurality of GAM1770 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1770 RNA, herein designated GAM RNA, and which when bound by GAM1770 RNA causes inhibition of translation of the GAM1770 target mRNA into a corresponding GAM1770 target protein.

The mechanism of the translational inhibition exerted by GAM1770 RNA, herein designated GAM RNA, on one or more GAM1770 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1770 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1770 RNA, herein designated GAM RNA, of GAM1770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1770 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1770 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1770 RNA correlate with, and may be deduced from, the identity of the GAM1770 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1782 6181 CTCTTAAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTAGAAATG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTACAGCATC Messenger 1782 (GAM1782) oligonucleotides modulates expression of respective target genes

TAGCTTCTCT whose function and utility is known in the art.

AGATCAATAA GAM1782 is a novel bioinformatically detectable regulatory, non protein coding,

TCACAGAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1782 was detected is

TTAAGTGCTG described with additional reference to Figs. 9-15.

ACCTCATAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATAAAGAG encoded by the human genome.

GAM1782 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1782 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1782 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1782 precursor RNA is designated SEQ ID:6181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6181 is located from position 136594090 to position 136594178 relative to chromosome X on the `+` strand.

GAM1782 precursor RNA folds onto itself, forming GAM1782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1782 precursor RNA, designated SEQ ID NO: 6181, and a schematic representation of a predicted secondary folding of GAM1782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1782 folded precursor RNA yielding a GAM1782 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1782 RNA, hereby incorporated herein. Expression of GAM1782 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM1782 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1782 target RNA, herein designated GAM TARGET RNA. GAM1782 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1782 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1782 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1782 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1782 RNA, herein designated GAM RNA, to target binding sites on GAM1782 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1782 target RNA into GAM1782 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1782 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1782 target genes. The mRNA of each one of this plurality of GAM1782 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1782 RNA, herein designated GAM RNA, and which when bound by GAM1782 RNA causes inhibition of translation of the GAM1782 target mRNA into a corresponding GAM1782 target protein.

The mechanism of the translational inhibition exerted by GAM1782 RNA, herein designated GAM RNA, on one or more GAM1782 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1782 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1782 RNA, herein designated GAM RNA, of GAM1782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1782 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1782 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1782 RNA correlate with, and may be deduced from, the identity of the GAM1782 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1820 6266 CTTGATCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CACCCAGGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGTGTAGT Messenger 1820 (GAM1820) oligonucleotides modulates expression of respective target genes

GGCATGATCT whose function and utility is known in the art.

CGGCTCACTG GAM1820 is a novel bioinformatically detectable regulatory, non protein coding,

CAACCCCCGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1820 was detected is

CTCCTGGGTT described with additional reference to Figs. 9-15.

CAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1820 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1820

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1820

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1820 precursor RNA is designated SEQ ID:6266, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6266 is located from position 79670256 to position 79670329 relative to chromosome 14 on the `+` strand.

GAM1820 precursor RNA folds onto itself, forming GAM1820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1820 precursor RNA, designated SEQ ID NO: 6266, and a schematic representation of a predicted secondary folding of GAM1820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1820 folded precursor RNA yielding a GAM1820 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1820 RNA, hereby incorporated herein.

GAM1820 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1820 target RNA, herein designated GAM TARGET RNA. GAM1820 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1820 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1820 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1820 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1820 RNA, herein designated GAM RNA, to target binding sites on GAM1820 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1820 target RNA into GAM1820 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1820 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1820 target genes. The mRNA of each one of this plurality of GAM1820 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1820 RNA, herein designated GAM RNA, and which when bound by GAM1820 RNA causes inhibition of translation of the GAM1820 target mRNA into a corresponding GAM1820 target protein.

The mechanism of the translational inhibition exerted by GAM1820 RNA, herein designated GAM RNA, on one or more GAM1820 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1820 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1820 RNA, herein designated GAM RNA, of GAM1820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1820 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1820 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1820 RNA correlate with, and may be deduced from, the identity of the GAM1820 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1835 6959 TAATCTTAAC ATTCTCAACT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGATTACCA Messenger 1835 (GAM1835) oligonucleotides modulates expression of respective target genes

AAGCAGAAAA whose function and utility is known in the art.

ATAAAACACA GAM1835 is a novel bioinformatically detectable regulatory, non protein coding, TTAAATCACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1835 was detected is

TGCTGGCTTA described with additional reference to Figs. 9-15.

TGAAAGCCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CATCTTTAAG encoded by the human genome.

TGACATGTGC GAM1835 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1835

ACTCTCGTTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1835

ATAGTTCATT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar GGCCAAAGAA to the nucleotide sequence of GAM1835 precursor RNA is designated SEQ ID:6959, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6959 is located from position 115193597 to position 115193726 relative to chromosome 9 on the `+` strand.

GAM1835 precursor RNA folds onto itself, forming GAM1835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1835 precursor RNA, designated SEQ ID NO: 6959, and a schematic representation of a predicted secondary folding of GAM1835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1835 folded precursor RNA yielding a GAM1835 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1835 RNA, hereby incorporated herein.

GAM1835 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1835 target RNA, herein designated GAM TARGET RNA. GAM1835 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1835 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1835 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1835 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1835 RNA, herein designated GAM RNA, to target binding sites on GAM1835 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1835 target RNA into GAM1835 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1835 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1835 target genes. The mRNA of each one of this plurality of GAM1835 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1835 RNA, herein designated GAM RNA, and which when bound by GAM1835 RNA causes inhibition of translation of the GAM1835 target mRNA into a corresponding GAM1835 target protein.

The mechanism of the translational inhibition exerted by GAM1835 RNA, herein designated GAM RNA, on one or more GAM1835 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1835 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1835 RNA, herein designated GAM RNA, of GAM1835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1835 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1835 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1835 RNA correlate with, and may be deduced from, the identity of the GAM1835 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1860 7189 TGATGAAAAT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCACAATGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTGAGCTTC Messenger 1860 (GAM1860) oligonucleotides modulates expression of respective target genes
TGGTTGTGTA whose function and utility is known in the art.

ATGCTGGGGT GAM1860 is a novel bioinformatically detectable regulatory, non protein coding,
TTAAAGTCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1860 was detected is

CATTTGTGGG described with additional reference to Figs. 9-15.

TTTGGCATCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM1860 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1860

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1860
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1860 precursor RNA is designated SEQ ID:7189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7189 is located from position 92812997 to position 92813076 relative to chromosome 11 on the `+` strand.

GAM1860 precursor RNA folds onto itself, forming GAM1860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1860 precursor RNA, designated SEQ ID NO: 7189, and a schematic representation of a predicted secondary folding of GAM1860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1860 folded precursor RNA yielding a GAM1860 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1860 RNA, hereby incorporated herein.

GAM1860 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM1860 target RNA, herein designated GAM TARGET RNA. GAM1860 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1860 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1860 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1860 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1860 RNA, herein designated GAM RNA, to target binding sites on GAM1860 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1860 target RNA into GAM1860 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1860 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1860 target genes. The mRNA of each one of this plurality of GAM1860 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1860 RNA, herein designated GAM RNA, and which when bound by GAM1860 RNA causes inhibition of translation of the GAM1860 target mRNA into a corresponding GAM1860 target protein.

The mechanism of the translational inhibition exerted by GAM1860 RNA, herein designated GAM RNA, on one or more GAM1860 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1860 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1860 RNA, herein designated GAM RNA, of GAM1860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1860 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM1860 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1860 RNA correlate with, and may be deduced from, the identity of the GAM1860 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1863 7295 TTCAGTATAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAGGTGCTA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTTTTTTCC Messenger 1863 (GAM1863) oligonucleotides modulates expression of respective target genes
TTTCCCCACC whose function and utility is known in the art.

TGTCTCTTAG GAM1863 is a novel bioinformatically detectable regulatory, non protein coding,
CCTGGGGAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1863 was detected is

TAAATGAGAA described with additional reference to Figs. 9-15.

GCCTTAGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGTGGCCCT encoded by the human genome.

TGTGACCTGA GAM1863 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1863
A precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1863

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1863 precursor RNA is designated SEQ ID:7295, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7295 is located from position 65182629 to position 65182729 relative to chromosome X on the `+` strand.

GAM1863 precursor RNA folds onto itself, forming GAM1863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1863 precursor RNA, designated SEQ ID NO: 7295, and a schematic representation of a predicted secondary folding of GAM1863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1863 folded precursor RNA yielding a GAM1863 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1863 RNA, hereby incorporated herein.

GAM1863 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1863 target RNA, herein designated GAM TARGET RNA. GAM1863 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1863 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1863 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1863 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1863 RNA, herein designated GAM RNA, to target binding sites on GAM1863 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1863 target RNA into GAM1863 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1863 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1863 target genes. The mRNA of each one of this plurality of GAM1863 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1863 RNA, herein designated GAM RNA, and which when bound by GAM1863 RNA causes inhibition of translation of the GAM1863 target mRNA into a corresponding GAM1863 target protein.

The mechanism of the translational inhibition exerted by GAM1863 RNA, herein designated GAM RNA, on one or more GAM1863 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1863 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1863 RNA, herein designated GAM RNA, of GAM1863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1863 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1863 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1863 RNA correlate with, and may be deduced from, the identity of the GAM1863 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1864 6072 CCCAGCATGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCATACCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TAATCTTACC Messenger 1864 (GAM1864) oligonucleotides modulates expression of respective target genes
CATTCTTGAT whose function and utility is known in the art.

TTAGATGAGA GAM1864 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGGATTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM1864 was detected is

GAGTTGATGC described with additional reference to Figs. 9-15.

TAGAATGGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAATACTTTT encoded by the human genome.

GAGGATGTTG GAM1864 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1864
GG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1864

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1864 precursor RNA is designated SEQ ID:6072, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6072 is located from position 89090896 to position 89090997 relative to chromosome 1 on the `-` strand.

GAM1864 precursor RNA folds onto itself, forming GAM1864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1864 precursor RNA, designated SEQ ID NO: 6072, and a schematic representation of a predicted secondary folding of GAM1864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1864 folded precursor RNA yielding a GAM1864 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1864 RNA, hereby incorporated herein.

GAM1864 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1864 target RNA, herein designated GAM TARGET RNA. GAM1864 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1864 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1864 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1864 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1864 RNA, herein designated GAM RNA, to target binding sites on GAM1864 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1864 target RNA into GAM1864 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1864 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1864 target genes. The mRNA of each one of this plurality of GAM1864 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1864 RNA, herein designated GAM RNA, and which when bound by GAM1864 RNA causes inhibition of translation of the GAM1864 target mRNA into a corresponding GAM1864 target protein.

The mechanism of the translational inhibition exerted by GAM1864 RNA, herein designated GAM RNA, on one or more GAM1864 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1864 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1864 RNA, herein designated GAM RNA, of GAM1864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1864 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1864 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1864 RNA correlate with, and may be deduced from, the identity of the GAM1864 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1887 6132 CCTTTGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGTGTTAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGAGAAGC Messenger 1887 (GAM1887) oligonucleotides modulates expression of respective target genes

TTGTTTATTT whose function and utility is known in the art.

GAAGGCTGGG GAM1887 is a novel bioinformatically detectable regulatory, non protein coding,

TTCTCATTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1887 was detected is

CCCACAGGGG described with additional reference to Figs. 9-15.

TAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1887 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1887

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1887

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1887 precursor RNA is designated SEQ ID:6132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6132 is located from position 46615376 to position 46615449 relative to chromosome 20 on the `-` strand.

GAM1887 precursor RNA folds onto itself, forming GAM1887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1887 precursor RNA, designated SEQ ID NO: 6132, and a schematic representation of a predicted secondary folding of GAM1887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1887 folded precursor RNA yielding a GAM1887 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1887 RNA, hereby incorporated herein.

GAM1887 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1887 target RNA, herein designated GAM TARGET RNA. GAM1887 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1887 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1887 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1887 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1887 RNA, herein designated GAM RNA, to target binding sites on GAM1887 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1887 target RNA into GAM1887 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1887 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1887 target genes. The mRNA of each one of this plurality of GAM1887 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1887 RNA, herein designated GAM RNA, and which when bound by GAM1887 RNA causes inhibition of translation of the GAM1887 target mRNA into a corresponding GAM1887 target protein.

The mechanism of the translational inhibition exerted by GAM1887 RNA, herein designated GAM RNA, on one or more GAM1887 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1887 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1887 RNA, herein designated GAM RNA, of GAM1887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1887 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1887 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1887 RNA correlate with, and may be deduced from, the identity of the GAM1887 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1896 6059 CCATCTCTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTATTCCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCACGTCTT Messenger 1896 (GAM1896) oligonucleotides modulates expression of respective target genes

TCCCTTCTCC whose function and utility is known in the art.

TCTCTGCTCT GAM1896 is a novel bioinformatically detectable regulatory, non protein coding,

CATAAAGAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1896 was detected is

AATGGGAGAT described with additional reference to Figs. 9-15.

GAAAGTGGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGCAGCTGA encoded by the human genome.

GGTGG GAM1896 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1896

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1896

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1896 precursor RNA is designated SEQ ID:6059, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6059 is located from position 21174682 to position 21174776 relative to chromosome 20 on the `+` strand.

GAM1896 precursor RNA folds onto itself, forming GAM1896 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1896 precursor RNA, designated SEQ ID NO: 6059, and a schematic representation of a predicted secondary folding of GAM1896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1896 folded precursor RNA yielding a GAM1896 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1896 RNA, hereby incorporated herein. Expression of GAM1896 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM1896 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1896 target RNA, herein designated GAM TARGET RNA. GAM1896 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1896 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1896 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1896 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1896 RNA, herein designated GAM RNA, to target binding sites on GAM1896 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1896 target RNA into GAM1896 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1896 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1896 target genes. The mRNA of each one of this plurality of GAM1896 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1896 RNA, herein

designated GAM RNA, and which when bound by GAM1896 RNA causes inhibition of translation of the GAM1896 target mRNA into a corresponding GAM1896 target protein.

The mechanism of the translational inhibition exerted by GAM1896 RNA, herein designated GAM RNA, on one or more GAM1896 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1896 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1896 RNA, herein designated GAM RNA, of GAM1896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1896 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1896 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1896 RNA correlate with, and may be deduced from, the identity of the GAM1896 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1914 6471 GATCCAGATA Fig. 8 further provides a conceptual description of another novel bioinformatically
GATGATATGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCTACTAGT Messenger 1914 (GAM1914) oligonucleotides modulates expression of respective target genes
GGTTGATGGC whose function and utility is known in the art.

CTCTTTCAGC GAM1914 is a novel bioinformatically detectable regulatory, non protein coding,
TCCATCGCTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1914 was detected is

TGGAGGCGAG described with additional reference to Figs. 9-15.

GTTCATCAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACTCAGAGA encoded by the human genome.

AACTTGTGTC GAM1914 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1914
CAGAGTTGGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1914

C precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1914 precursor RNA is designated SEQ ID:6471, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6471 is located from position 93938738 to position 93938848 relative to chromosome 10 on the `-` strand.

GAM1914 precursor RNA folds onto itself, forming GAM1914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1914 precursor RNA, designated SEQ ID NO: 6471, and a schematic representation of a predicted secondary folding of GAM1914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1914 folded precursor RNA yielding a GAM1914 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1914 RNA, hereby incorporated herein.

GAM1914 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1914 target RNA, herein designated GAM TARGET RNA. GAM1914 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1914 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1914 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1914 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1914 RNA, herein designated GAM RNA, to target binding sites on GAM1914 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1914 target RNA into GAM1914 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1914 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1914 target genes. The mRNA of each one of this plurality of GAM1914 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1914 RNA, herein designated GAM RNA, and which when bound by GAM1914 RNA causes inhibition of translation of the GAM1914 target mRNA into a corresponding GAM1914 target protein.

The mechanism of the translational inhibition exerted by GAM1914 RNA, herein designated GAM RNA, on one or more GAM1914 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1914 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1914 RNA, herein designated GAM RNA, of GAM1914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1914 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1914 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1914 RNA correlate with, and may be deduced from, the identity of the GAM1914 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1937 5679 AATGTTTACT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGTATTCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGTGCTGG Messenger 1937 (GAM1937) oligonucleotides modulates expression of respective target genes
GTGGAGAAAG whose function and utility is known in the art.

AAGACTTAAA GAM1937 is a novel bioinformatically detectable regulatory, non protein coding,
GATTCCCTAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1937 was detected is

ACATCTCCTC described with additional reference to Figs. 9-15.

TCCCCTAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAGGACCAT encoded by the human genome.

GGCACTTATT GAM1937 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1937 TTCTAGTCAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1937 TATT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1937 precursor RNA is designated SEQ ID:5679, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5679 is located from position 35798279 to position 35798392 relative to chromosome 9 on the `+` strand.

GAM1937 precursor RNA folds onto itself, forming GAM1937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1937 precursor RNA, designated SEQ ID NO: 5679, and a schematic representation of a predicted secondary folding of GAM1937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1937 folded precursor RNA yielding a GAM1937 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1937 RNA, hereby incorporated herein.

GAM1937 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1937 target RNA, herein designated GAM TARGET RNA. GAM1937 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1937 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1937 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1937 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1937 RNA, herein designated GAM RNA, to target binding sites on GAM1937 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1937 target RNA into GAM1937 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1937 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1937 target genes. The mRNA of each one of this plurality of GAM1937 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1937 RNA, herein designated GAM RNA, and which when bound by GAM1937 RNA causes inhibition of translation of the GAM1937 target mRNA into a corresponding GAM1937 target protein.

The mechanism of the translational inhibition exerted by GAM1937 RNA, herein designated GAM RNA, on one or more GAM1937 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1937 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1937 RNA, herein designated GAM RNA, of GAM1937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1937 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1937 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1937 RNA correlate with, and may be deduced from, the identity of the GAM1937 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1942 6832 GGTAGTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCAAAGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATGGTAGC Messenger 1942 (GAM1942) oligonucleotides modulates expression of respective target genes
ATTGGAGAGG whose function and utility is known in the art.

ATGAGATATG GAM1942 is a novel bioinformatically detectable regulatory, non protein coding,
GTCAGATGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1942 was detected is

GATATATTTT described with additional reference to Figs. 9-15.

AAAAGTTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTAACAGGAT encoded by the human genome.

TTGCTGAGGA GAM1942 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1942

ATCAGAAGTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1942

AACC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1942 precursor RNA is designated SEQ ID:6832, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6832 is located from position 133099401 to position 133099514 relative to chromosome 7 on the `+` strand.

GAM1942 precursor RNA folds onto itself, forming GAM1942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1942 precursor RNA, designated SEQ ID NO: 6832, and a schematic representation of a predicted secondary folding of GAM1942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1942 folded precursor RNA yielding a GAM1942 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1942 RNA, hereby incorporated herein.

GAM1942 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1942 target RNA, herein designated GAM TARGET RNA. GAM1942 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1942 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1942 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1942 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1942 RNA, herein designated GAM RNA, to target binding sites on GAM1942 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1942 target RNA into GAM1942 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1942 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1942 target genes. The mRNA of each one of this plurality of GAM1942 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1942 RNA, herein designated GAM RNA, and which when bound by GAM1942 RNA causes inhibition of translation of the GAM1942 target mRNA into a corresponding GAM1942 target protein.

The mechanism of the translational inhibition exerted by GAM1942 RNA, herein designated GAM RNA, on one or more GAM1942 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1942 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1942 RNA, herein designated GAM RNA, of GAM1942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1942 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1942 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1942 RNA correlate with, and may be deduced from, the identity of the GAM1942 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1961 6749 GGCCTCCCAA AGTGCTGAGA TTACAGGCAT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 1961 (GAM1961) oligonucleotides modulates expression of respective target genes

GAGCCACTGC whose function and utility is known in the art.

ACCTGGCCCT GAM1961 is a novel bioinformatically detectable regulatory, non protein coding, TGCCTCTATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM1961 was detected is

TCAAAGCTAC described with additional reference to Figs. 9-15.

TTTGGTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1961 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1961

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1961

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1961 precursor RNA is designated SEQ ID:6749, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6749 is located from position 111433254 to position 111433332 relative to chromosome 12 on the `+` strand.

GAM1961 precursor RNA folds onto itself, forming GAM1961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1961 precursor RNA, designated SEQ ID NO: 6749, and a schematic representation of a predicted secondary folding of GAM1961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1961 folded precursor RNA yielding a GAM1961 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1961 RNA, hereby incorporated herein.

GAM1961 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1961 target RNA, herein designated GAM TARGET RNA. GAM1961 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1961 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1961 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1961 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1961 RNA, herein designated GAM RNA, to target binding sites on GAM1961 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1961 target RNA into GAM1961 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1961 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1961 target genes. The mRNA of each one of this plurality of GAM1961 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1961 RNA, herein designated GAM RNA, and which when bound by GAM1961 RNA causes inhibition of translation of the GAM1961 target mRNA into a corresponding GAM1961 target protein.

The mechanism of the translational inhibition exerted by GAM1961 RNA, herein designated GAM RNA, on one or more GAM1961 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1961 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1961 RNA, herein designated GAM RNA, of GAM1961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1961 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1961 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1961 RNA correlate with, and may be deduced from, the identity of the GAM1961 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1975 5960 ATCTGTCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAAGCCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCGGGATCA Messenger 1975 (GAM1975) oligonucleotides modulates expression of respective target
genes
GAGTTTTTAA whose function and utility is known in the art.

GGATAATTTG GAM1975 is a novel bioinformatically detectable regulatory, non protein coding,
GTGGGGAGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1975 was detected is

GCTTGGGAAG described with additional reference to Figs. 9-15.

TGGGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
encoded by the human genome.

GAM1975 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1975

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM1975
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1975 precursor RNA is designated SEQ ID:5960, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5960 is located from position 55606620 to position 55606695 relative to chromosome X on the `-` strand.

GAM1975 precursor RNA folds onto itself, forming GAM1975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1975 precursor RNA, designated SEQ ID NO: 5960, and a schematic representation of a predicted secondary folding of GAM1975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1975 folded precursor RNA yielding a GAM1975 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1975 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1975 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1975 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1975 target RNA, herein designated GAM TARGET RNA. GAM1975 target
RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1975 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1975 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1975 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1975 RNA, herein designated GAM RNA, to target binding sites on GAM1975 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1975 target RNA into GAM1975 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1975 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1975 target genes. The mRNA of each one of this plurality of GAM1975 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1975 RNA, herein designated GAM RNA, and which when bound by GAM1975 RNA causes inhibition of translation of the GAM1975 target mRNA into a corresponding GAM1975 target protein.

The mechanism of the translational inhibition exerted by GAM1975 RNA, herein designated GAM RNA, on one or more GAM1975 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1975 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1975 RNA, herein designated GAM RNA, of GAM1975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1975 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1975 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1975 RNA correlate with, and may be deduced from, the identity of the GAM1975 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1976 6572 GGAAAATGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGAAGACCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTCCCTCT Messenger 1976 (GAM1976) oligonucleotides modulates expression of respective target genes

CTTCTCTCCC whose function and utility is known in the art.

GTTAGGCACA GAM1976 is a novel bioinformatically detectable regulatory, non protein coding,

AGACGGTGTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM1976 was detected is

AATCCTGGTC described with additional reference to Figs. 9-15.

TTCCTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM1976 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1976

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1976

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1976 precursor RNA is designated SEQ ID:6572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6572 is located from position 35292418 to position 35292494 relative to chromosome 21 on the `+` strand.

GAM1976 precursor RNA folds onto itself, forming GAM1976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1976 precursor RNA, designated SEQ ID NO: 6572, and a schematic representation of a predicted secondary folding of GAM1976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1976 folded precursor RNA yielding a GAM1976 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM1976 RNA, hereby incorporated herein.

GAM1976 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1976 target RNA, herein designated GAM TARGET RNA. GAM1976 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1976 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1976 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1976 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1976 RNA, herein designated GAM RNA, to target binding sites on GAM1976 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1976 target RNA into GAM1976 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1976 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1976 target genes. The mRNA of each one of this plurality of GAM1976 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1976 RNA, herein designated GAM RNA, and which when bound by GAM1976 RNA causes inhibition of translation of the GAM1976 target mRNA into a corresponding GAM1976 target protein.

The mechanism of the translational inhibition exerted by GAM1976 RNA, herein designated GAM RNA, on one or more GAM1976 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1976 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1976 RNA, herein designated GAM RNA, of GAM1976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1976 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1976 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1976 RNA correlate with, and may be deduced from, the identity of the GAM1976 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM1997 6880 GTCCCTATCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCGGAGCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGACCTGAGC Messenger 1997 (GAM1997) oligonucleotides modulates expression of respective target genes

TATGAGTCAT whose function and utility is known in the art.

CAGTGAGGTG GAM1997 is a novel bioinformatically detectable regulatory, non protein coding,

CTATACTCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM1997 was detected is

AGCCATTCCG described with additional reference to Figs. 9-15.

CTCAGGTCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGAGGAC encoded by the human genome.

GAM1997 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM1997

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM1997

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1997 precursor RNA is designated SEQ ID:6880, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6880 is located from position 79802871 to position 79802957 relative to chromosome 4 on the `+` strand.

GAM1997 precursor RNA folds onto itself, forming GAM1997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM1997 precursor RNA, designated SEQ ID NO: 6880, and a schematic representation of a predicted secondary folding of GAM1997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM1997 folded precursor RNA

yielding a GAM1997 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM1997 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM1997 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM1997 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1997 target RNA, herein designated GAM TARGET RNA. GAM1997 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM1997 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1997 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1997 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM1997 RNA, herein designated GAM RNA, to target binding sites on GAM1997 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1997 target RNA into GAM1997 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM1997 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1997 target genes. The mRNA of each one of this plurality of GAM1997 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1997 RNA, herein designated GAM RNA, and which when bound by GAM1997 RNA causes inhibition of translation of the GAM1997 target mRNA into a corresponding GAM1997 target protein.

The mechanism of the translational inhibition exerted by GAM1997 RNA, herein designated GAM RNA, on one or more GAM1997 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM1997 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM1997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM1997 RNA, herein designated GAM RNA, of GAM1997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM1997 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM1997 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM1997 RNA correlate with, and may be deduced from, the identity of the GAM1997 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2010 5689 ACAGGAGAAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCTTGAACC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGAGGTGG Messenger 2010 (GAM2010) oligonucleotides modulates expression of respective target genes

AGGTTGCAGT whose function and utility is known in the art.

GAGCCGAGAT GAM2010 is a novel bioinformatically detectable regulatory, non protein coding,

TGCACCATTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2010 was detected is

CACTCCACCC described with additional reference to Figs. 9-15.

TAGGCAACAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCAAAACT encoded by the human genome.

CTGT GAM2010 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2010

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2010

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2010 precursor RNA is designated SEQ ID:5689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5689 is located from position 22660388 to position 22660481 relative to chromosome 15 on the `+` strand.

GAM2010 precursor RNA folds onto itself, forming GAM2010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2010 precursor RNA, designated SEQ ID NO: 5689, and a schematic representation of a predicted secondary folding of GAM2010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2010 folded precursor RNA yielding a GAM2010 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2010 RNA, hereby incorporated herein.

GAM2010 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2010 target RNA, herein designated GAM TARGET RNA. GAM2010 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2010 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2010 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2010 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2010 RNA, herein designated GAM RNA, to target binding sites on GAM2010 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2010 target RNA into GAM2010 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2010 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2010 target genes. The mRNA of each one of this plurality of GAM2010 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2010 RNA, herein designated GAM RNA, and which when bound by GAM2010 RNA causes inhibition of translation of the GAM2010 target mRNA into a corresponding GAM2010 target protein.

The mechanism of the translational inhibition exerted by GAM2010 RNA, herein designated GAM RNA, on one or more GAM2010 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2010 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2010 RNA, herein designated GAM RNA, of GAM2010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2010 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2010 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2010 RNA correlate with, and may be deduced from, the identity of the GAM2010 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2014 6737 GGCAGGGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGACGAGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGCAGAGC Messenger 2014 (GAM2014) oligonucleotides modulates expression of respective target genes

GGATGGAAGC whose function and utility is known in the art.

CGGAGATCCC GAM2014 is a novel bioinformatically detectable regulatory, non protein coding,

AGGTTCCCGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2014 was detected is

AATACTCCGG described with additional reference to Figs. 9-15.

CTGGGGCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGGGCTTCTC encoded by the human genome.

CTGTCCCCTC GAM2014 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2014

CCTACCCCCG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2014

TGCCTCGGGT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TTCTCCCTCC to the nucleotide sequence of GAM2014 precursor RNA is designated SEQ ID:6737, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6737 is located from position 76816688 to position 76816817 relative to chromosome 17 on the `-` strand.

GAM2014 precursor RNA folds onto itself, forming GAM2014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2014 precursor RNA, designated SEQ ID NO: 6737, and a schematic representation of a predicted secondary folding of GAM2014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2014 folded precursor RNA yielding a GAM2014 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2014 RNA, hereby incorporated herein.

GAM2014 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2014 target RNA, herein designated GAM TARGET RNA. GAM2014 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2014 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2014 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2014 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2014 RNA, herein designated GAM RNA, to target binding sites on GAM2014 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2014 target RNA into GAM2014 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2014 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2014 target genes. The mRNA of each one of this plurality of GAM2014 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2014 RNA, herein designated GAM RNA, and which when bound by GAM2014 RNA causes inhibition of translation

of the GAM2014 target mRNA into a corresponding GAM2014 target protein.

The mechanism of the translational inhibition exerted by GAM2014 RNA, herein designated GAM RNA, on one or more GAM2014 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2014 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2014 RNA, herein designated GAM RNA, of GAM2014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2014 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2014 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2014 RNA correlate with, and may be deduced from, the identity of the GAM2014 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2022 6313 GACCATGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGAGTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGACTCCT Messenger 2022 (GAM2022) oligonucleotides modulates expression of respective target genes
CACTCAACCT whose function and utility is known in the art.

CGGCCATGGA GAM2022 is a novel bioinformatically detectable regulatory, non protein coding,
CGCAGGTTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2022 was detected is

GTGTGAGGGG described with additional reference to Figs. 9-15.

GGTCCCAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCGGTCTT encoded by the human genome.

CTATTTC GAM2022 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2022
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2022
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM2022 precursor RNA is designated SEQ ID:6313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6313 is located from position 47568406 to position 47568502 relative to chromosome 10 on the `+` strand.

GAM2022 precursor RNA folds onto itself, forming GAM2022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2022 precursor RNA, designated SEQ ID NO: 6313, and a schematic representation of a predicted secondary folding of GAM2022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2022 folded precursor RNA yielding a GAM2022 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2022 RNA, hereby incorporated herein.

GAM2022 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2022 target RNA, herein designated GAM TARGET RNA. GAM2022 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2022 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2022 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2022 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2022 RNA, herein designated GAM RNA, to target binding sites on GAM2022 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2022 target RNA into GAM2022 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2022 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2022 target genes. The mRNA of each one of this plurality of GAM2022 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2022 RNA, herein designated GAM RNA, and which when bound by GAM2022 RNA causes inhibition of translation of the GAM2022 target mRNA into a corresponding GAM2022 target protein.

The mechanism of the translational inhibition exerted by GAM2022 RNA, herein designated GAM RNA, on one or more GAM2022 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2022 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2022 RNA, herein designated GAM RNA, of GAM2022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2022 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2022 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2022 RNA correlate with, and may be deduced from, the identity of the GAM2022 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2027 6522 GCTACTTCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGTCCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTACTGCCA Messenger 2027 (GAM2027) oligonucleotides modulates expression of respective target genes
CAGAAGAGTC whose function and utility is known in the art.

TCAGCTCTCT GAM2027 is a novel bioinformatically detectable regulatory, non protein coding,
CCAGGATTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2027 was detected is

GTTCTAAGGT described with additional reference to Figs. 9-15.

CAGTGCCTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATAAAAATG encoded by the human genome.

GAGTGT GAM2027 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2027 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2027 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2027 precursor RNA is designated SEQ ID:6522, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6522 is located from position 3662454 to position 3662549 relative to chromosome 17 on the `-` strand.

GAM2027 precursor RNA folds onto itself, forming GAM2027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2027 precursor RNA, designated SEQ ID NO: 6522, and a schematic representation of a predicted secondary folding of GAM2027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2027 folded precursor RNA yielding a GAM2027 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2027 RNA, hereby incorporated herein.

GAM2027 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2027 target RNA, herein designated GAM TARGET RNA. GAM2027 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2027 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2027 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2027 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2027 RNA, herein designated GAM RNA, to target

binding sites on GAM2027 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2027 target RNA into GAM2027 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2027 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2027 target genes. The mRNA of each one of this plurality of GAM2027 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2027 RNA, herein designated GAM RNA, and which when bound by GAM2027 RNA causes inhibition of translation of the GAM2027 target mRNA into a corresponding GAM2027 target protein.

The mechanism of the translational inhibition exerted by GAM2027 RNA, herein designated GAM RNA, on one or more GAM2027 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2027 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2027 RNA, herein designated GAM RNA, of GAM2027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2027 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2027 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2027 RNA correlate with, and may be deduced from, the identity of the GAM2027 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2033 6291 GAAGAAGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATGGGTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGAGAGGGT Messenger 2033 (GAM2033) oligonucleotides modulates expression of respective target genes
TCCAATATTA whose function and utility is known in the art.

ACAACCCAAC GAM2033 is a novel bioinformatically detectable regulatory, non protein coding,
TTCAAGCTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2033 was detected is

TTCCTCTAAC described with additional reference to Figs. 9-15.

CTCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM2033 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2033 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2033 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2033 precursor RNA is designated SEQ ID:6291, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6291 is located from position 52243579 to position 52243654 relative to chromosome 1 on the `+` strand.

GAM2033 precursor RNA folds onto itself, forming GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2033 precursor RNA, designated SEQ ID NO: 6291, and a schematic representation of a predicted secondary folding of GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2033 folded precursor RNA yielding a GAM2033 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2033 RNA, hereby incorporated herein. Expression of GAM2033 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM2033 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2033 target RNA, herein designated GAM TARGET RNA. GAM2033 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2033 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2033 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2033 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2033 RNA, herein designated GAM RNA, to target binding sites on GAM2033 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2033 target RNA into GAM2033 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2033 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2033 target genes. The mRNA of each one of this plurality of GAM2033 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2033 RNA, herein designated GAM RNA, and which when bound by GAM2033 RNA causes inhibition of translation of the GAM2033 target mRNA into a corresponding GAM2033 target protein.

The mechanism of the translational inhibition exerted by GAM2033 RNA, herein designated GAM RNA, on one or more GAM2033 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2033 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2033 RNA, herein designated GAM RNA, of GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2033 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2033 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2033 RNA correlate with, and may be deduced from, the identity of the GAM2033 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2051 6003 CACTCTGTAA TAAAGAACTT GGAAAGGGAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 2051 (GAM2051) oligonucleotides modulates expression of respective target genes

GTTCCAAGAT whose function and utility is known in the art.

GGCCAAATAT GAM2051 is a novel bioinformatically detectable regulatory, non protein coding, GAACAGCTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2051 was detected is

AGTCTACAGC described with additional reference to Figs. 9-15.

CCCCAGCGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTG encoded by the human genome.

GAM2051 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2051 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2051 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2051 precursor RNA is designated SEQ ID:6003, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6003 is located from position 27725973 to position 27726056 relative to chromosome 11 on the `+` strand.

GAM2051 precursor RNA folds onto itself, forming GAM2051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2051 precursor RNA, designated SEQ ID NO: 6003, and a schematic representation of a predicted secondary folding of GAM2051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2051 folded precursor RNA yielding a GAM2051 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2051 RNA, hereby incorporated herein.

GAM2051 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2051 target RNA, herein designated GAM TARGET RNA. GAM2051 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2051 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2051 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2051 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2051 RNA, herein designated GAM RNA, to target binding sites on GAM2051 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2051 target RNA into GAM2051 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2051 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2051 target genes. The mRNA of each one of this plurality of GAM2051 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2051 RNA, herein designated GAM RNA, and which when bound by GAM2051 RNA causes inhibition of translation of the GAM2051 target mRNA into a corresponding GAM2051 target protein.

The mechanism of the translational inhibition exerted by GAM2051 RNA, herein designated GAM RNA, on one or more GAM2051 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2051 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2051 RNA, herein designated GAM RNA, of GAM2051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2051 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2051 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2051 RNA correlate with, and may be deduced from, the identity of the GAM2051 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2058 6568 GCTTTGAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGATGTGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGAAGACG Messenger 2058 (GAM2058) oligonucleotides modulates expression of respective target genes
AAGATGCCTT whose function and utility is known in the art.

TTGTTTGTCT GAM2058 is a novel bioinformatically detectable regulatory, non protein coding,
TTGGAGAATA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2058 was detected is

TTGCAACACT described with additional reference to Figs. 9-15.

ACAAAAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM2058 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2058

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2058
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2058 precursor RNA is designated SEQ ID:6568, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6568 is located from position 89111973 to position 89112050 relative to chromosome 15 on the `-` strand.

GAM2058 precursor RNA folds onto itself, forming GAM2058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2058 precursor RNA, designated SEQ ID NO: 6568, and a schematic representation of a predicted secondary folding of GAM2058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2058 folded precursor RNA yielding a GAM2058 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2058 RNA, hereby incorporated herein.

GAM2058 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2058 target RNA, herein designated GAM TARGET RNA. GAM2058 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2058 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2058 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2058 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2058 RNA, herein designated GAM RNA, to target binding sites on GAM2058 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2058 target RNA into GAM2058 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2058 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2058 target genes. The mRNA of each one of this plurality of GAM2058 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2058 RNA, herein designated GAM RNA, and which when bound by GAM2058 RNA causes inhibition of translation of the GAM2058 target mRNA into a corresponding GAM2058 target protein.

The mechanism of the translational inhibition exerted by GAM2058 RNA, herein designated GAM RNA, on one or more GAM2058 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2058 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2058 RNA, herein designated GAM RNA, of GAM2058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2058 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2058 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2058 RNA correlate with, and may be deduced from, the identity of the GAM2058 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2062 7236 TGGGCGCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TAATCTCAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TACTTGGGAG Messenger 2062 (GAM2062) oligonucleotides modulates expression of respective target genes

GCTGAGACAG whose function and utility is known in the art.

AGAATTGCTT GAM2062 is a novel bioinformatically detectable regulatory, non protein coding,

GAACCCAGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2062 was detected is

GGCGGAGGTT described with additional reference to Figs. 9-15.

GCAGTGAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TA encoded by the human genome.

GAM2062 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2062

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2062

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2062 precursor RNA is designated SEQ ID:7236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7236 is located from position 97732458 to position 97732539 relative to chromosome 13 on the `+` strand.

GAM2062 precursor RNA folds onto itself, forming GAM2062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2062 precursor RNA, designated SEQ ID NO: 7236, and a schematic representation of a predicted secondary folding of GAM2062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2062 folded precursor RNA yielding a GAM2062 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2062 RNA, hereby incorporated herein.

GAM2062 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2062 target RNA, herein designated GAM TARGET RNA. GAM2062 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2062 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2062 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2062 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2062 RNA, herein designated GAM RNA, to target binding sites on GAM2062 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2062 target RNA into GAM2062 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2062 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2062 target genes. The mRNA of each one of this plurality of GAM2062 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2062 RNA, herein designated GAM RNA, and which when bound by GAM2062 RNA causes inhibition of translation of the GAM2062 target mRNA into a corresponding GAM2062 target protein.

The mechanism of the translational inhibition exerted by GAM2062 RNA, herein designated GAM RNA, on one or more GAM2062 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2062 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2062 RNA, herein designated GAM RNA, of GAM2062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM2062 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2062 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2062 RNA correlate with, and may be deduced from, the identity of the GAM2062 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2098 6252 CTTCACCAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGTCATTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCACAGTTT Messenger 2098 (GAM2098) oligonucleotides modulates expression of respective target genes
GAGGAGTGTA whose function and utility is known in the art.

AGACAGTCAT GAM2098 is a novel bioinformatically detectable regulatory, non protein coding,
GCGGACTTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2098 was detected is

GGGGTACAAG described with additional reference to Figs. 9-15.

GGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM2098 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2098

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2098
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2098 precursor RNA is designated SEQ ID:6252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6252 is located from position 64216383 to position 64216457 relative to chromosome 15 on the `+` strand.

GAM2098 precursor RNA folds onto itself, forming GAM2098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2098 precursor RNA, designated SEQ ID NO: 6252, and a schematic representation of a predicted secondary folding of GAM2098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2098 folded precursor RNA yielding a GAM2098 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2098 RNA, hereby incorporated herein.

GAM2098 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2098 target RNA, herein designated GAM TARGET RNA. GAM2098 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2098 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2098 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2098 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2098 RNA, herein designated GAM RNA, to target binding sites on GAM2098 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2098 target RNA into GAM2098 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2098 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2098 target genes. The mRNA of each one of this plurality of GAM2098 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2098 RNA, herein designated GAM RNA, and which when bound by GAM2098 RNA causes inhibition of translation of the GAM2098 target mRNA into a corresponding GAM2098 target protein.

The mechanism of the translational inhibition exerted by GAM2098 RNA, herein designated GAM RNA, on one or more GAM2098 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2098 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2098 RNA, herein designated GAM RNA, of

GAM2098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2098 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2098 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2098 RNA correlate with, and may be deduced from, the identity of the GAM2098 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2171 6165 CTCCCAGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATATTCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATAGGCTGCC Messenger 2171 (GAM2171) oligonucleotides modulates expression of respective target genes

AGTTGGACTA whose function and utility is known in the art.

AGGAAGCCAC GAM2171 is a novel bioinformatically detectable regulatory, non protein coding,

TCCTGCGGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2171 was detected is

CCCTGGGAG described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2171 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2171

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2171

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2171 precursor RNA is designated SEQ ID:6165, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6165 is located from position 54026270 to position 54026338 relative to chromosome 8 on the `+` strand.

GAM2171 precursor RNA folds onto itself, forming GAM2171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2171 precursor RNA, designated SEQ ID NO: 6165, and a schematic representation of a predicted secondary folding of GAM2171 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2171 folded precursor RNA yielding a GAM2171 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2171 RNA, hereby incorporated herein.

GAM2171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2171 target RNA, herein designated GAM TARGET RNA. GAM2171 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2171 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2171 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2171 RNA, herein designated GAM RNA, to target binding sites on GAM2171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2171 target RNA into GAM2171 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2171 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2171 target genes. The mRNA of each one of this plurality of GAM2171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2171 RNA, herein designated GAM RNA, and which when bound by GAM2171 RNA causes inhibition of translation of the GAM2171 target mRNA into a corresponding GAM2171 target protein.

The mechanism of the translational inhibition exerted by GAM2171 RNA, herein designated GAM RNA, on one or more GAM2171 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2171 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM2171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2171 RNA, herein designated GAM RNA, of GAM2171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2171 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2171 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2171 RNA correlate with, and may be deduced from, the identity of the GAM2171 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2221 5975 ATGTCCAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCAACAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGACTACTT Messenger 2221 (GAM2221) oligonucleotides modulates expression of respective target genes

TTCTTCCACT whose function and utility is known in the art.

CATTTTAAAG GAM2221 is a novel bioinformatically detectable regulatory, non protein coding,

AAAAATGTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2221 was detected is

ATGAAGTGTT described with additional reference to Figs. 9-15.

TTGGATAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2221 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2221

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2221

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2221 precursor RNA is designated SEQ ID:5975, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5975 is located from position 13327337 to position 13327414 relative to chromosome 20 on the `+` strand.

GAM2221 precursor RNA folds onto itself, forming GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2221 precursor RNA, designated SEQ ID NO: 5975, and a schematic representation of a predicted secondary folding of GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2221 folded precursor RNA yielding a GAM2221 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2221 RNA, hereby incorporated herein.

GAM2221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2221 target RNA, herein designated GAM TARGET RNA. GAM2221 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2221 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2221 RNA, herein designated GAM RNA, to target binding sites on GAM2221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2221 target RNA into GAM2221 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2221 target genes. The mRNA of each one of this plurality of GAM2221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2221 RNA, herein designated GAM RNA, and which when bound by GAM2221 RNA causes inhibition of translation of the GAM2221 target mRNA into a corresponding GAM2221 target protein.

The mechanism of the translational inhibition exerted by GAM2221 RNA, herein designated GAM RNA, on one or more GAM2221 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2221 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2221 RNA, herein designated GAM RNA, of GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2221 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2221 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2221 RNA correlate with, and may be deduced from, the identity of the GAM2221 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2223 7077 TCTTACCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATCCTATT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCTCATACC Messenger 2223 (GAM2223) oligonucleotides modulates expression of respective target genes

TAAGGCAGTG whose function and utility is known in the art.

ATGGTTTCTC GAM2223 is a novel bioinformatically detectable regulatory, non protein coding,

AGACCTCTTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2223 was detected is

GATTGAGAAG described with additional reference to Figs. 9-15.

ATGTGGCATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTGTAAGG encoded by the human genome.

GAM2223 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2223

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2223

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2223 precursor RNA is designated SEQ ID:7077, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7077 is located from position 50175599 to position 50175687 relative to chromosome 20 on the `-` strand.

GAM2223 precursor RNA folds onto itself, forming GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2223 precursor RNA, designated SEQ ID NO: 7077, and a schematic representation of a predicted secondary folding of GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2223 folded precursor RNA yielding a GAM2223 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2223 RNA, hereby incorporated herein.

GAM2223 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2223 target RNA, herein designated GAM TARGET RNA. GAM2223 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2223 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2223 RNA, herein designated GAM RNA, to target binding sites on GAM2223 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2223 target RNA into GAM2223 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2223 target genes. The mRNA of each one of this plurality of GAM2223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2223 RNA, herein

designated GAM RNA, and which when bound by GAM2223 RNA causes inhibition of translation of the GAM2223 target mRNA into a corresponding GAM2223 target protein.

The mechanism of the translational inhibition exerted by GAM2223 RNA, herein designated GAM RNA, on one or more GAM2223 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2223 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2223 RNA, herein designated GAM RNA, of GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2223 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2223 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2223 RNA correlate with, and may be deduced from, the identity of the GAM2223 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2233 5810 AGTCTCTCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGCTGGACC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGACTGCAG Messenger 2233 (GAM2233) oligonucleotides modulates expression of respective target genes
TCACACTCTA whose function and utility is known in the art.

AGAGCTCCTC GAM2233 is a novel bioinformatically detectable regulatory, non protein coding,
TTTCTACACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2233 was detected is

TCTGCCAGTG described with additional reference to Figs. 9-15.

GGCGTTCGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGACAAG encoded by the human genome.

CT GAM2233 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2233
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2233

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2233 precursor RNA is designated SEQ ID:5810, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5810 is located from position 167487173 to position 167487264 relative to chromosome 6 on the `-` strand.

GAM2233 precursor RNA folds onto itself, forming GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2233 precursor RNA, designated SEQ ID NO: 5810, and a schematic representation of a predicted secondary folding of GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2233 folded precursor RNA yielding a GAM2233 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2233 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2233 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2233 target RNA, herein designated GAM TARGET RNA. GAM2233 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2233 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2233 RNA, herein designated GAM RNA, to target binding sites on GAM2233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2233 target RNA into GAM2233 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM2233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2233 target genes. The mRNA of each one of this plurality of GAM2233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2233 RNA, herein designated GAM RNA, and which when bound by GAM2233 RNA causes inhibition of translation of the GAM2233 target mRNA into a corresponding GAM2233 target protein.

The mechanism of the translational inhibition exerted by GAM2233 RNA, herein designated GAM RNA, on one or more GAM2233 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2233 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2233 RNA, herein designated GAM RNA, of GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2233 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2233 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2233 RNA correlate with, and may be deduced from, the identity of the GAM2233 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2251 7227 TGGCCTCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GACTCAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTCCTCTTT Messenger 2251 (GAM2251) oligonucleotides modulates expression of respective target genes

AAAATGGTGC whose function and utility is known in the art.

TAATAATAGC GAM2251 is a novel bioinformatically detectable regulatory, non protein coding,

ACCCACCCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2251 was detected is

TGTGAGGAGG described with additional reference to Figs. 9-15.

ATGCTGTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACAAAATGA encoded by the human genome.

GATCA GAM2251 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2251 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2251 precursor RNA is designated SEQ ID:7227, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7227 is located from position 17124868 to position 17124962 relative to chromosome 7 on the `+` strand.

GAM2251 precursor RNA folds onto itself, forming GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2251 precursor RNA, designated SEQ ID NO: 7227, and a schematic representation of a predicted secondary folding of GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2251 folded precursor RNA yielding a GAM2251 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2251 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2251 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2251 target RNA, herein designated GAM TARGET RNA. GAM2251 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2251 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2251 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2251 RNA, herein designated GAM RNA, to target binding sites on GAM2251 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2251 target RNA into GAM2251 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2251 target genes. The mRNA of each one of this plurality of GAM2251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2251 RNA, herein designated GAM RNA, and which when bound by GAM2251 RNA causes inhibition of translation of the GAM2251 target mRNA into a corresponding GAM2251 target protein.

The mechanism of the translational inhibition exerted by GAM2251 RNA, herein designated GAM RNA, on one or more GAM2251 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2251 RNA, herein designated GAM RNA, of GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2251 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2251 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2251 RNA correlate with, and may be deduced from, the identity of the GAM2251 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2260 6579 GGAAGCATCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGCTGCGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

CGCTTTCACT Messenger 2260 (GAM2260) oligonucleotides modulates expression of respective target genes

TCTAAAGAGT whose function and utility is known in the art.

CTTGTCTGCT GAM2260 is a novel bioinformatically detectable regulatory, non protein coding,

AATAAGAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2260 was detected is

CCCATGGCCC described with additional reference to Figs. 9-15.

AGGGTGGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGGGGGATT encoded by the human genome.

TAGAAAGGGC GAM2260 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2260

ATGATGATGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2260

CACTAGCGGC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TGCTTTC to the nucleotide sequence of GAM2260 precursor RNA is designated SEQ ID:6579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6579 is located from position 29926532 to position 29926658 relative to chromosome 10 on the `+` strand.

GAM2260 precursor RNA folds onto itself, forming GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2260 precursor RNA, designated SEQ ID NO: 6579, and a schematic representation of a predicted secondary folding of GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2260 folded precursor RNA yielding a GAM2260 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2260 RNA, hereby incorporated herein.

GAM2260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2260 target RNA, herein designated GAM TARGET RNA. GAM2260 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2260 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2260 RNA, herein designated GAM RNA, to target binding sites on GAM2260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2260 target RNA into GAM2260 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2260 target genes. The mRNA of each one of this plurality of GAM2260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2260 RNA, herein designated GAM RNA, and which when bound by GAM2260 RNA causes inhibition of translation of the GAM2260 target mRNA into a corresponding GAM2260 target protein.

The mechanism of the translational inhibition exerted by GAM2260 RNA, herein designated GAM RNA, on one or more GAM2260 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2260 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2260 RNA, herein designated GAM RNA, of GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2260 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2260 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2260 RNA correlate with, and may be deduced from, the identity of the GAM2260 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2262 5779 AGGCTGAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGATGATTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CTAGCTAGAG Messenger 2262 (GAM2262) oligonucleotides modulates expression of respective target genes
TCCAGGAGTT whose function and utility is known in the art.

CAGGATTAAA GAM2262 is a novel bioinformatically detectable regulatory, non protein coding,
ATGAGCTATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2262 was detected is

ATCATACCAC described with additional reference to Figs. 9-15.

TGCACTCCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCT encoded by the human genome.

GAM2262 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2262

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2262

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2262 precursor RNA is designated SEQ ID:5779, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5779 is located from position 42901138 to position 42901220 relative to chromosome 20 on the `+` strand.

GAM2262 precursor RNA folds onto itself, forming GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2262 precursor RNA, designated SEQ ID NO: 5779, and a schematic representation of a predicted secondary folding of GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2262 folded precursor RNA yielding a GAM2262 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2262 RNA, hereby incorporated herein.

GAM2262 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2262 target RNA, herein designated GAM TARGET RNA. GAM2262 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2262 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2262 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2262 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2262 RNA, herein designated GAM RNA, to target binding sites on GAM2262 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2262 target RNA into GAM2262 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2262 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2262 target genes. The mRNA of each one of this plurality of GAM2262 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2262 RNA, herein designated GAM RNA, and which when bound by GAM2262 RNA causes inhibition of translation of the GAM2262 target mRNA into a corresponding GAM2262 target protein.

The mechanism of the translational inhibition exerted by GAM2262 RNA, herein designated GAM RNA, on one or more GAM2262 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2262 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2262 RNA, herein designated GAM RNA, of GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2262 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2262 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2262 RNA correlate with, and may be deduced from, the identity of the GAM2262 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2263 5674 AATGAAGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCAAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCAAGAAAAT Messenger 2263 (GAM2263) oligonucleotides modulates expression of respective target genes
TTAGAATCGT whose function and utility is known in the art.

TTCTGATAGG GAM2263 is a novel bioinformatically detectable regulatory, non protein coding,
GACTTTCCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2263 was detected is

TATCCTAAAT described with additional reference to Figs. 9-15.

GTGTTTTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCACACGTT encoded by the human genome.

ATTTCCATTG GAM2263 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2263
TCATT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2263

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2263 precursor RNA is designated SEQ ID:5674, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5674 is located from position 40238503 to position 40238607 relative to chromosome 22 on the `-` strand.

GAM2263 precursor RNA folds onto itself, forming GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2263 precursor RNA, designated SEQ ID NO: 5674, and a schematic representation of a predicted secondary folding of GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2263 folded precursor RNA yielding a GAM2263 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2263 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2263 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2263 target RNA, herein designated GAM TARGET RNA. GAM2263 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2263 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2263 RNA, herein designated GAM RNA, to target binding sites on GAM2263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2263 target RNA into GAM2263 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2263 target genes. The mRNA of each one of this plurality of GAM2263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2263 RNA, herein designated GAM RNA, and which when bound by GAM2263 RNA causes inhibition of translation of the GAM2263 target mRNA into a corresponding GAM2263 target protein.

The mechanism of the translational inhibition exerted by GAM2263 RNA, herein designated GAM RNA, on one or more GAM2263 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2263 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2263 RNA, herein designated GAM RNA, of GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2263 target RNA, herein designated GAM

TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2263 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2263 RNA correlate with, and may be deduced from, the identity of the GAM2263 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2270 6896 GTGACTTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGTGTCACA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGTGAGTGG Messenger 2270 (GAM2270) oligonucleotides modulates expression of respective target genes
CATAATCAGA whose function and utility is known in the art.

GTACAATTTG GAM2270 is a novel bioinformatically detectable regulatory, non protein coding,
AGTCATGCCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2270 was detected is

ATACATCACA described with additional reference to Figs. 9-15.

TTGCCAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTACCCAAGG encoded by the human genome.

AAAGTGAC GAM2270 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2270
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2270
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2270 precursor RNA is designated SEQ ID:6896, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6896 is located from position 19237261 to position 19237358 relative to chromosome X on the `-` strand.

GAM2270 precursor RNA folds onto itself, forming GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2270 precursor RNA, designated SEQ ID NO: 6896, and a schematic representation of a predicted secondary folding of GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2270 folded precursor RNA yielding a GAM2270 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor

product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2270 RNA, hereby incorporated herein. Expression of GAM2270 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM2270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2270 target RNA, herein designated GAM TARGET RNA. GAM2270 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2270 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2270 RNA, herein designated GAM RNA, to target binding sites on GAM2270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2270 target RNA into GAM2270 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2270 target genes. The mRNA of each one of this plurality of GAM2270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2270 RNA, herein designated GAM RNA, and which when bound by GAM2270 RNA causes inhibition of translation of the GAM2270 target mRNA into a corresponding GAM2270 target protein.

The mechanism of the translational inhibition exerted by GAM2270 RNA, herein designated GAM RNA, on one or more GAM2270 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2270 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2270 RNA, herein designated GAM RNA, of GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2270 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2270 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2270 RNA correlate with, and may be deduced from, the identity of the GAM2270 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2272 5946 ATAAGCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTAATTGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAATTCACA Messenger 2272 (GAM2272) oligonucleotides modulates expression of respective target genes

TGTGGTTGTA whose function and utility is known in the art.

TGCAGCTTTA GAM2272 is a novel bioinformatically detectable regulatory, non protein coding,

CTGGGAGACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2272 was detected is

GAAGTGTATC described with additional reference to Figs. 9-15.

TGCATGTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGCTGTGA encoded by the human genome.

TGGACACTTG GAM2272 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2272

T precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2272

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2272 precursor RNA is designated SEQ ID:5946, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5946 is located from position 62131109 to position 62131209 relative to chromosome 9 on the `-` strand.

GAM2272 precursor RNA folds onto itself, forming GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2272 precursor RNA, designated SEQ ID NO: 5946, and a

schematic representation of a predicted secondary folding of GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2272 folded precursor RNA yielding a GAM2272 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2272 RNA, hereby incorporated herein.

GAM2272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2272 target RNA, herein designated GAM TARGET RNA. GAM2272 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2272 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2272 RNA, herein designated GAM RNA, to target binding sites on GAM2272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2272 target RNA into GAM2272 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2272 target genes. The mRNA of each one of this plurality of GAM2272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2272 RNA, herein designated GAM RNA, and which when bound by GAM2272 RNA causes inhibition of translation of the GAM2272 target mRNA into a corresponding GAM2272 target protein.

The mechanism of the translational inhibition exerted by GAM2272 RNA, herein designated GAM RNA, on one or more GAM2272 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2272 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2272 RNA, herein designated GAM RNA, of GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2272 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2272 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2272 RNA correlate with, and may be deduced from, the identity of the GAM2272 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2290 5685 ACACTGCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGATTGTTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTTGTCCAA Messenger 2290 (GAM2290) oligonucleotides modulates expression of respective target genes

GAGAGAGATC whose function and utility is known in the art.

ATGGAGAGAG GAM2290 is a novel bioinformatically detectable regulatory, non protein coding,

TCTCTCTCGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2290 was detected is

TCACGGAGGC described with additional reference to Figs. 9-15.

TCTGTCTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGGAGTATG encoded by the human genome.

TGT GAM2290 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2290

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2290

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2290 precursor RNA is designated SEQ ID:5685, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5685 is located from position 148621116 to position 148621208 relative to chromosome X on the `+` strand.

GAM2290 precursor RNA folds onto itself, forming GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2290 precursor RNA, designated SEQ ID NO: 5685, and a schematic representation of a predicted secondary folding of GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2290 folded precursor RNA yielding a GAM2290 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2290 RNA, hereby incorporated herein.

GAM2290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2290 target RNA, herein designated GAM TARGET RNA. GAM2290 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2290 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2290 RNA, herein designated GAM RNA, to target binding sites on GAM2290 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2290 target RNA into GAM2290 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2290 target genes. The mRNA of each one of this plurality of GAM2290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2290 RNA, herein designated GAM RNA, and which when bound by GAM2290 RNA causes inhibition of translation of the GAM2290 target mRNA into a corresponding GAM2290 target protein.

The mechanism of the translational inhibition exerted by GAM2290 RNA, herein

designated GAM RNA, on one or more GAM2290 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2290 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2290 RNA, herein designated GAM RNA, of GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2290 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2290 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2290 RNA correlate with, and may be deduced from, the identity of the GAM2290 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2300 5720 AGACAGTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGTCAAACA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCTTTATTT Messenger 2300 (GAM2300) oligonucleotides modulates expression of respective target genes
TAGCAGTTGT whose function and utility is known in the art.

GAGACCCTAG GAM2300 is a novel bioinformatically detectable regulatory, non protein coding,
AGAACTCCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2300 was detected is

TGGTGTTTTG described with additional reference to Figs. 9-15.

GGGTCTCCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCATGCACA encoded by the human genome.

ATGGGGGTTA GAM2300 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2300
TGCTAGCATC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2300
TCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2300 precursor RNA is designated SEQ ID:5720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5720 is located from position 22354493 to position 22354605 relative to chromosome 22

on the `-` strand.

GAM2300 precursor RNA folds onto itself, forming GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2300 precursor RNA, designated SEQ ID NO: 5720, and a schematic representation of a predicted secondary folding of GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2300 folded precursor RNA yielding a GAM2300 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2300 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2300 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2300 target RNA, herein designated GAM TARGET RNA. GAM2300 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2300 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2300 RNA, herein designated GAM RNA, to target binding sites on GAM2300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2300 target RNA into GAM2300 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2300 target genes. The mRNA of each one of this

plurality of GAM2300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2300 RNA, herein designated GAM RNA, and which when bound by GAM2300 RNA causes inhibition of translation of the GAM2300 target mRNA into a corresponding GAM2300 target protein.

The mechanism of the translational inhibition exerted by GAM2300 RNA, herein designated GAM RNA, on one or more GAM2300 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2300 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2300 RNA, herein designated GAM RNA, of GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2300 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2300 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2300 RNA correlate with, and may be deduced from, the identity of the GAM2300 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2306 7343 TTTGAGATTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TATTGAGTAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TACTAATCTT Messenger 2306 (GAM2306) oligonucleotides modulates expression of respective target genes
GACATATTTT whose function and utility is known in the art.

GGTTGGCACC GAM2306 is a novel bioinformatically detectable regulatory, non protein coding,
ACATTCTTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2306 was detected is

TATAGTGGGT described with additional reference to Figs. 9-15.

TAGTGGTTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAGTTTGCA encoded by the human genome.

GA GAM2306 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2306

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2306 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2306 precursor RNA is designated SEQ ID:7343, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7343 is located from position 78004552 to position 78004643 relative to chromosome 9 on the `+` strand.

GAM2306 precursor RNA folds onto itself, forming GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2306 precursor RNA, designated SEQ ID NO: 7343, and a schematic representation of a predicted secondary folding of GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2306 folded precursor RNA yielding a GAM2306 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2306 RNA, hereby incorporated herein.

GAM2306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2306 target RNA, herein designated GAM TARGET RNA. GAM2306 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2306 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2306 RNA, herein designated GAM RNA, to target binding sites on GAM2306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2306 target RNA

into GAM2306 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2306 target genes. The mRNA of each one of this plurality of GAM2306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2306 RNA, herein designated GAM RNA, and which when bound by GAM2306 RNA causes inhibition of translation of the GAM2306 target mRNA into a corresponding GAM2306 target protein.

The mechanism of the translational inhibition exerted by GAM2306 RNA, herein designated GAM RNA, on one or more GAM2306 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2306 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2306 RNA, herein designated GAM RNA, of GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2306 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2306 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2306 RNA correlate with, and may be deduced from, the identity of the GAM2306 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2309 6076 CCCCACCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGGAGCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTTCCAGTA Messenger 2309 (GAM2309) oligonucleotides modulates expression of respective target genes

GGTCTAAACT whose function and utility is known in the art.

GGTTTGATTG GAM2309 is a novel bioinformatically detectable regulatory, non protein coding,

AGTTCCATGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2309 was detected is

AAAACAACAA described with additional reference to Figs. 9-15.

AGTGGGGTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGG encoded by the human genome.

GAM2309 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2309 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2309 precursor RNA is designated SEQ ID:6076, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6076 is located from position 124008737 to position 124008820 relative to chromosome 9 on the `+` strand.

GAM2309 precursor RNA folds onto itself, forming GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2309 precursor RNA, designated SEQ ID NO: 6076, and a schematic representation of a predicted secondary folding of GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2309 folded precursor RNA yielding a GAM2309 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2309 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2309 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2309 target RNA, herein designated GAM TARGET RNA. GAM2309 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2309 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2309 RNA, herein designated GAM RNA, to target binding sites on GAM2309 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2309 target RNA into GAM2309 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2309 target genes. The mRNA of each one of this plurality of GAM2309 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2309 RNA, herein designated GAM RNA, and which when bound by GAM2309 RNA causes inhibition of translation of the GAM2309 target mRNA into a corresponding GAM2309 target protein.

The mechanism of the translational inhibition exerted by GAM2309 RNA, herein designated GAM RNA, on one or more GAM2309 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2309 RNA, herein designated GAM RNA, of GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2309 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2309 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2309 RNA correlate with, and may be deduced from, the identity of the GAM2309 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2350 5647 AAACGGATGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCTGGGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CACTTTGCAC Messenger 2350 (GAM2350) oligonucleotides modulates expression of respective target genes

AGGGTTCTCC whose function and utility is known in the art.

AGAGCCCTGC GAM2350 is a novel bioinformatically detectable regulatory, non protein coding,

CCATCCTGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2350 was detected is

TCCACCACTT described with additional reference to Figs. 9-15.

CCTGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2350 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2350

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2350

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2350 precursor RNA is designated SEQ ID:5647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5647 is located from position 47322081 to position 47322157 relative to chromosome 11 on the `+` strand.

GAM2350 precursor RNA folds onto itself, forming GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2350 precursor RNA, designated SEQ ID NO: 5647, and a schematic representation of a predicted secondary folding of GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2350 folded precursor RNA yielding a GAM2350 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2350 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2350 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2350 target RNA, herein designated GAM TARGET RNA. GAM2350 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2350 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2350 RNA, herein designated GAM RNA, to target binding sites on GAM2350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2350 target RNA into GAM2350 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2350 target genes. The mRNA of each one of this plurality of GAM2350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2350 RNA, herein designated GAM RNA, and which when bound by GAM2350 RNA causes inhibition of translation of the GAM2350 target mRNA into a corresponding GAM2350 target protein.

The mechanism of the translational inhibition exerted by GAM2350 RNA, herein designated GAM RNA, on one or more GAM2350 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2350 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2350 RNA, herein designated GAM RNA, of GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2350 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2350 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2350 RNA correlate with, and may be deduced from, the identity of the GAM2350 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2384 7017 TCATTCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAATCTTCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TAAAATGGAC Messenger 2384 (GAM2384) oligonucleotides modulates expression of respective target genes
AAGTATTCAT whose function and utility is known in the art.

TGAGCACCTA GAM2384 is a novel bioinformatically detectable regulatory, non protein coding,
ATGCGTGTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2384 was detected is

AGTATGGTGG described with additional reference to Figs. 9-15.

GAGATGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATGA encoded by the human genome.

GAM2384 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2384

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2384

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2384 precursor RNA is designated SEQ ID:7017, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7017 is located from position 35442640 to position 35442723 relative to chromosome 7 on the `+` strand.

GAM2384 precursor RNA folds onto itself, forming GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2384 precursor RNA, designated SEQ ID NO: 7017, and a schematic representation of a predicted secondary folding of GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2384 folded precursor RNA yielding a GAM2384 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2384 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2384 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2384 target RNA, herein designated GAM TARGET RNA. GAM2384 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN

CODING and 3`UTR respectively.

GAM2384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2384 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2384 RNA, herein designated GAM RNA, to target binding sites on GAM2384 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2384 target RNA into GAM2384 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2384 target genes. The mRNA of each one of this plurality of GAM2384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2384 RNA, herein designated GAM RNA, and which when bound by GAM2384 RNA causes inhibition of translation of the GAM2384 target mRNA into a corresponding GAM2384 target protein.

The mechanism of the translational inhibition exerted by GAM2384 RNA, herein designated GAM RNA, on one or more GAM2384 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2384 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2384 RNA, herein designated GAM RNA, of GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2384 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2384 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2384 RNA

correlate with, and may be deduced from, the identity of the GAM2384 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2391 6908 GTGCTGGGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AAACAGCCTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TATTTTAGCA Messenger 2391 (GAM2391) oligonucleotides modulates expression of respective target genes
GTTGTGAGAC whose function and utility is known in the art.

CCTAGAGAAC GAM2391 is a novel bioinformatically detectable regulatory, non protein coding,
TCCTTTGGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2391 was detected is

TTTTGGGGTC described with additional reference to Figs. 9-15.

TCCCCAGCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCACAATGGG encoded by the human genome.

GGTTATGCTA GAM2391 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2391
GCAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2391

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2391 precursor RNA is designated SEQ ID:6908, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6908 is located from position 22354497 to position 22354600 relative to chromosome 22 on the `-` strand.

GAM2391 precursor RNA folds onto itself, forming GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2391 precursor RNA, designated SEQ ID NO: 6908, and a schematic representation of a predicted secondary folding of GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2391 folded precursor RNA yielding a GAM2391 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2391 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2391 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2391 target RNA, herein designated GAM TARGET RNA. GAM2391 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2391 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2391 RNA, herein designated GAM RNA, to target binding sites on GAM2391 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2391 target RNA into GAM2391 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2391 target genes. The mRNA of each one of this plurality of GAM2391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2391 RNA, herein designated GAM RNA, and which when bound by GAM2391 RNA causes inhibition of translation of the GAM2391 target mRNA into a corresponding GAM2391 target protein.

The mechanism of the translational inhibition exerted by GAM2391 RNA, herein designated GAM RNA, on one or more GAM2391 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2391 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2391 RNA, herein designated GAM RNA, of GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM2391 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2391 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2391 RNA correlate with, and may be deduced from, the identity of the GAM2391 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2393 5830 AGTTTGGGTA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGAAGCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAGATTTGC Messenger 2393 (GAM2393) oligonucleotides modulates expression of respective target genes
TGATACATTT whose function and utility is known in the art.

GCTAGGCACG GAM2393 is a novel bioinformatically detectable regulatory, non protein coding,
ACTTCTGGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2393 was detected is

ATTTAGAAAG described with additional reference to Figs. 9-15.

CTATTTTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTTCATCAA encoded by the human genome.

TAAGGTATTC GAM2393 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2393
CCCAGCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2393
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2393 precursor RNA is designated SEQ ID:5830, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5830 is located from position 99981233 to position 99981339 relative to chromosome 3 on the `+` strand.

GAM2393 precursor RNA folds onto itself, forming GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2393 precursor RNA, designated SEQ ID NO: 5830, and a schematic representation of a predicted secondary folding of GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2393 folded precursor RNA yielding a GAM2393 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2393 RNA, hereby incorporated herein.

GAM2393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2393 target RNA, herein designated GAM TARGET RNA. GAM2393 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2393 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2393 RNA, herein designated GAM RNA, to target binding sites on GAM2393 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2393 target RNA into GAM2393 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2393 target genes. The mRNA of each one of this plurality of GAM2393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2393 RNA, herein designated GAM RNA, and which when bound by GAM2393 RNA causes inhibition of translation of the GAM2393 target mRNA into a corresponding GAM2393 target protein.

The mechanism of the translational inhibition exerted by GAM2393 RNA, herein designated GAM RNA, on one or more GAM2393 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2393 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2393 RNA, herein designated GAM RNA, of

GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2393 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2393 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2393 RNA correlate with, and may be deduced from, the identity of the GAM2393 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2398 5666 AAGCCCTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGGCTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCCTTTCTC Messenger 2398 (GAM2398) oligonucleotides modulates expression of respective target genes

TCAGAGATGC whose function and utility is known in the art.

CCTGCCCAGT GAM2398 is a novel bioinformatically detectable regulatory, non protein coding,

GAGGAGGAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2398 was detected is

CTAGAGAGGC described with additional reference to Figs. 9-15.

AGTCTGGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGTTGCTT encoded by the human genome.

GAM2398 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2398

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2398

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2398 precursor RNA is designated SEQ ID:5666, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5666 is located from position 63185944 to position 63186032 relative to chromosome 11 on the `-` strand.

GAM2398 precursor RNA folds onto itself, forming GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2398 precursor RNA, designated SEQ ID NO: 5666, and a schematic representation of a predicted secondary folding of GAM2398 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2398 folded precursor RNA yielding a GAM2398 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2398 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2398 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2398 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2398 target RNA, herein designated GAM TARGET RNA. GAM2398 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2398 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2398 RNA, herein designated GAM RNA, to target binding sites on GAM2398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2398 target RNA into GAM2398 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2398 target genes. The mRNA of each one of this plurality of GAM2398 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2398 RNA, herein designated GAM RNA, and which when bound by GAM2398 RNA causes inhibition of translation of the GAM2398 target mRNA into a corresponding GAM2398 target protein.

The mechanism of the translational inhibition exerted by GAM2398 RNA, herein designated GAM RNA, on one or more GAM2398 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2398 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2398 RNA, herein designated GAM RNA, of GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2398 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2398 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2398 RNA correlate with, and may be deduced from, the identity of the GAM2398 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2424 7052 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTAGTAG Messenger 2424 (GAM2424) oligonucleotides modulates expression of respective target genes

TGAGCTGAAG whose function and utility is known in the art.

TCCCGCCACT GAM2424 is a novel bioinformatically detectable regulatory, non protein coding,

GCACTCCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2424 was detected is

CTGGGCAACA described with additional reference to Figs. 9-15.

GAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2424 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2424

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2424

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2424 precursor RNA is designated SEQ ID:7052, and is provided hereinbelow with reference to the sequence listing part.

GAM2424 precursor RNA folds onto itself, forming GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2424 precursor RNA, designated SEQ ID NO: 7052, and a schematic representation of a predicted secondary folding of GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2424 folded precursor RNA yielding a GAM2424 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2424 RNA, hereby incorporated herein. Expression of GAM2424 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM2424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2424 target RNA, herein designated GAM TARGET RNA. GAM2424 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2424 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2424 RNA, herein designated GAM RNA, to target binding sites on GAM2424 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2424 target RNA into GAM2424 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2424 target genes. The mRNA of each one of this plurality of GAM2424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2424 RNA, herein designated GAM RNA, and which when bound by GAM2424 RNA causes inhibition of translation of the GAM2424 target mRNA into a corresponding GAM2424 target protein.

The mechanism of the translational inhibition exerted by GAM2424 RNA, herein

designated GAM RNA, on one or more GAM2424 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2424 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2424 RNA, herein designated GAM RNA, of GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2424 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2424 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2424 RNA correlate with, and may be deduced from, the identity of the GAM2424 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2440 7311 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAAGAGGCG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 2440 (GAM2440) oligonucleotides modulates expression of respective target genes

TGAGCTAAGA whose function and utility is known in the art.

TCATGCCACT GAM2440 is a novel bioinformatically detectable regulatory, non protein coding,

GCACTCCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2440 was detected is

CTGGGTGACA described with additional reference to Figs. 9-15.

GAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2440

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2440

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2440 precursor RNA is designated SEQ ID:7311, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7311 is located from position 29072015 to position 29072090 relative to chromosome 14

on the `+` strand.

GAM2440 precursor RNA folds onto itself, forming GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2440 precursor RNA, designated SEQ ID NO: 7311, and a schematic representation of a predicted secondary folding of GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2440 folded precursor RNA yielding a GAM2440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2440 RNA, hereby incorporated herein.

GAM2440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2440 target RNA, herein designated GAM TARGET RNA. GAM2440 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2440 RNA, herein designated GAM RNA, to target binding sites on GAM2440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2440 target RNA into GAM2440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2440 target genes. The mRNA of each one of this plurality of GAM2440 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM2440 RNA, herein designated GAM RNA, and which when bound by GAM2440 RNA causes inhibition of translation of the GAM2440 target mRNA into a corresponding GAM2440 target protein.

The mechanism of the translational inhibition exerted by GAM2440 RNA, herein designated GAM RNA, on one or more GAM2440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2440 RNA, herein designated GAM RNA, of GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2440 RNA correlate with, and may be deduced from, the identity of the GAM2440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2514 7214 TGGAACTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAGCTGTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGTCAGCC Messenger 2514 (GAM2514) oligonucleotides modulates expression of respective target genes
TGAAATAATC whose function and utility is known in the art.

AAAAGGATCA GAM2514 is a novel bioinformatically detectable regulatory, non protein coding,
AAAATCCTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2514 was detected is

TTTAGGCAAC described with additional reference to Figs. 9-15.

ATAGGAAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCAACTCTA encoded by the human genome.

GAM2514 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2514

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2514

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2514 precursor RNA is designated SEQ ID:7214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7214 is located from position 93198982 to position 93199071 relative to chromosome 1 on the `+` strand.

GAM2514 precursor RNA folds onto itself, forming GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2514 precursor RNA, designated SEQ ID NO: 7214, and a schematic representation of a predicted secondary folding of GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2514 folded precursor RNA yielding a GAM2514 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2514 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2514 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2514 target RNA, herein designated GAM TARGET RNA. GAM2514 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2514 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2514 RNA, herein designated GAM RNA, to target binding sites on GAM2514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2514 target RNA into GAM2514 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM2514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2514 target genes. The mRNA of each one of this plurality of GAM2514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2514 RNA, herein designated GAM RNA, and which when bound by GAM2514 RNA causes inhibition of translation of the GAM2514 target mRNA into a corresponding GAM2514 target protein.

The mechanism of the translational inhibition exerted by GAM2514 RNA, herein designated GAM RNA, on one or more GAM2514 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2514 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2514 RNA, herein designated GAM RNA, of GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2514 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2514 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2514 RNA correlate with, and may be deduced from, the identity of the GAM2514 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2519 5968 ATGATGCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GACTGCAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGGGACTT Messenger 2519 (GAM2519) oligonucleotides modulates expression of respective target genes

GTGGCAGATG whose function and utility is known in the art.

CACAGGGTGC GAM2519 is a novel bioinformatically detectable regulatory, non protein coding,

CTCTGGCTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2519 was detected is

CTGGAGCTCC described with additional reference to Figs. 9-15.

ACACTGCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCAGCTCTG encoded by the human genome.

T GAM2519 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2519 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2519 precursor RNA is designated SEQ ID:5968, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5968 is located from position 80675207 to position 80675297 relative to chromosome 10 on the `+` strand.

GAM2519 precursor RNA folds onto itself, forming GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2519 precursor RNA, designated SEQ ID NO: 5968, and a schematic representation of a predicted secondary folding of GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2519 folded precursor RNA yielding a GAM2519 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2519 RNA, hereby incorporated herein.

GAM2519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2519 target RNA, herein designated GAM TARGET RNA. GAM2519 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2519 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2519 RNA, herein designated GAM RNA, to target binding sites on GAM2519 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2519 target RNA into GAM2519 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2519 target genes. The mRNA of each one of this plurality of GAM2519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2519 RNA, herein designated GAM RNA, and which when bound by GAM2519 RNA causes inhibition of translation of the GAM2519 target mRNA into a corresponding GAM2519 target protein.

The mechanism of the translational inhibition exerted by GAM2519 RNA, herein designated GAM RNA, on one or more GAM2519 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2519 RNA, herein designated GAM RNA, of GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2519 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2519 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2519 RNA correlate with, and may be deduced from, the identity of the GAM2519 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2543 7207 TGCTGTAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTATGCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAATGCTAAT Messenger 2543 (GAM2543) oligonucleotides modulates expression of respective target genes
CGTGATAGGG whose function and utility is known in the art.

GTTTTTGCCT GAM2543 is a novel bioinformatically detectable regulatory, non protein coding,
CCAACTGACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2543 was detected is

CCTACATATT described with additional reference to Figs. 9-15.

AGCATTAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGTATGATG encoded by the human genome.

CCTGTTACTA GAM2543 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2543

GCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2543

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2543 precursor RNA is designated SEQ ID:7207, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7207 is located from position 25868146 to position 25868248 relative to chromosome 21 on the `+` strand.

GAM2543 precursor RNA folds onto itself, forming GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2543 precursor RNA, designated SEQ ID NO: 7207, and a schematic representation of a predicted secondary folding of GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2543 folded precursor RNA yielding a GAM2543 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2543 RNA, hereby incorporated herein.

GAM2543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2543 target RNA, herein designated GAM TARGET RNA. GAM2543 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2543 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2543 RNA, herein designated GAM RNA, to target binding sites on GAM2543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2543 target RNA into GAM2543 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2543 target genes. The mRNA of each one of this plurality of GAM2543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2543 RNA, herein designated GAM RNA, and which when bound by GAM2543 RNA causes inhibition of translation of the GAM2543 target mRNA into a corresponding GAM2543 target protein.

The mechanism of the translational inhibition exerted by GAM2543 RNA, herein designated GAM RNA, on one or more GAM2543 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2543 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2543 RNA, herein designated GAM RNA, of GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2543 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2543 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2543 RNA correlate with, and may be deduced from, the identity of the GAM2543 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2565 6361 GAGCCTTTTA ATGACACAGT GGGGCCAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 2565 (GAM2565) oligonucleotides modulates expression of respective target genes

GGAGCACTGA whose function and utility is known in the art.

TCCTGGTCAT GAM2565 is a novel bioinformatically detectable regulatory, non protein coding,
TACTCCTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2565 was detected is

CCCTGGCCTG described with additional reference to Figs. 9-15.

CAGCCTTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCAGTGTCT encoded by the human genome.

TATTTGGGCT GAM2565 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2565
T precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2565
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2565 precursor RNA is designated SEQ ID:6361, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6361 is located from position 17811037 to position 17811137 relative to chromosome 22 on the `-` strand.

GAM2565 precursor RNA folds onto itself, forming GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2565 precursor RNA, designated SEQ ID NO: 6361, and a schematic representation of a predicted secondary folding of GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2565 folded precursor RNA yielding a GAM2565 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2565 RNA, hereby incorporated herein.

GAM2565 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2565 target RNA, herein designated GAM TARGET RNA. GAM2565 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2565 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2565 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2565 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2565 RNA, herein designated GAM RNA, to target binding sites on GAM2565 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2565 target RNA into GAM2565 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2565 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2565 target genes. The mRNA of each one of this plurality of GAM2565 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2565 RNA, herein designated GAM RNA, and which when bound by GAM2565 RNA causes inhibition of translation of the GAM2565 target mRNA into a corresponding GAM2565 target protein.

The mechanism of the translational inhibition exerted by GAM2565 RNA, herein designated GAM RNA, on one or more GAM2565 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2565 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2565 RNA, herein designated GAM RNA, of GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2565 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2565 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2565 RNA correlate with, and may be deduced from, the identity of the GAM2565 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2591 6099 CCGGTAGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGAATGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTGTGTCAC Messenger 2591 (GAM2591) oligonucleotides modulates expression of respective target genes

TGTGGTATTA whose function and utility is known in the art.

CGATATTTTG GAM2591 is a novel bioinformatically detectable regulatory, non protein coding,

ACTGGTTATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2591 was detected is

ATAACCACAG described with additional reference to Figs. 9-15.

TGTCACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCATCAAAA encoded by the human genome.

ACCCATGCCT GAM2591 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2591

GG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2591

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2591 precursor RNA is designated SEQ ID:6099, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6099 is located from position 104342178 to position 104342279 relative to chromosome 14 on the `-` strand.

GAM2591 precursor RNA folds onto itself, forming GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2591 precursor RNA, designated SEQ ID NO: 6099, and a schematic representation of a predicted secondary folding of GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2591 folded precursor RNA yielding a GAM2591 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2591 RNA, hereby incorporated herein.

GAM2591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2591 target RNA, herein designated GAM TARGET RNA. GAM2591 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2591 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2591 RNA, herein designated GAM RNA, to target binding sites on GAM2591 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2591 target RNA into GAM2591 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2591 target genes. The mRNA of each one of this plurality of GAM2591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2591 RNA, herein designated GAM RNA, and which when bound by GAM2591 RNA causes inhibition of translation of the GAM2591 target mRNA into a corresponding GAM2591 target protein.

The mechanism of the translational inhibition exerted by GAM2591 RNA, herein designated GAM RNA, on one or more GAM2591 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2591 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2591 RNA, herein designated GAM RNA, of GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2591 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2591 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2591 RNA correlate with, and may be deduced from, the identity of the GAM2591 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2608 6276 CTTTTGAGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTTCTTATA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGTGTCTCT Messenger 2608 (GAM2608) oligonucleotides modulates expression of respective target genes
TGTGTTAAGG whose function and utility is known in the art.

TGCATCTAGT GAM2608 is a novel bioinformatically detectable regulatory, non protein coding,
GCAGTTAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2608 was detected is

AAGCAGCTTA described with additional reference to Figs. 9-15.

GAATCTACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCCTAAATGC encoded by the human genome.

CCCTTCTGGC GAM2608 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2608
ACAGGCTGCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2608
TAATATACAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CATTTTAAAA to the nucleotide sequence of GAM2608 precursor RNA is designated SEQ ID:6276, and is

G provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6276 is located from position 131249037 to position 131249167 relative to chromosome X on the `-` strand.

GAM2608 precursor RNA folds onto itself, forming GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2608 precursor RNA, designated SEQ ID NO: 6276, and a schematic representation of a predicted secondary folding of GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2608 folded precursor RNA yielding a GAM2608 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM2608 RNA, hereby incorporated herein. Expression of GAM2608 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM2608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2608 target RNA, herein designated GAM TARGET RNA. GAM2608 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2608 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2608 RNA, herein designated GAM RNA, to target binding sites on GAM2608 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2608 target RNA into GAM2608 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2608 target genes. The mRNA of each one of this plurality of GAM2608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2608 RNA, herein designated GAM RNA, and which when bound by GAM2608 RNA causes inhibition of translation of the GAM2608 target mRNA into a corresponding GAM2608 target protein.

The mechanism of the translational inhibition exerted by GAM2608 RNA, herein designated GAM RNA, on one or more GAM2608 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2608 RNA, herein designated GAM RNA, of GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2608 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2608 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2608 RNA correlate with, and may be deduced from, the identity of the GAM2608 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2618 7275 TGTGGGAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCTGGCAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGCTGGAGG Messenger 2618 (GAM2618) oligonucleotides modulates expression of respective target genes
GCCCTGGAGG whose function and utility is known in the art.

CAAAGGGCCT GAM2618 is a novel bioinformatically detectable regulatory, non protein coding,
GCCTCGACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2618 was detected is

TGCCCCCCAT described with additional reference to Figs. 9-15.

AACCCACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM2618 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2618

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2618
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2618 precursor RNA is designated SEQ ID:7275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7275 is located from position 10351230 to position 10351307 relative to chromosome 19 on the `+` strand.

GAM2618 precursor RNA folds onto itself, forming GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2618 precursor RNA, designated SEQ ID NO: 7275, and a schematic representation of a predicted secondary folding of GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2618 folded precursor RNA yielding a GAM2618 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2618 RNA, hereby incorporated herein.

GAM2618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2618 target RNA, herein designated GAM TARGET RNA. GAM2618 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2618 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2618 RNA, herein designated GAM RNA, to target binding sites on GAM2618 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2618 target RNA into GAM2618 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2618 target genes. The mRNA of each one of this plurality of GAM2618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2618 RNA, herein designated GAM RNA, and which when bound by GAM2618 RNA causes inhibition of translation of the GAM2618 target mRNA into a corresponding GAM2618 target protein.

The mechanism of the translational inhibition exerted by GAM2618 RNA, herein designated GAM RNA, on one or more GAM2618 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2618 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2618 RNA, herein designated GAM RNA, of GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2618 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2618 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2618 RNA correlate with, and may be deduced from, the identity of the GAM2618 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2624 5958 ATCGTCTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCAGGAGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGGCTGCA Messenger 2624 (GAM2624) oligonucleotides modulates expression of respective target genes

GTGAGCTACA whose function and utility is known in the art.

ATCACACCCC GAM2624 is a novel bioinformatically detectable regulatory, non protein coding,

TGCACTCAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2624 was detected is

CCTGGGTTAC described with additional reference to Figs. 9-15.

AGAGTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2624 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2624

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2624

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2624 precursor RNA is designated SEQ ID:5958, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5958 is located from position 128731509 to position 128731586 relative to chromosome X on the `-` strand.

GAM2624 precursor RNA folds onto itself, forming GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2624 precursor RNA, designated SEQ ID NO: 5958, and a schematic representation of a predicted secondary folding of GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2624 folded precursor RNA yielding a GAM2624 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2624 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2624 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2624 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2624 target RNA, herein designated GAM TARGET RNA. GAM2624 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2624 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2624 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2624 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2624 RNA, herein designated GAM RNA, to target binding sites on GAM2624 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2624 target RNA into GAM2624 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2624 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2624 target genes. The mRNA of each one of this plurality of GAM2624 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2624 RNA, herein designated GAM RNA, and which when bound by GAM2624 RNA causes inhibition of translation of the GAM2624 target mRNA into a corresponding GAM2624 target protein.

The mechanism of the translational inhibition exerted by GAM2624 RNA, herein designated GAM RNA, on one or more GAM2624 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2624 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2624 RNA, herein designated GAM RNA, of GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2624 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2624 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2624 RNA correlate with, and may be deduced from, the identity of the GAM2624 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2628 6901 GTGCACTACA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACTCCAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCCTTTGAA Messenger 2628 (GAM2628) oligonucleotides modulates expression of respective target genes

GCCAGGTTCC whose function and utility is known in the art.

AGAGCTTCCT GAM2628 is a novel bioinformatically detectable regulatory, non protein coding,

CCCTTTGGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2628 was detected is

TGGAACCTCA described with additional reference to Figs. 9-15.

ACAGCAGGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGGATGAGG encoded by the human genome.

ATGGAAGTGT GAM2628 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2628

AC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2628

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2628 precursor RNA is designated SEQ ID:6901, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6901 is located from position 15653139 to position 15653240 relative to chromosome 17 on the `-` strand.

GAM2628 precursor RNA folds onto itself, forming GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2628 precursor RNA, designated SEQ ID NO: 6901, and a schematic representation of a predicted secondary folding of GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2628 folded precursor RNA yielding a GAM2628 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2628 RNA, hereby incorporated herein.

GAM2628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2628 target RNA, herein designated GAM TARGET RNA. GAM2628 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2628 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2628 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2628 RNA, herein designated GAM RNA, to target binding sites on GAM2628 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2628 target RNA into GAM2628 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2628 target genes. The mRNA of each one of this plurality of GAM2628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2628 RNA, herein designated GAM RNA, and which when bound by GAM2628 RNA causes inhibition of translation

of the GAM2628 target mRNA into a corresponding GAM2628 target protein.

The mechanism of the translational inhibition exerted by GAM2628 RNA, herein designated GAM RNA, on one or more GAM2628 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2628 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2628 RNA, herein designated GAM RNA, of GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2628 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2628 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2628 RNA correlate with, and may be deduced from, the identity of the GAM2628 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2631 7210 TGCTTCCTTA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTACAAGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
AATTTAGAAG Messenger 2631 (GAM2631) oligonucleotides modulates expression of respective target genes
TTGGTGCAAA whose function and utility is known in the art.

TGGCATTTCC GAM2631 is a novel bioinformatically detectable regulatory, non protein coding,
ATGAGTACTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2631 was detected is

CTCATGCATC described with additional reference to Figs. 9-15.

TTTGCATATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCACCTGGGG encoded by the human genome.

GGAAGCA GAM2631 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2631
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2631
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM2631 precursor RNA is designated SEQ ID:7210, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7210 is located from position 8927224 to position 8927320 relative to chromosome 8 on the `+` strand.

GAM2631 precursor RNA folds onto itself, forming GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2631 precursor RNA, designated SEQ ID NO: 7210, and a schematic representation of a predicted secondary folding of GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2631 folded precursor RNA yielding a GAM2631 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2631 RNA, hereby incorporated herein.

GAM2631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2631 target RNA, herein designated GAM TARGET RNA. GAM2631 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2631 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2631 RNA, herein designated GAM RNA, to target binding sites on GAM2631 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2631 target RNA into GAM2631 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2631 target genes. The mRNA of each one of this plurality of GAM2631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2631 RNA, herein designated GAM RNA, and which when bound by GAM2631 RNA causes inhibition of translation of the GAM2631 target mRNA into a corresponding GAM2631 target protein.

The mechanism of the translational inhibition exerted by GAM2631 RNA, herein designated GAM RNA, on one or more GAM2631 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2631 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2631 RNA, herein designated GAM RNA, of GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2631 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2631 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2631 RNA correlate with, and may be deduced from, the identity of the GAM2631 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2640 7260 TGGTTTCATT Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAATGTGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTTGGCTG Messenger 2640 (GAM2640) oligonucleotides modulates expression of respective target genes

GGTGCAGTAA whose function and utility is known in the art.

CTCATGCCTG GAM2640 is a novel bioinformatically detectable regulatory, non protein coding,

TAATCCCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2640 was detected is

ATTTTAGGAG described with additional reference to Figs. 9-15.

ACCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2640 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2640 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2640 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2640 precursor RNA is designated SEQ ID:7260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7260 is located from position 13483969 to position 13484042 relative to chromosome 10 on the `-` strand.

GAM2640 precursor RNA folds onto itself, forming GAM2640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2640 precursor RNA, designated SEQ ID NO: 7260, and a schematic representation of a predicted secondary folding of GAM2640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2640 folded precursor RNA yielding a GAM2640 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2640 RNA, hereby incorporated herein.

GAM2640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2640 target RNA, herein designated GAM TARGET RNA. GAM2640 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2640 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2640 RNA, herein designated GAM RNA, to target

binding sites on GAM2640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2640 target RNA into GAM2640 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2640 target genes. The mRNA of each one of this plurality of GAM2640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2640 RNA, herein designated GAM RNA, and which when bound by GAM2640 RNA causes inhibition of translation of the GAM2640 target mRNA into a corresponding GAM2640 target protein.

The mechanism of the translational inhibition exerted by GAM2640 RNA, herein designated GAM RNA, on one or more GAM2640 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2640 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2640 RNA, herein designated GAM RNA, of GAM2640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2640 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2640 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2640 RNA correlate with, and may be deduced from, the identity of the GAM2640 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2672 6512 GCCTGCGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TATTGTAGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACGCTGCGCT Messenger 2672 (GAM2672) oligonucleotides modulates expression of respective target genes
GCCTATCACA whose function and utility is known in the art.

GCTTGTGATG GAM2672 is a novel bioinformatically detectable regulatory, non protein coding,
TGACACGTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2672 was detected is

ATTCTGCAAG described with additional reference to Figs. 9-15.

TTTAAACTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCTAGGT encoded by the human genome.

GAM2672 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2672 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2672 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2672 precursor RNA is designated SEQ ID:6512, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6512 is located from position 97817966 to position 97818053 relative to chromosome 13 on the `+` strand.

GAM2672 precursor RNA folds onto itself, forming GAM2672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2672 precursor RNA, designated SEQ ID NO: 6512, and a schematic representation of a predicted secondary folding of GAM2672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2672 folded precursor RNA yielding a GAM2672 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2672 RNA, hereby incorporated herein.

GAM2672 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2672 target RNA, herein designated GAM TARGET RNA. GAM2672 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2672 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2672 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2672 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2672 RNA, herein designated GAM RNA, to target binding sites on GAM2672 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2672 target RNA into GAM2672 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2672 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2672 target genes. The mRNA of each one of this plurality of GAM2672 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2672 RNA, herein designated GAM RNA, and which when bound by GAM2672 RNA causes inhibition of translation of the GAM2672 target mRNA into a corresponding GAM2672 target protein.

The mechanism of the translational inhibition exerted by GAM2672 RNA, herein designated GAM RNA, on one or more GAM2672 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2672 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2672 RNA, herein designated GAM RNA, of GAM2672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2672 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2672 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2672 RNA correlate with, and may be deduced from, the identity of the GAM2672 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2732 6840 GGTCTGTGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGCATCACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCAGGGAT Messenger 2732 (GAM2732) oligonucleotides modulates expression of respective target genes
TACTAATGGT whose function and utility is known in the art.

GGGGCAGCAG GAM2732 is a novel bioinformatically detectable regulatory, non protein coding, GTCTGTGAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2732 was detected is

TAAGTTATCT described with additional reference to Figs. 9-15.

CTTGACCTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCTCATGTC encoded by the human genome.

AACACAAATG GAM2732 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2732

TAATTCCTAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2732

ACAAGATGCA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar TTGCCAGTCT to the nucleotide sequence of GAM2732 precursor RNA is designated SEQ ID:6840, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6840 is located from position 49257580 to position 49257709 relative to chromosome 7 on the `-` strand.

GAM2732 precursor RNA folds onto itself, forming GAM2732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2732 precursor RNA, designated SEQ ID NO: 6840, and a schematic representation of a predicted secondary folding of GAM2732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2732 folded precursor RNA yielding a GAM2732 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2732 RNA, hereby incorporated herein.

GAM2732 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2732 target RNA, herein designated GAM TARGET RNA. GAM2732 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2732 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2732 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2732 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2732 RNA, herein designated GAM RNA, to target binding sites on GAM2732 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2732 target RNA into GAM2732 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2732 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2732 target genes. The mRNA of each one of this plurality of GAM2732 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2732 RNA, herein designated GAM RNA, and which when bound by GAM2732 RNA causes inhibition of translation of the GAM2732 target mRNA into a corresponding GAM2732 target protein.

The mechanism of the translational inhibition exerted by GAM2732 RNA, herein designated GAM RNA, on one or more GAM2732 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2732 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2732 RNA, herein designated GAM RNA, of GAM2732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2732 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2732 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2732 RNA correlate with, and may be deduced from, the identity of the GAM2732 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2762 6255 CTTCTCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCCTTCACA detected oligonucleotides of the present invention, referred to here as Genomic Address
CACAGTCGTG Messenger 2762 (GAM2762) oligonucleotides modulates expression of respective target genes
TAGTTTTGCG whose function and utility is known in the art.

CTTGCTTGAT GAM2762 is a novel bioinformatically detectable regulatory, non protein coding,
TAATCTCTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2762 was detected is

GCCTCAGTCG described with additional reference to Figs. 9-15.

GTTTTCTACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATATGGAGTT encoded by the human genome.

GGTTCATTCT GAM2762 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2762
CTCGAATGGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2762
TGTGTAGTCC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
AGTGTGTGGG to the nucleotide sequence of GAM2762 precursor RNA is designated SEQ ID:6255, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6255 is located from position 110144402 to position 110144531 relative to chromosome 13 on the `-` strand.

GAM2762 precursor RNA folds onto itself, forming GAM2762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2762 precursor RNA, designated SEQ ID NO: 6255, and a schematic representation of a predicted secondary folding of GAM2762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2762 folded precursor RNA yielding a GAM2762 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2762 RNA, hereby incorporated herein.

GAM2762 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2762 target RNA, herein designated GAM TARGET RNA. GAM2762 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2762 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2762 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2762 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2762 RNA, herein designated GAM RNA, to target binding sites on GAM2762 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2762 target RNA into GAM2762 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2762 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2762 target genes. The mRNA of each one of this plurality of GAM2762 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2762 RNA, herein designated GAM RNA, and which when bound by GAM2762 RNA causes inhibition of translation of the GAM2762 target mRNA into a corresponding GAM2762 target protein.

The mechanism of the translational inhibition exerted by GAM2762 RNA, herein designated GAM RNA, on one or more GAM2762 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2762 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2762 RNA, herein designated GAM RNA, of GAM2762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2762 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2762 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2762 RNA correlate with, and may be deduced from, the identity of the GAM2762 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2770 6592 GGACTACAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACATGCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CACATCTGGC Messenger 2770 (GAM2770) oligonucleotides modulates expression of respective target genes

TAATTTTCTT whose function and utility is known in the art.

GAGTTTTAGT GAM2770 is a novel bioinformatically detectable regulatory, non protein coding,

AGAGACTGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2770 was detected is

TCTCATTATG described with additional reference to Figs. 9-15.

TTGTCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCCCAAG encoded by the human genome.

CTCCTGAGTT GAM2770 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2770

C precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2770

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2770 precursor RNA is designated SEQ ID:6592, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6592 is located from position 69984108 to position 69984208 relative to chromosome 16 on the `-` strand.

GAM2770 precursor RNA folds onto itself, forming GAM2770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2770 precursor RNA, designated SEQ ID NO: 6592, and a schematic representation of a predicted secondary folding of GAM2770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2770 folded precursor RNA yielding a GAM2770 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM2770 RNA, hereby incorporated herein.

GAM2770 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2770 target RNA, herein designated GAM TARGET RNA. GAM2770 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2770 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2770 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2770 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2770 RNA, herein designated GAM RNA, to target binding sites on GAM2770 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2770 target RNA into GAM2770 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2770 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2770 target genes. The mRNA of each one of this plurality of GAM2770 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2770 RNA, herein designated GAM RNA, and which when bound by GAM2770 RNA causes inhibition of translation of the GAM2770 target mRNA into a corresponding GAM2770 target protein.

The mechanism of the translational inhibition exerted by GAM2770 RNA, herein designated GAM RNA, on one or more GAM2770 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2770 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2770 RNA, herein designated GAM RNA, of GAM2770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2770 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2770 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2770 RNA correlate with, and may be deduced from, the identity of the GAM2770 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2780 6229 CTGGGAGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTTGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGATCAGGAA Messenger 2780 (GAM2780) oligonucleotides modulates expression of respective target genes

TTGTGCCACT whose function and utility is known in the art.

GCACTCCAAC GAM2780 is a novel bioinformatically detectable regulatory, non protein coding,

CTGAGTGACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2780 was detected is

GAGCAACACT described with additional reference to Figs. 9-15.

CTGTCTTAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM2780 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2780

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2780

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2780 precursor RNA is designated SEQ ID:6229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6229 is located from position 101905422 to position 101905503 relative to chromosome 11 on the `+` strand.

GAM2780 precursor RNA folds onto itself, forming GAM2780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2780 precursor RNA, designated SEQ ID NO: 6229, and a schematic representation of a predicted secondary folding of GAM2780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2780 folded precursor RNA

yielding a GAM2780 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2780 RNA, hereby incorporated herein.

GAM2780 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2780 target RNA, herein designated GAM TARGET RNA. GAM2780 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2780 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2780 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2780 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2780 RNA, herein designated GAM RNA, to target binding sites on GAM2780 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2780 target RNA into GAM2780 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2780 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2780 target genes. The mRNA of each one of this plurality of GAM2780 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2780 RNA, herein designated GAM RNA, and which when bound by GAM2780 RNA causes inhibition of translation of the GAM2780 target mRNA into a corresponding GAM2780 target protein.

The mechanism of the translational inhibition exerted by GAM2780 RNA, herein designated GAM RNA, on one or more GAM2780 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2780 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2780 RNA, herein designated GAM RNA, of GAM2780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2780 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2780 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2780 RNA correlate with, and may be deduced from, the identity of the GAM2780 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2799 5809 AGTCTCACTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTTGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGGAGTGC Messenger 2799 (GAM2799) oligonucleotides modulates expression of respective target genes

AGTGGTGCGA whose function and utility is known in the art.

TCTCAGCTCA GAM2799 is a novel bioinformatically detectable regulatory, non protein coding,

CTGCAACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2799 was detected is

CACCTCCTGG described with additional reference to Figs. 9-15.

GTTCAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCT encoded by the human genome.

GAM2799 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2799

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2799

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2799 precursor RNA is designated SEQ ID:5809, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5809 is located from position 67595564 to position 67595647 relative to chromosome 17 on the `+` strand.

GAM2799 precursor RNA folds onto itself, forming GAM2799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2799 precursor RNA, designated SEQ ID NO: 5809, and a

schematic representation of a predicted secondary folding of GAM2799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2799 folded precursor RNA yielding a GAM2799 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2799 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2799 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2799 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2799 target RNA, herein designated GAM TARGET RNA. GAM2799 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2799 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2799 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2799 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2799 RNA, herein designated GAM RNA, to target binding sites on GAM2799 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2799 target RNA into GAM2799 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2799 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2799 target genes. The mRNA of each one of this plurality of GAM2799 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2799 RNA, herein designated GAM RNA, and which when bound by GAM2799 RNA causes inhibition of translation of the GAM2799 target mRNA into a corresponding GAM2799 target protein.

The mechanism of the translational inhibition exerted by GAM2799 RNA, herein designated GAM RNA, on one or more GAM2799 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2799 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2799 RNA, herein designated GAM RNA, of GAM2799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2799 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2799 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2799 RNA correlate with, and may be deduced from, the identity of the GAM2799 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2807 5981 ATTGTATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCAGGTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGCCTCAGT Messenger 2807 (GAM2807) oligonucleotides modulates expression of respective target genes

AAATCTCCAT whose function and utility is known in the art.

TTGTAAATGT GAM2807 is a novel bioinformatically detectable regulatory, non protein coding,

GACAGTCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2807 was detected is

AGAATCTCCA described with additional reference to Figs. 9-15.

GTTACAGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACTCAAAGCA encoded by the human genome.

AGCAGGGGCA GAM2807 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2807

TGCCACATAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2807

ATGTTCATAT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

ATAGT to the nucleotide sequence of GAM2807 precursor RNA is designated SEQ ID:5981, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5981 is located from position 79828330 to position 79828454 relative to chromosome 14 on the `-` strand.

GAM2807 precursor RNA folds onto itself, forming GAM2807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2807 precursor RNA, designated SEQ ID NO: 5981, and a schematic representation of a predicted secondary folding of GAM2807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2807 folded precursor RNA yielding a GAM2807 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2807 RNA, hereby incorporated herein.

GAM2807 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2807 target RNA, herein designated GAM TARGET RNA. GAM2807 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2807 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2807 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2807 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2807 RNA, herein designated GAM RNA, to target binding sites on GAM2807 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2807 target RNA into GAM2807 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2807 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2807 target genes. The mRNA of each one of this plurality of GAM2807 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2807 RNA, herein designated GAM RNA, and which when bound by GAM2807 RNA causes inhibition of translation of the GAM2807 target mRNA into a corresponding GAM2807 target protein.

The mechanism of the translational inhibition exerted by GAM2807 RNA, herein designated GAM RNA, on one or more GAM2807 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2807 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2807 RNA, herein designated GAM RNA, of GAM2807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2807 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2807 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2807 RNA correlate with, and may be deduced from, the identity of the GAM2807 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2808 6530 GCTATTGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAATCTTGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TACCATCCAT Messenger 2808 (GAM2808) oligonucleotides modulates expression of respective target genes
TAAGTGCTGC whose function and utility is known in the art.

TGATTTTGGA GAM2808 is a novel bioinformatically detectable regulatory, non protein coding,
AAGATCATGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2808 was detected is

AAAACGTCTT described with additional reference to Figs. 9-15.

TCCAAACATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGCACGTC encoded by the human genome.

GTTTGGGCAC GAM2808 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2808
AAGAGGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2808
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2808 precursor RNA is designated SEQ ID:6530, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6530 is located from position 53974898 to position 53975004 relative to chromosome 15 on the `-` strand.

GAM2808 precursor RNA folds onto itself, forming GAM2808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2808 precursor RNA, designated SEQ ID NO: 6530, and a schematic representation of a predicted secondary folding of GAM2808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2808 folded precursor RNA yielding a GAM2808 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2808 RNA, hereby incorporated herein.

GAM2808 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2808 target RNA, herein designated GAM TARGET RNA. GAM2808 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2808 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2808 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2808 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2808 RNA, herein designated GAM RNA, to target binding sites on GAM2808 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2808 target RNA into GAM2808 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2808 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2808 target genes. The mRNA of each one of this

plurality of GAM2808 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2808 RNA, herein designated GAM RNA, and which when bound by GAM2808 RNA causes inhibition of translation of the GAM2808 target mRNA into a corresponding GAM2808 target protein.

The mechanism of the translational inhibition exerted by GAM2808 RNA, herein designated GAM RNA, on one or more GAM2808 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2808 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2808 RNA, herein designated GAM RNA, of GAM2808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2808 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2808 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2808 RNA correlate with, and may be deduced from, the identity of the GAM2808 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2817 6475 GATGGTCTCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TAACTGAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
TATTAAAAAC Messenger 2817 (GAM2817) oligonucleotides modulates expression of respective target genes
TTAAATTGTA whose function and utility is known in the art.

TACTTTAAGT GAM2817 is a novel bioinformatically detectable regulatory, non protein coding,
TGGTGATTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2817 was detected is

ATGATATATG described with additional reference to Figs. 9-15.

AGTTTTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM2817 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2817

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2817

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2817 precursor RNA is designated SEQ ID:6475, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6475 is located from position 15101514 to position 15101592 relative to chromosome 16 on the `-` strand.

GAM2817 precursor RNA folds onto itself, forming GAM2817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2817 precursor RNA, designated SEQ ID NO: 6475, and a schematic representation of a predicted secondary folding of GAM2817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2817 folded precursor RNA yielding a GAM2817 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2817 RNA, hereby incorporated herein.

GAM2817 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2817 target RNA, herein designated GAM TARGET RNA. GAM2817 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2817 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2817 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2817 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2817 RNA, herein designated GAM RNA, to target binding sites on GAM2817 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2817 target RNA

into GAM2817 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2817 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2817 target genes. The mRNA of each one of this plurality of GAM2817 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2817 RNA, herein designated GAM RNA, and which when bound by GAM2817 RNA causes inhibition of translation of the GAM2817 target mRNA into a corresponding GAM2817 target protein.

The mechanism of the translational inhibition exerted by GAM2817 RNA, herein designated GAM RNA, on one or more GAM2817 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2817 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2817 RNA, herein designated GAM RNA, of GAM2817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2817 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2817 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2817 RNA correlate with, and may be deduced from, the identity of the GAM2817 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2839 6184 CTCTTGACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGGTCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGAGGGAC Messenger 2839 (GAM2839) oligonucleotides modulates expression of respective target genes

ATTTTACCTG whose function and utility is known in the art.

CCAGGGGACA GAM2839 is a novel bioinformatically detectable regulatory, non protein coding,

TTTCCAATGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2839 was detected is

TTGGGGACAC described with additional reference to Figs. 9-15.

TTTTGGTTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAG encoded by the human genome.

GAM2839 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2839 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2839 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2839 precursor RNA is designated SEQ ID:6184, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6184 is located from position 21329921 to position 21330005 relative to chromosome 5 on the `+` strand.

GAM2839 precursor RNA folds onto itself, forming GAM2839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2839 precursor RNA, designated SEQ ID NO: 6184, and a schematic representation of a predicted secondary folding of GAM2839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2839 folded precursor RNA yielding a GAM2839 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2839 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2839 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2839 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2839 target RNA, herein designated GAM TARGET RNA. GAM2839 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2839 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2839 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2839 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2839 RNA, herein designated GAM RNA, to target binding sites on GAM2839 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2839 target RNA into GAM2839 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2839 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2839 target genes. The mRNA of each one of this plurality of GAM2839 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2839 RNA, herein designated GAM RNA, and which when bound by GAM2839 RNA causes inhibition of translation of the GAM2839 target mRNA into a corresponding GAM2839 target protein.

The mechanism of the translational inhibition exerted by GAM2839 RNA, herein designated GAM RNA, on one or more GAM2839 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2839 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2839 RNA, herein designated GAM RNA, of GAM2839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2839 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2839 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2839 RNA correlate with, and may be deduced from, the identity of the GAM2839 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2846 6159 CTCAGCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCTGATGTA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCTGGGTTC Messenger 2846 (GAM2846) oligonucleotides modulates expression of respective target genes
CTTGTGTGGC whose function and utility is known in the art.

AACAGTAATG GAM2846 is a novel bioinformatically detectable regulatory, non protein coding,

GGAAGAAAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2846 was detected is

ACCTGAAATA described with additional reference to Figs. 9-15.

TTAGTTGATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCAAGGGACC encoded by the human genome.

CTCTAAGGTT GAM2846 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2846

AGAGAGGCAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2846

AG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2846 precursor RNA is designated SEQ ID:6159, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6159 is located from position 143268257 to position 143268368 relative to chromosome 7 on the `+` strand.

GAM2846 precursor RNA folds onto itself, forming GAM2846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2846 precursor RNA, designated SEQ ID NO: 6159, and a schematic representation of a predicted secondary folding of GAM2846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2846 folded precursor RNA yielding a GAM2846 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2846 RNA, hereby incorporated herein.

GAM2846 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2846 target RNA, herein designated GAM TARGET RNA. GAM2846 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2846 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2846 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2846 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2846 RNA, herein designated GAM RNA, to target binding sites on GAM2846 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2846 target RNA into GAM2846 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2846 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2846 target genes. The mRNA of each one of this plurality of GAM2846 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2846 RNA, herein designated GAM RNA, and which when bound by GAM2846 RNA causes inhibition of translation of the GAM2846 target mRNA into a corresponding GAM2846 target protein.

The mechanism of the translational inhibition exerted by GAM2846 RNA, herein designated GAM RNA, on one or more GAM2846 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2846 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2846 RNA, herein designated GAM RNA, of GAM2846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2846 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2846 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2846 RNA correlate with, and may be deduced from, the identity of the GAM2846 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2868 6101 CCGTGGCCCG TGTTCTCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTTGTCCCC Messenger 2868 (GAM2868) oligonucleotides modulates expression of respective target genes

ATAGTGTGAC whose function and utility is known in the art.

TCCGCCAGGA GAM2868 is a novel bioinformatically detectable regulatory, non protein coding, ACTTGGAATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2868 was detected is

GCTGAAGACT described with additional reference to Figs. 9-15.

GTGAATGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCATGGGTC encoded by the human genome.

TGTGG GAM2868 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2868 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2868 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2868 precursor RNA is designated SEQ ID:6101, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6101 is located from position 78873561 to position 78873655 relative to chromosome 17 on the `+` strand.

GAM2868 precursor RNA folds onto itself, forming GAM2868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2868 precursor RNA, designated SEQ ID NO: 6101, and a schematic representation of a predicted secondary folding of GAM2868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2868 folded precursor RNA yielding a GAM2868 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2868 RNA, hereby incorporated herein.

GAM2868 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2868 target RNA, herein designated GAM TARGET RNA. GAM2868 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2868 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2868 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2868 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2868 RNA, herein designated GAM RNA, to target binding sites on GAM2868 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2868 target RNA into GAM2868 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2868 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2868 target genes. The mRNA of each one of this plurality of GAM2868 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2868 RNA, herein designated GAM RNA, and which when bound by GAM2868 RNA causes inhibition of translation of the GAM2868 target mRNA into a corresponding GAM2868 target protein.

The mechanism of the translational inhibition exerted by GAM2868 RNA, herein designated GAM RNA, on one or more GAM2868 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2868 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2868 RNA, herein designated GAM RNA, of GAM2868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2868 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2868 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2868 RNA correlate with, and may be deduced from, the identity of the GAM2868 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2887 6844 GGTGCAAACA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCCGTTCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTAACACGGG Messenger 2887 (GAM2887) oligonucleotides modulates expression of respective target genes

CCTGAGGTCA whose function and utility is known in the art.

GCAGTAGAGG GAM2887 is a novel bioinformatically detectable regulatory, non protein coding,

ACCAGTATTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2887 was detected is

GTTTTGGCCC described with additional reference to Figs. 9-15.

CAGCCTCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGGATGGAT encoded by the human genome.

TGAACGCC GAM2887 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2887

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2887

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2887 precursor RNA is designated SEQ ID:6844, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6844 is located from position 69517026 to position 69517123 relative to chromosome 11 on the `-` strand.

GAM2887 precursor RNA folds onto itself, forming GAM2887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2887 precursor RNA, designated SEQ ID NO: 6844, and a schematic representation of a predicted secondary folding of GAM2887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2887 folded precursor RNA yielding a GAM2887 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2887 RNA, hereby incorporated herein.

GAM2887 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2887 target RNA, herein designated GAM TARGET RNA. GAM2887 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2887 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2887 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2887 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2887 RNA, herein designated GAM RNA, to target binding sites on GAM2887 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2887 target RNA into GAM2887 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2887 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2887 target genes. The mRNA of each one of this plurality of GAM2887 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2887 RNA, herein designated GAM RNA, and which when bound by GAM2887 RNA causes inhibition of translation of the GAM2887 target mRNA into a corresponding GAM2887 target protein.

The mechanism of the translational inhibition exerted by GAM2887 RNA, herein designated GAM RNA, on one or more GAM2887 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2887 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2887 RNA, herein designated GAM RNA, of GAM2887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2887 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2887 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2887 RNA correlate with, and may be deduced from, the identity of the GAM2887 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2908 6735 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAGGAGGCA Messenger 2908 (GAM2908) oligonucleotides modulates expression of respective target genes

GAGATTGCAG whose function and utility is known in the art.

TGAGTCAAGA GAM2908 is a novel bioinformatically detectable regulatory, non protein coding,

TCATGCCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2908 was detected is

GCACTCCAGC described with additional reference to Figs. 9-15.

ACTCCAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGTGACAGA encoded by the human genome.

GCAAGATCCT GAM2908 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2908

GTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2908

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2908 precursor RNA is designated SEQ ID:6735, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6735 is located from position 51977188 to position 51977290 relative to chromosome 19 on the `+` strand.

GAM2908 precursor RNA folds onto itself, forming GAM2908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2908 precursor RNA, designated SEQ ID NO: 6735, and a schematic representation of a predicted secondary folding of GAM2908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2908 folded precursor RNA yielding a GAM2908 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM2908 RNA, hereby incorporated herein.

GAM2908 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2908 target RNA, herein designated GAM TARGET RNA. GAM2908 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2908 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2908 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2908 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2908 RNA, herein designated GAM RNA, to target binding sites on GAM2908 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2908 target RNA into GAM2908 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2908 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2908 target genes. The mRNA of each one of this plurality of GAM2908 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2908 RNA, herein designated GAM RNA, and which when bound by GAM2908 RNA causes inhibition of translation of the GAM2908 target mRNA into a corresponding GAM2908 target protein.

The mechanism of the translational inhibition exerted by GAM2908 RNA, herein designated GAM RNA, on one or more GAM2908 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2908 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2908 RNA, herein designated GAM RNA, of GAM2908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2908 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2908 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2908 RNA correlate with, and may be deduced from, the identity of the GAM2908 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2911 6220 CTGCCTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCAGGCCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCTTTGCTC Messenger 2911 (GAM2911) oligonucleotides modulates expression of respective target genes
GGTTGATCTT whose function and utility is known in the art.

GCAGAGCCTA GAM2911 is a novel bioinformatically detectable regulatory, non protein coding,
AGACACAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM2911 was detected is

CCAGAGAGGC described with additional reference to Figs. 9-15.

AG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM2911 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2911

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2911
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2911 precursor RNA is designated SEQ ID:6220, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6220 is located from position 50818311 to position 50818382 relative to chromosome 19 on the `+` strand.

GAM2911 precursor RNA folds onto itself, forming GAM2911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2911 precursor RNA, designated SEQ ID NO: 6220, and a schematic representation of a predicted secondary folding of GAM2911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2911 folded precursor RNA

yielding a GAM2911 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2911 RNA, hereby incorporated herein.

GAM2911 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2911 target RNA, herein designated GAM TARGET RNA. GAM2911 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2911 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2911 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2911 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2911 RNA, herein designated GAM RNA, to target binding sites on GAM2911 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2911 target RNA into GAM2911 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2911 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2911 target genes. The mRNA of each one of this plurality of GAM2911 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2911 RNA, herein designated GAM RNA, and which when bound by GAM2911 RNA causes inhibition of translation of the GAM2911 target mRNA into a corresponding GAM2911 target protein.

The mechanism of the translational inhibition exerted by GAM2911 RNA, herein designated GAM RNA, on one or more GAM2911 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2911 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2911 RNA, herein designated GAM RNA, of GAM2911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2911 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2911 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2911 RNA correlate with, and may be deduced from, the identity of the GAM2911 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2920 6761 GGCTGAGACC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCCTTGCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCCCTTCT Messenger 2920 (GAM2920) oligonucleotides modulates expression of respective target genes

TTCTGCCTTA whose function and utility is known in the art.

AGAATGTCCT GAM2920 is a novel bioinformatically detectable regulatory, non protein coding,

TTTAGGCTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM2920 was detected is

GCATGGTGGC described with additional reference to Figs. 9-15.

TCACGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM2920 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2920

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2920

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2920 precursor RNA is designated SEQ ID:6761, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6761 is located from position 1319193 to position 1319269 relative to chromosome 17 on the `-` strand.

GAM2920 precursor RNA folds onto itself, forming GAM2920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2920 precursor RNA, designated SEQ ID NO: 6761, and a

schematic representation of a predicted secondary folding of GAM2920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2920 folded precursor RNA yielding a GAM2920 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM2920 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2920 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM2920 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2920 target RNA, herein designated GAM TARGET RNA. GAM2920 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2920 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2920 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2920 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2920 RNA, herein designated GAM RNA, to target binding sites on GAM2920 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2920 target RNA into GAM2920 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2920 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2920 target genes. The mRNA of each one of this plurality of GAM2920 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2920 RNA, herein designated GAM RNA, and which when bound by GAM2920 RNA causes inhibition of translation of the GAM2920 target mRNA into a corresponding GAM2920 target protein.

The mechanism of the translational inhibition exerted by GAM2920 RNA, herein designated GAM RNA, on one or more GAM2920 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2920 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2920 RNA, herein designated GAM RNA, of GAM2920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2920 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2920 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2920 RNA correlate with, and may be deduced from, the identity of the GAM2920 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2927 6056 CCAGTATATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTGCAGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTATGTTTT Messenger 2927 (GAM2927) oligonucleotides modulates expression of respective target genes

TCCCCCTAAG whose function and utility is known in the art.

AACCTCAGCT GAM2927 is a novel bioinformatically detectable regulatory, non protein coding,

GAGAAATAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2927 was detected is

GCAGGTTAAC described with additional reference to Figs. 9-15.

AAAGCTGTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAATGTCAC encoded by the human genome.

TGG GAM2927 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2927

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2927

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2927 precursor RNA is designated SEQ ID:6056, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6056 is located from position 12168404 to position 12168496 relative to chromosome 10 on the `-` strand.

GAM2927 precursor RNA folds onto itself, forming GAM2927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2927 precursor RNA, designated SEQ ID NO: 6056, and a schematic representation of a predicted secondary folding of GAM2927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2927 folded precursor RNA yielding a GAM2927 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2927 RNA, hereby incorporated herein.

GAM2927 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2927 target RNA, herein designated GAM TARGET RNA. GAM2927 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2927 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2927 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2927 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2927 RNA, herein designated GAM RNA, to target binding sites on GAM2927 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2927 target RNA into GAM2927 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2927 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2927 target genes. The mRNA of each one of this plurality of GAM2927 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2927 RNA, herein designated GAM RNA, and which when bound by GAM2927 RNA causes inhibition of translation of the GAM2927 target mRNA into a corresponding GAM2927 target protein.

The mechanism of the translational inhibition exerted by GAM2927 RNA, herein designated GAM RNA, on one or more GAM2927 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2927 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2927 RNA, herein designated GAM RNA, of GAM2927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2927 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2927 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2927 RNA correlate with, and may be deduced from, the identity of the GAM2927 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2931 6723 GGATTAGTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGAGAGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTTGCTAA Messenger 2931 (GAM2931) oligonucleotides modulates expression of respective target genes
GAAGAATCTG whose function and utility is known in the art.

GCTTCTTCAG GAM2931 is a novel bioinformatically detectable regulatory, non protein coding,
TCAGCGCTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM2931 was detected is

TGCTTCCTAT described with additional reference to Figs. 9-15.

CTCTCCATGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATCT encoded by the human genome.

GAM2931 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2931

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2931

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2931 precursor RNA is designated SEQ ID:6723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6723 is located from position 97874565 to position 97874649 relative to chromosome 8 on the `+` strand.

GAM2931 precursor RNA folds onto itself, forming GAM2931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2931 precursor RNA, designated SEQ ID NO: 6723, and a schematic representation of a predicted secondary folding of GAM2931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2931 folded precursor RNA yielding a GAM2931 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2931 RNA, hereby incorporated herein.

GAM2931 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2931 target RNA, herein designated GAM TARGET RNA. GAM2931 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2931 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2931 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2931 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2931 RNA, herein designated GAM RNA, to target binding sites on GAM2931 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2931 target RNA into GAM2931 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2931 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2931 target genes. The mRNA of each one of this

plurality of GAM2931 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2931 RNA, herein designated GAM RNA, and which when bound by GAM2931 RNA causes inhibition of translation of the GAM2931 target mRNA into a corresponding GAM2931 target protein.

The mechanism of the translational inhibition exerted by GAM2931 RNA, herein designated GAM RNA, on one or more GAM2931 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2931 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2931 RNA, herein designated GAM RNA, of GAM2931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2931 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2931 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2931 RNA correlate with, and may be deduced from, the identity of the GAM2931 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM2950 6060 CCATCTGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACACTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAAAAGAGGT Messenger 2950 (GAM2950) oligonucleotides modulates expression of respective target genes

TCTGATTCTG whose function and utility is known in the art.

GCCTGTTACT GAM2950 is a novel bioinformatically detectable regulatory, non protein coding,

TGCTGTACAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM2950 was detected is

ACTTGCACAA described with additional reference to Figs. 9-15.

GGCCAGAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACTCTCTTT encoded by the human genome.

TCCCATCTGC GAM2950 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM2950

AAAGTGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM2950 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2950 precursor RNA is designated SEQ ID:6060, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6060 is located from position 170095979 to position 170096085 relative to chromosome 5 on the `-` strand.

GAM2950 precursor RNA folds onto itself, forming GAM2950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM2950 precursor RNA, designated SEQ ID NO: 6060, and a schematic representation of a predicted secondary folding of GAM2950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM2950 folded precursor RNA yielding a GAM2950 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM2950 RNA, hereby incorporated herein.

GAM2950 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2950 target RNA, herein designated GAM TARGET RNA. GAM2950 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM2950 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2950 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2950 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM2950 RNA, herein designated GAM RNA, to target binding sites on GAM2950 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2950 target RNA

into GAM2950 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM2950 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2950 target genes. The mRNA of each one of this plurality of GAM2950 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2950 RNA, herein designated GAM RNA, and which when bound by GAM2950 RNA causes inhibition of translation of the GAM2950 target mRNA into a corresponding GAM2950 target protein.

The mechanism of the translational inhibition exerted by GAM2950 RNA, herein designated GAM RNA, on one or more GAM2950 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM2950 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM2950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM2950 RNA, herein designated GAM RNA, of GAM2950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM2950 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM2950 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM2950 RNA correlate with, and may be deduced from, the identity of the GAM2950 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3004 6092 CCCTGTCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTTCGAGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTGTTTTTA Messenger 3004 (GAM3004) oligonucleotides modulates expression of respective target genes

ATGCTGGGTG whose function and utility is known in the art.

TCGATCGAGA GAM3004 is a novel bioinformatically detectable regulatory, non protein coding,

CAACAAGCGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3004 was detected is

TCAGAGCAAA described with additional reference to Figs. 9-15.

GCAAGGATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTACGGGG encoded by the human genome.

GAM3004 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3004 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3004 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3004 precursor RNA is designated SEQ ID:6092, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6092 is located from position 79931895 to position 79931983 relative to chromosome 17 on the `-` strand.

GAM3004 precursor RNA folds onto itself, forming GAM3004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3004 precursor RNA, designated SEQ ID NO: 6092, and a schematic representation of a predicted secondary folding of GAM3004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3004 folded precursor RNA yielding a GAM3004 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3004 RNA, hereby incorporated herein.

GAM3004 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3004 target RNA, herein designated GAM TARGET RNA. GAM3004 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3004 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3004 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3004 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3004 RNA, herein designated GAM RNA, to target binding sites on GAM3004 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3004 target RNA into GAM3004 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3004 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3004 target genes. The mRNA of each one of this plurality of GAM3004 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3004 RNA, herein designated GAM RNA, and which when bound by GAM3004 RNA causes inhibition of translation of the GAM3004 target mRNA into a corresponding GAM3004 target protein.

The mechanism of the translational inhibition exerted by GAM3004 RNA, herein designated GAM RNA, on one or more GAM3004 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3004 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3004 RNA, herein designated GAM RNA, of GAM3004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3004 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3004 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3004 RNA correlate with, and may be deduced from, the identity of the GAM3004 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3028 5798 AGGTTCTGGT GAATTCAGGA TGGTATTTTT GTCTTTGAAT AGTTTCTGGT TGCATTTCTA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3028 (GAM3028) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM3028 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM3028 was detected is

TAGTGGGGGT described with additional reference to Figs. 9-15.

GAAGCTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAACTTCTGT encoded by the human genome.

GATCTTCCTG GAM3028 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3028

AGGTCACTTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3028

AAAGTGCCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3028 precursor RNA is designated SEQ ID:5798, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5798 is located from position 1293547 to position 1293665 relative to chromosome 18 on the `+` strand.

GAM3028 precursor RNA folds onto itself, forming GAM3028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3028 precursor RNA, designated SEQ ID NO: 5798, and a schematic representation of a predicted secondary folding of GAM3028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3028 folded precursor RNA yielding a GAM3028 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3028 RNA, hereby incorporated herein.

GAM3028 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3028 target RNA, herein designated GAM TARGET RNA. GAM3028 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3028 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3028 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3028 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3028 RNA, herein designated GAM RNA, to target binding sites on GAM3028 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3028 target RNA into GAM3028 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3028 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3028 target genes. The mRNA of each one of this plurality of GAM3028 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3028 RNA, herein designated GAM RNA, and which when bound by GAM3028 RNA causes inhibition of translation of the GAM3028 target mRNA into a corresponding GAM3028 target protein.

The mechanism of the translational inhibition exerted by GAM3028 RNA, herein designated GAM RNA, on one or more GAM3028 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3028 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3028 RNA, herein designated GAM RNA, of GAM3028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3028 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3028 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3028 RNA correlate with, and may be deduced from, the identity of the GAM3028 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3057 6272 CTTTCTGTGC CACTCAGGAA GCAATGGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3057 (GAM3057) oligonucleotides modulates expression of respective target genes

TGATTCAGCA whose function and utility is known in the art.

GAGGAGAGGA GAM3057 is a novel bioinformatically detectable regulatory, non protein coding, GAGTTTAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3057 was detected is

CTGGTTATGC described with additional reference to Figs. 9-15.

TTCCTTCTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACCCTCCCT encoded by the human genome.

GCAAAAACAC GAM3057 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3057

TGGCCAGCTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3057

CTGACATCAC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

AGTAAGACAG to the nucleotide sequence of GAM3057 precursor RNA is designated SEQ ID:6272, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6272 is located from position 8202273 to position 8202402 relative to chromosome 19 on the `+` strand.

GAM3057 precursor RNA folds onto itself, forming GAM3057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3057 precursor RNA, designated SEQ ID NO: 6272, and a schematic representation of a predicted secondary folding of GAM3057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3057 folded precursor RNA yielding a GAM3057 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3057 RNA, hereby incorporated herein.

GAM3057 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3057 target RNA, herein designated GAM TARGET RNA. GAM3057 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3057 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM3057 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3057 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3057 RNA, herein designated GAM RNA, to target binding sites on GAM3057 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3057 target RNA into GAM3057 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3057 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3057 target genes. The mRNA of each one of this plurality of GAM3057 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3057 RNA, herein designated GAM RNA, and which when bound by GAM3057 RNA causes inhibition of translation of the GAM3057 target mRNA into a corresponding GAM3057 target protein.

The mechanism of the translational inhibition exerted by GAM3057 RNA, herein designated GAM RNA, on one or more GAM3057 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3057 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3057 RNA, herein designated GAM RNA, of GAM3057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3057 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3057 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3057 RNA correlate with, and may be deduced from, the identity of the GAM3057 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3061 6305 GAATCTGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTTCCTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGATCACTTG Messenger 3061 (GAM3061) oligonucleotides modulates expression of respective target genes

ACATGGACAG whose function and utility is known in the art.

GGTTTGGAAA GAM3061 is a novel bioinformatically detectable regulatory, non protein coding,

ACTATTTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3061 was detected is

CATTACGGAG described with additional reference to Figs. 9-15.

ACTGTCACCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCAAGAGGTG encoded by the human genome.

TTTATTATCA GAM3061 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3061

TTAGGTTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3061

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3061 precursor RNA is designated SEQ ID:6305, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6305 is located from position 94124802 to position 94124909 relative to chromosome 9 on the `+` strand.

GAM3061 precursor RNA folds onto itself, forming GAM3061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3061 precursor RNA, designated SEQ ID NO: 6305, and a schematic representation of a predicted secondary folding of GAM3061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3061 folded precursor RNA yielding a GAM3061 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3061 RNA, hereby incorporated herein.

GAM3061 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3061 target RNA, herein designated GAM TARGET RNA. GAM3061 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3061 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3061 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3061 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3061 RNA, herein designated GAM RNA, to target binding sites on GAM3061 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3061 target RNA into GAM3061 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3061 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3061 target genes. The mRNA of each one of this plurality of GAM3061 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3061 RNA, herein designated GAM RNA, and which when bound by GAM3061 RNA causes inhibition of translation of the GAM3061 target mRNA into a corresponding GAM3061 target protein.

The mechanism of the translational inhibition exerted by GAM3061 RNA, herein designated GAM RNA, on one or more GAM3061 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3061 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3061 RNA, herein designated GAM RNA, of GAM3061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3061 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3061 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3061 RNA correlate with, and may be deduced from, the identity of the GAM3061 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3064 6726 GGCACTTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
ACCGTCTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAATATAGC Messenger 3064 (GAM3064) oligonucleotides modulates expression of respective target genes
TTGGTAATTG whose function and utility is known in the art.

AACTGCTTAA GAM3064 is a novel bioinformatically detectable regulatory, non protein coding,
GCTTATTATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3064 was detected is

AATATTTAAG described with additional reference to Figs. 9-15.

CTATAGTTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGCCCATTC encoded by the human genome.

CAGAGGTCCC GAM3064 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3064
CCAGCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3064

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3064 precursor RNA is designated SEQ ID:6726, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6726 is located from position 69459978 to position 69460083 relative to chromosome 16 on the `+` strand.

GAM3064 precursor RNA folds onto itself, forming GAM3064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3064 precursor RNA, designated SEQ ID NO: 6726, and a schematic representation of a predicted secondary folding of GAM3064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3064 folded precursor RNA yielding a GAM3064 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM3064 RNA, hereby incorporated herein.

GAM3064 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3064 target RNA, herein designated GAM TARGET RNA. GAM3064 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3064 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3064 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3064 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3064 RNA, herein designated GAM RNA, to target binding sites on GAM3064 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3064 target RNA into GAM3064 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3064 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3064 target genes. The mRNA of each one of this plurality of GAM3064 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3064 RNA, herein designated GAM RNA, and which when bound by GAM3064 RNA causes inhibition of translation of the GAM3064 target mRNA into a corresponding GAM3064 target protein.

The mechanism of the translational inhibition exerted by GAM3064 RNA, herein designated GAM RNA, on one or more GAM3064 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3064 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3064 RNA, herein designated GAM RNA, of GAM3064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3064 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3064 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3064 RNA correlate with, and may be deduced from, the identity of the GAM3064 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3065 6704 GGAGACATGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTAGCAGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GATGGGACTG Messenger 3065 (GAM3065) oligonucleotides modulates expression of respective target genes
TCTTACATAA whose function and utility is known in the art.

CTGGATCTTT GAM3065 is a novel bioinformatically detectable regulatory, non protein coding,
TAGAACTATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3065 was detected is

GAAGATTAAG described with additional reference to Figs. 9-15.

TAGTAAAATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTATAAAAAG encoded by the human genome.

TTTCTTGACA GAM3065 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3065
ATGTTATTTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3065
CC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3065 precursor RNA is designated SEQ ID:6704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6704 is located from position 120332544 to position 120332655 relative to chromosome 11 on the `+` strand.

GAM3065 precursor RNA folds onto itself, forming GAM3065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3065 precursor RNA, designated SEQ ID NO: 6704, and a schematic representation of a predicted secondary folding of GAM3065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3065 folded precursor RNA

yielding a GAM3065 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3065 RNA, hereby incorporated herein.

GAM3065 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3065 target RNA, herein designated GAM TARGET RNA. GAM3065 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3065 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3065 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3065 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3065 RNA, herein designated GAM RNA, to target binding sites on GAM3065 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3065 target RNA into GAM3065 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3065 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3065 target genes. The mRNA of each one of this plurality of GAM3065 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3065 RNA, herein designated GAM RNA, and which when bound by GAM3065 RNA causes inhibition of translation of the GAM3065 target mRNA into a corresponding GAM3065 target protein.

The mechanism of the translational inhibition exerted by GAM3065 RNA, herein designated GAM RNA, on one or more GAM3065 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3065 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3065 RNA, herein designated GAM RNA, of GAM3065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3065 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3065 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3065 RNA correlate with, and may be deduced from, the identity of the GAM3065 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3077 6030 CAGGTGTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTACCATGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGCTAATTT Messenger 3077 (GAM3077) oligonucleotides modulates expression of respective target genes

TTGTATTTTT whose function and utility is known in the art.

GGTAGAAACA GAM3077 is a novel bioinformatically detectable regulatory, non protein coding,

GGGTTTTACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3077 was detected is

ATGTTGGCCA described with additional reference to Figs. 9-15.

GGCTGGTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAACTTCTG encoded by the human genome.

GAM3077 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3077

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3077

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3077 precursor RNA is designated SEQ ID:6030, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6030 is located from position 127843803 to position 127843891 relative to chromosome 7 on the `+` strand.

GAM3077 precursor RNA folds onto itself, forming GAM3077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3077 precursor RNA, designated SEQ ID NO: 6030, and a

schematic representation of a predicted secondary folding of GAM3077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3077 folded precursor RNA yielding a GAM3077 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3077 RNA, hereby incorporated herein.

GAM3077 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3077 target RNA, herein designated GAM TARGET RNA. GAM3077 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3077 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3077 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3077 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3077 RNA, herein designated GAM RNA, to target binding sites on GAM3077 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3077 target RNA into GAM3077 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3077 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3077 target genes. The mRNA of each one of this plurality of GAM3077 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3077 RNA, herein designated GAM RNA, and which when bound by GAM3077 RNA causes inhibition of translation of the GAM3077 target mRNA into a corresponding GAM3077 target protein.

The mechanism of the translational inhibition exerted by GAM3077 RNA, herein designated GAM RNA, on one or more GAM3077 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3077 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3077 RNA, herein designated GAM RNA, of GAM3077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3077 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3077 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3077 RNA correlate with, and may be deduced from, the identity of the GAM3077 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3081 6109 CCTCAGCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAAAGTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGATTACAG Messenger 3081 (GAM3081) oligonucleotides modulates expression of respective target genes

GTGTGAACCA whose function and utility is known in the art.

CCATGCCCGG GAM3081 is a novel bioinformatically detectable regulatory, non protein coding,

CAGTGATTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3081 was detected is

TTTCTAAACC described with additional reference to Figs. 9-15.

CAGCTTGTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGGTGAGG encoded by the human genome.

GAM3081 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3081

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3081

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3081 precursor RNA is designated SEQ ID:6109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6109 is located from position 23059753 to position 23059842 relative to chromosome 19 on the `+` strand.

GAM3081 precursor RNA folds onto itself, forming GAM3081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3081 precursor RNA, designated SEQ ID NO: 6109, and a schematic representation of a predicted secondary folding of GAM3081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3081 folded precursor RNA yielding a GAM3081 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3081 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3081 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3081 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3081 target RNA, herein designated GAM TARGET RNA. GAM3081 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3081 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3081 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3081 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3081 RNA, herein designated GAM RNA, to target binding sites on GAM3081 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3081 target RNA into GAM3081 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3081 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3081 target genes. The mRNA of each one of this plurality of GAM3081 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3081 RNA, herein designated GAM RNA, and which when bound by GAM3081 RNA causes inhibition of translation of the GAM3081 target mRNA into a corresponding GAM3081 target protein.

The mechanism of the translational inhibition exerted by GAM3081 RNA, herein designated GAM RNA, on one or more GAM3081 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3081 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3081 RNA, herein designated GAM RNA, of GAM3081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3081 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3081 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3081 RNA correlate with, and may be deduced from, the identity of the GAM3081 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3089 7090 TGACACTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTAAACGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCTGTGCTT Messenger 3089 (GAM3089) oligonucleotides modulates expression of respective target genes
TTCTCCCATT whose function and utility is known in the art.

TGTACTGCCC GAM3089 is a novel bioinformatically detectable regulatory, non protein coding,
TGTATATCCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3089 was detected is

CGTTCAGCAT described with additional reference to Figs. 9-15.

TGCCAGTGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCAGCCACC encoded by the human genome.

TCTTAAAGCA GAM3089 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3089
TTCTGAAGTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3089
TCA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3089 precursor RNA is designated SEQ ID:7090, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:7090 is located from position 39513226 to position 39513338 relative to chromosome 19 on the `+` strand.

GAM3089 precursor RNA folds onto itself, forming GAM3089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3089 precursor RNA, designated SEQ ID NO: 7090, and a schematic representation of a predicted secondary folding of GAM3089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3089 folded precursor RNA yielding a GAM3089 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3089 RNA, hereby incorporated herein.

GAM3089 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3089 target RNA, herein designated GAM TARGET RNA. GAM3089 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3089 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3089 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3089 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3089 RNA, herein designated GAM RNA, to target binding sites on GAM3089 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3089 target RNA into GAM3089 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3089 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3089 target genes. The mRNA of each one of this

plurality of GAM3089 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3089 RNA, herein designated GAM RNA, and which when bound by GAM3089 RNA causes inhibition of translation of the GAM3089 target mRNA into a corresponding GAM3089 target protein.

The mechanism of the translational inhibition exerted by GAM3089 RNA, herein designated GAM RNA, on one or more GAM3089 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3089 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3089 RNA, herein designated GAM RNA, of GAM3089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3089 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3089 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3089 RNA correlate with, and may be deduced from, the identity of the GAM3089 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3091 6308 GACAGCAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTTTCTATC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAAATGAATG Messenger 3091 (GAM3091) oligonucleotides modulates expression of respective target genes
CCGTCCCATG whose function and utility is known in the art.

GAAAGTGGCT GAM3091 is a novel bioinformatically detectable regulatory, non protein coding,
GTCCTGGGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3091 was detected is

GCTACACGTT described with additional reference to Figs. 9-15.

TCTCCAATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGATGCTGTT encoded by the human genome.

GAM3091 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3091

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3091

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3091 precursor RNA is designated SEQ ID:6308, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6308 is located from position 96671073 to position 96671162 relative to chromosome 9 on the `+` strand.

GAM3091 precursor RNA folds onto itself, forming GAM3091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3091 precursor RNA, designated SEQ ID NO: 6308, and a schematic representation of a predicted secondary folding of GAM3091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3091 folded precursor RNA yielding a GAM3091 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3091 RNA, hereby incorporated herein.

GAM3091 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3091 target RNA, herein designated GAM TARGET RNA. GAM3091 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3091 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3091 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3091 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3091 RNA, herein designated GAM RNA, to target binding sites on GAM3091 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3091 target RNA

into GAM3091 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3091 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3091 target genes. The mRNA of each one of this plurality of GAM3091 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3091 RNA, herein designated GAM RNA, and which when bound by GAM3091 RNA causes inhibition of translation of the GAM3091 target mRNA into a corresponding GAM3091 target protein.

The mechanism of the translational inhibition exerted by GAM3091 RNA, herein designated GAM RNA, on one or more GAM3091 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3091 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3091 RNA, herein designated GAM RNA, of GAM3091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3091 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3091 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3091 RNA correlate with, and may be deduced from, the identity of the GAM3091 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3123 6105 CCTACCATGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGTTCTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTTTGAAGT Messenger 3123 (GAM3123) oligonucleotides modulates expression of respective target genes
TGAGCATACC whose function and utility is known in the art.

GATGCGCCAC GAM3123 is a novel bioinformatically detectable regulatory, non protein coding,
TCCTGCTTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3123 was detected is

ATGCTTGAGA described with additional reference to Figs. 9-15.

AGTCGTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3123 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3123 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3123 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3123 precursor RNA is designated SEQ ID:6105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6105 is located from position 63390513 to position 63390591 relative to chromosome 17 on the `+` strand.

GAM3123 precursor RNA folds onto itself, forming GAM3123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3123 precursor RNA, designated SEQ ID NO: 6105, and a schematic representation of a predicted secondary folding of GAM3123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3123 folded precursor RNA yielding a GAM3123 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3123 RNA, hereby incorporated herein.

GAM3123 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3123 target RNA, herein designated GAM TARGET RNA. GAM3123 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3123 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3123 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3123 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3123 RNA, herein designated GAM RNA, to target binding sites on GAM3123 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3123 target RNA into GAM3123 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3123 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3123 target genes. The mRNA of each one of this plurality of GAM3123 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3123 RNA, herein designated GAM RNA, and which when bound by GAM3123 RNA causes inhibition of translation of the GAM3123 target mRNA into a corresponding GAM3123 target protein.

The mechanism of the translational inhibition exerted by GAM3123 RNA, herein designated GAM RNA, on one or more GAM3123 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3123 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3123 RNA, herein designated GAM RNA, of GAM3123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3123 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3123 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3123 RNA correlate with, and may be deduced from, the identity of the GAM3123 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3126 7267 TGTGAAACAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCCAGTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTGATGACT Messenger 3126 (GAM3126) oligonucleotides modulates expression of respective target genes
CAAAACGTAC whose function and utility is known in the art.

TTTGTGATCT GAM3126 is a novel bioinformatically detectable regulatory, non protein coding,
TGCCAAGCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3126 was detected is

TGAGATCATC described with additional reference to Figs. 9-15.

GTTACAAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCATTTTGGT encoded by the human genome.

TGTGAAAAAC GAM3126 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3126

A precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3126

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3126 precursor RNA is designated SEQ ID:7267, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7267 is located from position 43395837 to position 43395937 relative to chromosome 17 on the `+` strand.

GAM3126 precursor RNA folds onto itself, forming GAM3126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3126 precursor RNA, designated SEQ ID NO: 7267, and a schematic representation of a predicted secondary folding of GAM3126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3126 folded precursor RNA yielding a GAM3126 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3126 RNA, hereby incorporated herein.

GAM3126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3126 target RNA, herein designated GAM TARGET RNA. GAM3126 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3126 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3126 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3126 RNA, herein designated GAM RNA, to target binding sites on GAM3126 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3126 target RNA into GAM3126 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3126 target genes. The mRNA of each one of this plurality of GAM3126 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3126 RNA, herein designated GAM RNA, and which when bound by GAM3126 RNA causes inhibition of translation of the GAM3126 target mRNA into a corresponding GAM3126 target protein.

The mechanism of the translational inhibition exerted by GAM3126 RNA, herein designated GAM RNA, on one or more GAM3126 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3126 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3126 RNA, herein designated GAM RNA, of GAM3126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3126 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3126 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3126 RNA correlate with, and may be deduced from, the identity of the GAM3126 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3132 5752 AGCTATTGTG ACAATCTTGG TTACCATCCA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3132 (GAM3132) oligonucleotides modulates expression of respective target genes

TTAAGTGCTG whose function and utility is known in the art.

CTGATTTTGG GAM3132 is a novel bioinformatically detectable regulatory, non protein coding, AAAGATCATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3132 was detected is

AAAAACGTCT described with additional reference to Figs. 9-15.

TTCCAAACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAGGCACGT encoded by the human genome.

CGTTTGGGCA GAM3132 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3132

CAAGAGGCAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3132

ATCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3132 precursor RNA is designated SEQ ID:5752, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5752 is located from position 53974892 to position 53975005 relative to chromosome 15 on the `-` strand.

GAM3132 precursor RNA folds onto itself, forming GAM3132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3132 precursor RNA, designated SEQ ID NO: 5752, and a schematic representation of a predicted secondary folding of GAM3132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3132 folded precursor RNA yielding a GAM3132 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3132 RNA, hereby incorporated herein.

GAM3132 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3132 target RNA, herein designated GAM TARGET RNA. GAM3132 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3132 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3132 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3132 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3132 RNA, herein designated GAM RNA, to target binding sites on GAM3132 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3132 target RNA into GAM3132 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3132 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3132 target genes. The mRNA of each one of this plurality of GAM3132 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3132 RNA, herein designated GAM RNA, and which when bound by GAM3132 RNA causes inhibition of translation of the GAM3132 target mRNA into a corresponding GAM3132 target protein.

The mechanism of the translational inhibition exerted by GAM3132 RNA, herein designated GAM RNA, on one or more GAM3132 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3132 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3132 RNA, herein designated GAM RNA, of GAM3132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3132 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3132 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3132 RNA correlate with, and may be deduced from, the identity of the GAM3132 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3138 5707 ACTCTTTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGACTGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGAATGGAG Messenger 3138 (GAM3138) oligonucleotides modulates expression of respective target genes
CAGTCTTTGA whose function and utility is known in the art.

AAGGCACCAA GAM3138 is a novel bioinformatically detectable regulatory, non protein coding,
CCCTTCCTAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3138 was detected is

CTGATGGTGG described with additional reference to Figs. 9-15.

TCTCTTGAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGGCTCTTC encoded by the human genome.

CAAATTTGTC GAM3138 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3138
TTCTGAAAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3138
GT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3138 precursor RNA is designated SEQ ID:5707, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5707 is located from position 33981295 to position 33981406 relative to chromosome 15 on the `+` strand.

GAM3138 precursor RNA folds onto itself, forming GAM3138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3138 precursor RNA, designated SEQ ID NO: 5707, and a schematic representation of a predicted secondary folding of GAM3138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3138 folded precursor RNA yielding a GAM3138 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3138 RNA, hereby incorporated herein.

GAM3138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3138 target RNA, herein designated GAM TARGET RNA. GAM3138 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3138 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3138 RNA, herein designated GAM RNA, to target binding sites on GAM3138 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3138 target RNA into GAM3138 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3138 target genes. The mRNA of each one of this plurality of GAM3138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3138 RNA, herein designated GAM RNA, and which when bound by GAM3138 RNA causes inhibition of translation of the GAM3138 target mRNA into a corresponding GAM3138 target protein.

The mechanism of the translational inhibition exerted by GAM3138 RNA, herein designated GAM RNA, on one or more GAM3138 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3138 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3138 RNA, herein designated GAM RNA, of GAM3138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3138 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3138 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3138 RNA correlate with, and may be deduced from, the identity of the GAM3138 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3140 5818 AGTGTGAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAAAGCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTCTAAGGA Messenger 3140 (GAM3140) oligonucleotides modulates expression of respective target genes
TGGTGGAGCA whose function and utility is known in the art.

GAAAGGCAGG GAM3140 is a novel bioinformatically detectable regulatory, non protein coding,
AGTCCTGCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3140 was detected is

CCTGGCACCA described with additional reference to Figs. 9-15.

TCATGGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCCCAGCCC encoded by the human genome.

AGATCTGCCC GAM3140 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3140
CCCTCTGAAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3140
TTCCTGTTGC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
ATT to the nucleotide sequence of GAM3140 precursor RNA is designated SEQ ID:5818, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5818 is located from position 38591279 to position 38591401 relative to chromosome 17 on the `+` strand.

GAM3140 precursor RNA folds onto itself, forming GAM3140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3140 precursor RNA, designated SEQ ID NO: 5818, and a schematic representation of a predicted secondary folding of GAM3140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3140 folded precursor RNA yielding a GAM3140 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3140 RNA, hereby incorporated herein.

GAM3140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3140 target RNA, herein designated GAM TARGET RNA. GAM3140 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3140 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3140 RNA, herein designated GAM RNA, to target binding sites on GAM3140 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3140 target RNA into GAM3140 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3140 target genes. The mRNA of each one of this plurality of GAM3140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3140 RNA, herein designated GAM RNA, and which when bound by GAM3140 RNA causes inhibition of translation of the GAM3140 target mRNA into a corresponding GAM3140 target protein.

The mechanism of the translational inhibition exerted by GAM3140 RNA, herein designated GAM RNA, on one or more GAM3140 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3140 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3140 RNA, herein designated GAM RNA, of GAM3140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM3140 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3140 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3140 RNA correlate with, and may be deduced from, the identity of the GAM3140 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3143 6754 GGCGTATCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTTCAGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGCGGCTGG Messenger 3143 (GAM3143) oligonucleotides modulates expression of respective target genes
GAACGGGAGT whose function and utility is known in the art.

AGAGGTGAGG GAM3143 is a novel bioinformatically detectable regulatory, non protein coding,
GGTCGTTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3143 was detected is

TCTGTCGCGG described with additional reference to Figs. 9-15.

TGTGTATCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGGGGGTTC encoded by the human genome.

AGCGCC GAM3143 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3143
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3143
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3143 precursor RNA is designated SEQ ID:6754, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6754 is located from position 81003842 to position 81003937 relative to chromosome 15 on the `+` strand.

GAM3143 precursor RNA folds onto itself, forming GAM3143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3143 precursor RNA, designated SEQ ID NO: 6754, and a schematic representation of a predicted secondary folding of GAM3143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3143 folded precursor RNA yielding a GAM3143 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3143 RNA, hereby incorporated herein.

GAM3143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3143 target RNA, herein designated GAM TARGET RNA. GAM3143 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3143 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3143 RNA, herein designated GAM RNA, to target binding sites on GAM3143 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3143 target RNA into GAM3143 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3143 target genes. The mRNA of each one of this plurality of GAM3143 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3143 RNA, herein designated GAM RNA, and which when bound by GAM3143 RNA causes inhibition of translation of the GAM3143 target mRNA into a corresponding GAM3143 target protein.

The mechanism of the translational inhibition exerted by GAM3143 RNA, herein designated GAM RNA, on one or more GAM3143 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3143 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3143 RNA, herein designated GAM RNA, of

GAM3143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3143 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3143 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3143 RNA correlate with, and may be deduced from, the identity of the GAM3143 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3157 7340 TTGTTGAAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCAGTGAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGGTTTCAG Messenger 3157 (GAM3157) oligonucleotides modulates expression of respective target genes

GTTTGGTTTT whose function and utility is known in the art.

ACAAACCTGT GAM3157 is a novel bioinformatically detectable regulatory, non protein coding,

TAACTACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3157 was detected is

CTGTCCAGCT described with additional reference to Figs. 9-15.

TGACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3157 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3157

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3157

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3157 precursor RNA is designated SEQ ID:7340, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7340 is located from position 21733645 to position 21733720 relative to chromosome 14 on the `-` strand.

GAM3157 precursor RNA folds onto itself, forming GAM3157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3157 precursor RNA, designated SEQ ID NO: 7340, and a schematic representation of a predicted secondary folding of GAM3157 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3157 folded precursor RNA yielding a GAM3157 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3157 RNA, hereby incorporated herein.

GAM3157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3157 target RNA, herein designated GAM TARGET RNA. GAM3157 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3157 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3157 RNA, herein designated GAM RNA, to target binding sites on GAM3157 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3157 target RNA into GAM3157 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3157 target genes. The mRNA of each one of this plurality of GAM3157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3157 RNA, herein designated GAM RNA, and which when bound by GAM3157 RNA causes inhibition of translation of the GAM3157 target mRNA into a corresponding GAM3157 target protein.

The mechanism of the translational inhibition exerted by GAM3157 RNA, herein designated GAM RNA, on one or more GAM3157 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3157 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM3157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3157 RNA, herein designated GAM RNA, of GAM3157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3157 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3157 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3157 RNA correlate with, and may be deduced from, the identity of the GAM3157 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3163 7074 TCTGCTCATG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTACTGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAATACCACT Messenger 3163 (GAM3163) oligonucleotides modulates expression of respective target genes

GCAATGACTG whose function and utility is known in the art.

TCAGAACAAT GAM3163 is a novel bioinformatically detectable regulatory, non protein coding,

TCTTGTGAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3163 was detected is

GTTGTTTTTA described with additional reference to Figs. 9-15.

TAAGCCTTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTTTGTTGA encoded by the human genome.

AGTTGAGGTT GAM3163 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3163

CAAGGGCAGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3163

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3163 precursor RNA is designated SEQ ID:7074, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7074 is located from position 28262669 to position 28262778 relative to chromosome 9 on the `-` strand.

GAM3163 precursor RNA folds onto itself, forming GAM3163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3163 precursor RNA, designated SEQ ID NO: 7074, and a schematic representation of a predicted secondary folding of GAM3163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3163 folded precursor RNA yielding a GAM3163 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3163 RNA, hereby incorporated herein.

GAM3163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3163 target RNA, herein designated GAM TARGET RNA. GAM3163 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3163 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3163 RNA, herein designated GAM RNA, to target binding sites on GAM3163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3163 target RNA into GAM3163 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3163 target genes. The mRNA of each one of this plurality of GAM3163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3163 RNA, herein designated GAM RNA, and which when bound by GAM3163 RNA causes inhibition of translation of the GAM3163 target mRNA into a corresponding GAM3163 target protein.

The mechanism of the translational inhibition exerted by GAM3163 RNA, herein designated GAM RNA, on one or more GAM3163 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3163 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3163 RNA, herein designated GAM RNA, of GAM3163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3163 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3163 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3163 RNA correlate with, and may be deduced from, the identity of the GAM3163 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3174 5711 ACTTTTGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CATTTTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCATGTGAC Messenger 3174 (GAM3174) oligonucleotides modulates expression of respective target genes

CTGGGATTAT whose function and utility is known in the art.

AAATGTGAAA GAM3174 is a novel bioinformatically detectable regulatory, non protein coding,

TTAGGTTTAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3174 was detected is

GAAAGGATCC described with additional reference to Figs. 9-15.

AGTGTCATTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCATCATGG encoded by the human genome.

GCAAGGAGT GAM3174 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3174

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3174

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3174 precursor RNA is designated SEQ ID:5711, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5711 is located from position 42623627 to position 42623725 relative to chromosome 13 on the `+` strand.

GAM3174 precursor RNA folds onto itself, forming GAM3174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3174 precursor RNA, designated SEQ ID NO: 5711, and a schematic representation of a predicted secondary folding of GAM3174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3174 folded precursor RNA yielding a GAM3174 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3174 RNA, hereby incorporated herein.

GAM3174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3174 target RNA, herein designated GAM TARGET RNA. GAM3174 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3174 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3174 RNA, herein designated GAM RNA, to target binding sites on GAM3174 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3174 target RNA into GAM3174 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3174 target genes. The mRNA of each one of this plurality of GAM3174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3174 RNA, herein

designated GAM RNA, and which when bound by GAM3174 RNA causes inhibition of translation of the GAM3174 target mRNA into a corresponding GAM3174 target protein.

The mechanism of the translational inhibition exerted by GAM3174 RNA, herein designated GAM RNA, on one or more GAM3174 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3174 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3174 RNA, herein designated GAM RNA, of GAM3174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3174 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3174 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3174 RNA correlate with, and may be deduced from, the identity of the GAM3174 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3183 5961 ATCTTGTACA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTTCCCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTTGGAATC Messenger 3183 (GAM3183) oligonucleotides modulates expression of respective target genes
AGCCATTCCT whose function and utility is known in the art.

CCAGGGAGTG GAM3183 is a novel bioinformatically detectable regulatory, non protein coding,
CAGGTTCACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3183 was detected is

GGCTGGGCTC described with additional reference to Figs. 9-15.

TAAGAGAATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAAGGT encoded by the human genome.

GAM3183 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3183

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3183

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3183 precursor RNA is designated SEQ ID:5961, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5961 is located from position 36044102 to position 36044188 relative to chromosome 17 on the `+` strand.

GAM3183 precursor RNA folds onto itself, forming GAM3183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3183 precursor RNA, designated SEQ ID NO: 5961, and a schematic representation of a predicted secondary folding of GAM3183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3183 folded precursor RNA yielding a GAM3183 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3183 RNA, hereby incorporated herein.

GAM3183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3183 target RNA, herein designated GAM TARGET RNA. GAM3183 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3183 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3183 RNA, herein designated GAM RNA, to target binding sites on GAM3183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3183 target RNA into GAM3183 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3183 target genes. The mRNA of each one of this plurality of GAM3183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3183 RNA, herein designated GAM RNA, and which when bound by GAM3183 RNA causes inhibition of translation of the GAM3183 target mRNA into a corresponding GAM3183 target protein.

The mechanism of the translational inhibition exerted by GAM3183 RNA, herein designated GAM RNA, on one or more GAM3183 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3183 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3183 RNA, herein designated GAM RNA, of GAM3183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3183 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3183 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3183 RNA correlate with, and may be deduced from, the identity of the GAM3183 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3190 6470 GATCATTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACCAGAAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCAGGCTGT Messenger 3190 (GAM3190) oligonucleotides modulates expression of respective target genes

AGTGCACTAT whose function and utility is known in the art.

GATGATCGTA GAM3190 is a novel bioinformatically detectable regulatory, non protein coding,

CGTATGAACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3190 was detected is

GCCATTGCAC described with additional reference to Figs. 9-15.

TCCAGCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAATTCAGC encoded by the human genome.

AAGACATC GAM3190 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3190 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3190 precursor RNA is designated SEQ ID:6470, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6470 is located from position 95449990 to position 95450087 relative to chromosome 4 on the `+` strand.

GAM3190 precursor RNA folds onto itself, forming GAM3190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3190 precursor RNA, designated SEQ ID NO: 6470, and a schematic representation of a predicted secondary folding of GAM3190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3190 folded precursor RNA yielding a GAM3190 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3190 RNA, hereby incorporated herein. Expression of GAM3190 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM3190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3190 target RNA, herein designated GAM TARGET RNA. GAM3190 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3190 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3190 RNA, herein designated GAM RNA, to target binding sites on GAM3190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3190 target RNA into GAM3190 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3190 target genes. The mRNA of each one of this plurality of GAM3190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3190 RNA, herein designated GAM RNA, and which when bound by GAM3190 RNA causes inhibition of translation of the GAM3190 target mRNA into a corresponding GAM3190 target protein.

The mechanism of the translational inhibition exerted by GAM3190 RNA, herein designated GAM RNA, on one or more GAM3190 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3190 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3190 RNA, herein designated GAM RNA, of GAM3190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3190 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3190 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3190 RNA correlate with, and may be deduced from, the identity of the GAM3190 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3195 6939 GTTCCTTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCACACCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCTCCCTGG Messenger 3195 (GAM3195) oligonucleotides modulates expression of respective target genes
ACTGCCTGAC whose function and utility is known in the art.

CTCGCTCCAA GAM3195 is a novel bioinformatically detectable regulatory, non protein coding,

GGCTCAGGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3195 was detected is

AAGGTTCTGA described with additional reference to Figs. 9-15.

GGGCAGGTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAAATGCTT encoded by the human genome.

GGAAT GAM3195 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3195 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3195 precursor RNA is designated SEQ ID:6939, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6939 is located from position 68013720 to position 68013814 relative to chromosome 11 on the `+` strand.

GAM3195 precursor RNA folds onto itself, forming GAM3195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3195 precursor RNA, designated SEQ ID NO: 6939, and a schematic representation of a predicted secondary folding of GAM3195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3195 folded precursor RNA yielding a GAM3195 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3195 RNA, hereby incorporated herein.

GAM3195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3195 target RNA, herein designated GAM TARGET RNA. GAM3195 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3195 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3195 RNA, herein designated GAM RNA, to target binding sites on GAM3195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3195 target RNA into GAM3195 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3195 target genes. The mRNA of each one of this plurality of GAM3195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3195 RNA, herein designated GAM RNA, and which when bound by GAM3195 RNA causes inhibition of translation of the GAM3195 target mRNA into a corresponding GAM3195 target protein.

The mechanism of the translational inhibition exerted by GAM3195 RNA, herein designated GAM RNA, on one or more GAM3195 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3195 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3195 RNA, herein designated GAM RNA, of GAM3195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3195 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3195 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3195 RNA correlate with, and may be deduced from, the identity of the GAM3195 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3211 7039 TCCTCCCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCATTCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCACTGTTCC Messenger 3211 (GAM3211) oligonucleotides modulates expression of respective target genes

TTTTTGTTGA whose function and utility is known in the art.

GATCATTCTC GAM3211 is a novel bioinformatically detectable regulatory, non protein coding, GGTGTCTCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3211 was detected is

ATAGCTGGGT described with additional reference to Figs. 9-15.

TGCAGCTCCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCTTTGCCA encoded by the human genome.

GGAGGTGGTA GAM3211 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3211

ATAGAGGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3211

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3211 precursor RNA is designated SEQ ID:7039, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7039 is located from position 55666192 to position 55666299 relative to chromosome 19 on the `+` strand.

GAM3211 precursor RNA folds onto itself, forming GAM3211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3211 precursor RNA, designated SEQ ID NO: 7039, and a schematic representation of a predicted secondary folding of GAM3211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3211 folded precursor RNA yielding a GAM3211 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3211 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3211 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3211 target RNA, herein designated GAM TARGET RNA. GAM3211 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3211 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3211 RNA, herein designated GAM RNA, to target binding sites on GAM3211 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3211 target RNA into GAM3211 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3211 target genes. The mRNA of each one of this plurality of GAM3211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3211 RNA, herein designated GAM RNA, and which when bound by GAM3211 RNA causes inhibition of translation of the GAM3211 target mRNA into a corresponding GAM3211 target protein.

The mechanism of the translational inhibition exerted by GAM3211 RNA, herein designated GAM RNA, on one or more GAM3211 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3211 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3211 RNA, herein designated GAM RNA, of GAM3211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3211 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3211 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3211 RNA correlate with, and may be deduced from, the identity of the GAM3211 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3227 6673 GGAGAATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTGAACCCG detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGCGGAC Messenger 3227 (GAM3227) oligonucleotides modulates expression of respective target genes
GTTGCAGTGA whose function and utility is known in the art.

GCCGAGATTG GAM3227 is a novel bioinformatically detectable regulatory, non protein coding,
CACCACTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3227 was detected is

CTCCAGCCTG described with additional reference to Figs. 9-15.

GGCAACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAGACTCC encoded by the human genome.

GAM3227 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3227

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3227
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3227 precursor RNA is designated SEQ ID:6673, and is provided hereinbelow with reference to the sequence listing part.

GAM3227 precursor RNA folds onto itself, forming GAM3227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3227 precursor RNA, designated SEQ ID NO: 6673, and a schematic representation of a predicted secondary folding of GAM3227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3227 folded precursor RNA yielding a GAM3227 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3227 RNA, hereby incorporated herein. Expression of GAM3227 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM3227 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM3227 target RNA, herein designated GAM TARGET RNA. GAM3227 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3227 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3227 RNA, herein designated GAM RNA, to target binding sites on GAM3227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3227 target RNA into GAM3227 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3227 target genes. The mRNA of each one of this plurality of GAM3227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3227 RNA, herein designated GAM RNA, and which when bound by GAM3227 RNA causes inhibition of translation of the GAM3227 target mRNA into a corresponding GAM3227 target protein.

The mechanism of the translational inhibition exerted by GAM3227 RNA, herein designated GAM RNA, on one or more GAM3227 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3227 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3227 RNA, herein designated GAM RNA, of GAM3227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3227 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM3227 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3227 RNA correlate with, and may be deduced from, the identity of the GAM3227 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3236 6490 GCAGCGACGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGTTTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAAGCCAAG Messenger 3236 (GAM3236) oligonucleotides modulates expression of respective target genes

ATGGCTGAGT whose function and utility is known in the art.

CCACAGGCTC GAM3236 is a novel bioinformatically detectable regulatory, non protein coding,

ACCCACGGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3236 was detected is

GCGTTTAGAC described with additional reference to Figs. 9-15.

TGGGATGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

C encoded by the human genome.

GAM3236 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3236

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3236

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3236 precursor RNA is designated SEQ ID:6490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6490 is located from position 48954882 to position 48954962 relative to chromosome 15 on the `+` strand.

GAM3236 precursor RNA folds onto itself, forming GAM3236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3236 precursor RNA, designated SEQ ID NO: 6490, and a schematic representation of a predicted secondary folding of GAM3236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3236 folded precursor RNA yielding a GAM3236 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3236 RNA, hereby incorporated herein.

GAM3236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3236 target RNA, herein designated GAM TARGET RNA. GAM3236 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3236 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3236 RNA, herein designated GAM RNA, to target binding sites on GAM3236 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3236 target RNA into GAM3236 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3236 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3236 target genes. The mRNA of each one of this plurality of GAM3236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3236 RNA, herein designated GAM RNA, and which when bound by GAM3236 RNA causes inhibition of translation of the GAM3236 target mRNA into a corresponding GAM3236 target protein.

The mechanism of the translational inhibition exerted by GAM3236 RNA, herein designated GAM RNA, on one or more GAM3236 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3236 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3236 RNA, herein designated GAM RNA, of GAM3236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3236 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3236 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3236 RNA correlate with, and may be deduced from, the identity of the GAM3236 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3263 6096 CCGAGGCTAC Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAAGGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTTTGCCTG Messenger 3263 (GAM3263) oligonucleotides modulates expression of respective target genes
GAGACATTTC whose function and utility is known in the art.

TACTGGTACC GAM3263 is a novel bioinformatically detectable regulatory, non protein coding,
TTACCAATGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3263 was detected is

GGGTATCCAG described with additional reference to Figs. 9-15.

TATCTCCGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTACCTTCA encoded by the human genome.

TCTGCCCCCG GAM3263 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3263
G precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3263

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3263 precursor RNA is designated SEQ ID:6096, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6096 is located from position 127750640 to position 127750740 relative to chromosome 7 on the `-` strand.

GAM3263 precursor RNA folds onto itself, forming GAM3263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3263 precursor RNA, designated SEQ ID NO: 6096, and a schematic representation of a predicted secondary folding of GAM3263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3263 folded precursor RNA yielding a GAM3263 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3263 RNA, hereby incorporated herein.

GAM3263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3263 target RNA, herein designated GAM TARGET RNA. GAM3263 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3263 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3263 RNA, herein designated GAM RNA, to target binding sites on GAM3263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3263 target RNA into GAM3263 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3263 target genes. The mRNA of each one of this plurality of GAM3263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3263 RNA, herein designated GAM RNA, and which when bound by GAM3263 RNA causes inhibition of translation of the GAM3263 target mRNA into a corresponding GAM3263 target protein.

The mechanism of the translational inhibition exerted by GAM3263 RNA, herein designated GAM RNA, on one or more GAM3263 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3263 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3263 RNA, herein designated GAM RNA, of GAM3263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3263 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3263 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3263 RNA correlate with, and may be deduced from, the identity of the GAM3263 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3266 6123 CCTGTACAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCAGCCTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCAGGAGGG Messenger 3266 (GAM3266) oligonucleotides modulates expression of respective target genes

AAAACCCCAA whose function and utility is known in the art.

GGCTCTGCAG GAM3266 is a novel bioinformatically detectable regulatory, non protein coding,

CCTCCCTGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3266 was detected is

CCCCTCCGTT described with additional reference to Figs. 9-15.

TAAGGCTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCAGG encoded by the human genome.

GAM3266 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3266

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3266

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3266 precursor RNA is designated SEQ ID:6123, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6123 is located from position 3852982 to position 3853067 relative to chromosome 20 on the `+` strand.

GAM3266 precursor RNA folds onto itself, forming GAM3266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3266 precursor RNA, designated SEQ ID NO: 6123, and a schematic representation of a predicted secondary folding of GAM3266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3266 folded precursor RNA yielding a GAM3266 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3266 RNA, hereby incorporated herein.

GAM3266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3266 target RNA, herein designated GAM TARGET RNA. GAM3266 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3266 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3266 RNA, herein designated GAM RNA, to target binding sites on GAM3266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3266 target RNA into GAM3266 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3266 target genes. The mRNA of each one of this plurality of GAM3266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3266 RNA, herein designated GAM RNA, and which when bound by GAM3266 RNA causes inhibition of translation of the GAM3266 target mRNA into a corresponding GAM3266 target protein.

The mechanism of the translational inhibition exerted by GAM3266 RNA, herein designated GAM RNA, on one or more GAM3266 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3266 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3266 RNA, herein designated GAM RNA, of GAM3266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3266 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3266 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3266 RNA correlate with, and may be deduced from, the identity of the GAM3266 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3271 6468 GATATGTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TACTAGTGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGATGGCCTC Messenger 3271 (GAM3271) oligonucleotides modulates expression of respective target genes

TTTCAGCTCC whose function and utility is known in the art.

ATCGCTATGG GAM3271 is a novel bioinformatically detectable regulatory, non protein coding,

AGGCGAGGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3271 was detected is

CATCAATAAC described with additional reference to Figs. 9-15.

TCAGAGAAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGTGTC encoded by the human genome.

GAM3271 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3271

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3271

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3271 precursor RNA is designated SEQ ID:6468, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6468 is located from position 93938749 to position 93938835 relative to chromosome 10 on the `-` strand.

GAM3271 precursor RNA folds onto itself, forming GAM3271 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3271 precursor RNA, designated SEQ ID NO: 6468, and a schematic representation of a predicted secondary folding of GAM3271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3271 folded precursor RNA yielding a GAM3271 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3271 RNA, hereby incorporated herein.

GAM3271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3271 target RNA, herein designated GAM TARGET RNA. GAM3271 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3271 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3271 RNA, herein designated GAM RNA, to target binding sites on GAM3271 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3271 target RNA into GAM3271 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3271 target genes. The mRNA of each one of this plurality of GAM3271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3271 RNA, herein designated GAM RNA, and which when bound by GAM3271 RNA causes inhibition of translation of the GAM3271 target mRNA into a corresponding GAM3271 target protein.

The mechanism of the translational inhibition exerted by GAM3271 RNA, herein designated GAM RNA, on one or more GAM3271 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3271 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3271 RNA, herein designated GAM RNA, of GAM3271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3271 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3271 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3271 RNA correlate with, and may be deduced from, the identity of the GAM3271 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3293 6053 CCAGGCCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGTCTCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGGAGTAT Messenger 3293 (GAM3293) oligonucleotides modulates expression of respective target genes

TTGTGTTGAA whose function and utility is known in the art.

GATGGGTGGT GAM3293 is a novel bioinformatically detectable regulatory, non protein coding,

AACGTTCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3293 was detected is

AAAAGCCATG described with additional reference to Figs. 9-15.

CCCAGGAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGGCACAGTA encoded by the human genome.

CCCATGG GAM3293 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3293

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3293

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3293 precursor RNA is designated SEQ ID:6053, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6053 is located from position 72746540 to position 72746636 relative to chromosome 11 on the `-` strand.

GAM3293 precursor RNA folds onto itself, forming GAM3293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3293 precursor RNA, designated SEQ ID NO: 6053, and a schematic representation of a predicted secondary folding of GAM3293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3293 folded precursor RNA yielding a GAM3293 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3293 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3293 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3293 target RNA, herein designated GAM TARGET RNA. GAM3293 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3293 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3293 RNA, herein designated GAM RNA, to target binding sites on GAM3293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3293 target RNA into GAM3293 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3293 target genes. The mRNA of each one of this plurality of GAM3293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3293 RNA, herein designated GAM RNA, and which when bound by GAM3293 RNA causes inhibition of translation of the GAM3293 target mRNA into a corresponding GAM3293 target protein.

The mechanism of the translational inhibition exerted by GAM3293 RNA, herein designated GAM RNA, on one or more GAM3293 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3293 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3293 RNA, herein designated GAM RNA, of GAM3293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3293 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3293 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3293 RNA correlate with, and may be deduced from, the identity of the GAM3293 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3298 7336 TTGGGTCCTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAGTACCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGCTCATA Messenger 3298 (GAM3298) oligonucleotides modulates expression of respective target genes

GTGCAGGTAG whose function and utility is known in the art.

TTTTGGCATG GAM3298 is a novel bioinformatically detectable regulatory, non protein coding,

ACTCTACTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3298 was detected is

AGTATGGGCA described with additional reference to Figs. 9-15.

CTTCCAGTAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTTGGATAA encoded by the human genome.

CAA GAM3298 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3298 precursor RNA is designated SEQ ID:7336, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7336 is located from position 131248823 to position 131248915 relative to chromosome X on the `-` strand.

GAM3298 precursor RNA folds onto itself, forming GAM3298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3298 precursor RNA, designated SEQ ID NO: 7336, and a schematic representation of a predicted secondary folding of GAM3298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3298 folded precursor RNA yielding a GAM3298 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3298 RNA, hereby incorporated herein. Expression of GAM3298 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM3298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3298 target RNA, herein designated GAM TARGET RNA. GAM3298 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3298 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3298 RNA, herein designated GAM RNA, to target binding sites on GAM3298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3298 target RNA into GAM3298 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3298 target genes. The mRNA of each one of this plurality of GAM3298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3298 RNA, herein designated GAM RNA, and which when bound by GAM3298 RNA causes inhibition of translation of the GAM3298 target mRNA into a corresponding GAM3298 target protein.

The mechanism of the translational inhibition exerted by GAM3298 RNA, herein designated GAM RNA, on one or more GAM3298 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3298 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3298 RNA, herein designated GAM RNA, of GAM3298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3298 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3298 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3298 RNA correlate with, and may be deduced from, the identity of the GAM3298 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3311 6781 GGGACTGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGCTGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACACTACACA Messenger 3311 (GAM3311) oligonucleotides modulates expression of respective target genes
CTACTACACT whose function and utility is known in the art.

GCTGTCTGCT GAM3311 is a novel bioinformatically detectable regulatory, non protein coding,
GTGTGTGATA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3311 was detected is

AGGACACAGA described with additional reference to Figs. 9-15.

TAGTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM3311 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3311 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3311 precursor RNA is designated SEQ ID:6781, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6781 is located from position 47179504 to position 47179580 relative to chromosome 18 on the `+` strand.

GAM3311 precursor RNA folds onto itself, forming GAM3311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3311 precursor RNA, designated SEQ ID NO: 6781, and a schematic representation of a predicted secondary folding of GAM3311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3311 folded precursor RNA yielding a GAM3311 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3311 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3311 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3311 target RNA, herein designated GAM TARGET RNA. GAM3311 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3311 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3311 RNA, herein designated GAM RNA, to target binding sites on GAM3311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3311 target RNA into GAM3311 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3311 target genes. The mRNA of each one of this plurality of GAM3311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3311 RNA, herein designated GAM RNA, and which when bound by GAM3311 RNA causes inhibition of translation of the GAM3311 target mRNA into a corresponding GAM3311 target protein.

The mechanism of the translational inhibition exerted by GAM3311 RNA, herein designated GAM RNA, on one or more GAM3311 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3311 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3311 RNA, herein designated GAM RNA, of GAM3311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3311 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3311 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3311 RNA correlate with, and may be deduced from, the identity of the GAM3311 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3330 6104 CCTACATGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTACACTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTGTAAATA Messenger 3330 (GAM3330) oligonucleotides modulates expression of respective target genes

ACTGTGAAGA whose function and utility is known in the art.

GGCAATTGTC GAM3330 is a novel bioinformatically detectable regulatory, non protein coding, AGATAGCAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3330 was detected is

TTGGGCACCT described with additional reference to Figs. 9-15.

GCTGTGTACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTATATTGCA encoded by the human genome.

CTGGGGCTGA GAM3330 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3330

CGGGTGTGTA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3330

GG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3330 precursor RNA is designated SEQ ID:6104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6104 is located from position 62164417 to position 62164528 relative to chromosome 20 on the `-` strand.

GAM3330 precursor RNA folds onto itself, forming GAM3330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3330 precursor RNA, designated SEQ ID NO: 6104, and a schematic representation of a predicted secondary folding of GAM3330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3330 folded precursor RNA yielding a GAM3330 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3330 RNA, hereby incorporated herein.

GAM3330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3330 target RNA, herein designated GAM TARGET RNA. GAM3330 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3330 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3330 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3330 RNA, herein designated GAM RNA, to target binding sites on GAM3330 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3330 target RNA into GAM3330 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3330 target genes. The mRNA of each one of this plurality of GAM3330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3330 RNA, herein designated GAM RNA, and which when bound by GAM3330 RNA causes inhibition of translation of the GAM3330 target mRNA into a corresponding GAM3330 target protein.

The mechanism of the translational inhibition exerted by GAM3330 RNA, herein designated GAM RNA, on one or more GAM3330 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3330 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3330 RNA, herein designated GAM RNA, of GAM3330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3330 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3330 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3330 RNA correlate with, and may be deduced from, the identity of the GAM3330 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3350 6949 GTTTTGACAA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGCAGATAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGTGTAACT Messenger 3350 (GAM3350) oligonucleotides modulates expression of respective target genes
GAACTTATGA whose function and utility is known in the art.

CTTTCCTTAT GAM3350 is a novel bioinformatically detectable regulatory, non protein coding,
AGAAACTTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3350 was detected is

GAAAGTTCCC described with additional reference to Figs. 9-15.

TCATACCCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TATCTCAATC encoded by the human genome.

TTGTCACTAC GAM3350 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3350
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3350
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3350 precursor RNA is designated SEQ ID:6949, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6949 is located from position 9289824 to position 9289923 relative to chromosome 8 on the `+` strand.

GAM3350 precursor RNA folds onto itself, forming GAM3350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3350 precursor RNA, designated SEQ ID NO: 6949, and a schematic representation of a predicted secondary folding of GAM3350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3350 folded precursor RNA yielding a GAM3350 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3350 RNA, hereby incorporated herein.

GAM3350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3350 target RNA, herein designated GAM TARGET RNA. GAM3350 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3350 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3350 RNA, herein designated GAM RNA, to target binding sites on GAM3350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3350 target RNA into GAM3350 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3350 target genes. The mRNA of each one of this plurality of GAM3350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3350 RNA, herein designated GAM RNA, and which when bound by GAM3350 RNA causes inhibition of translation of the GAM3350 target mRNA into a corresponding GAM3350 target protein.

The mechanism of the translational inhibition exerted by GAM3350 RNA, herein designated GAM RNA, on one or more GAM3350 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3350 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3350 RNA, herein designated GAM RNA, of GAM3350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3350 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3350 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3350 RNA correlate with, and may be deduced from, the identity of the GAM3350 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3368 7008 TCAGATCAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTGACATGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GATTTTCATA Messenger 3368 (GAM3368) oligonucleotides modulates expression of respective target genes
GGAGCAGAAA whose function and utility is known in the art.

CCCTATTGTG GAM3368 is a novel bioinformatically detectable regulatory, non protein coding,
AACTCCAAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3368 was detected is

ACAAGGGATC described with additional reference to Figs. 9-15.

TAGGTTATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACTACTTATG encoded by the human genome.

AGAATCTAAT GAM3368 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3368
GCCTGATGAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3368
CTGA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3368 precursor RNA is designated SEQ ID:7008, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7008 is located from position 72291796 to position 72291909 relative to chromosome 16 on the `-` strand.

GAM3368 precursor RNA folds onto itself, forming GAM3368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3368 precursor RNA, designated SEQ ID NO: 7008, and a schematic representation of a predicted secondary folding of GAM3368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3368 folded precursor RNA yielding a GAM3368 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3368 RNA, hereby incorporated herein.

GAM3368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3368 target RNA, herein designated GAM TARGET RNA. GAM3368 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3368 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3368 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3368 RNA, herein designated GAM RNA, to target binding sites on GAM3368 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3368 target RNA into GAM3368 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3368 target genes. The mRNA of each one of this plurality of GAM3368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3368 RNA, herein designated GAM RNA, and which when bound by GAM3368 RNA causes inhibition of translation of the GAM3368 target mRNA into a corresponding GAM3368 target protein.

The mechanism of the translational inhibition exerted by GAM3368 RNA, herein designated GAM RNA, on one or more GAM3368 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3368 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3368 RNA, herein designated GAM RNA, of GAM3368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM3368 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3368 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3368 RNA correlate with, and may be deduced from, the identity of the GAM3368 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3414 5972 ATGGCATGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
CGTGTTGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTAGTGGAG Messenger 3414 (GAM3414) oligonucleotides modulates expression of respective target genes
GCTATCTCCC whose function and utility is known in the art.

CAGTGGTCAA GAM3414 is a novel bioinformatically detectable regulatory, non protein coding,
AGGAGGTCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3414 was detected is

GCTGGAGAAA described with additional reference to Figs. 9-15.

TTATATTTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAACTTGAA encoded by the human genome.

GCAGCAGCTG GAM3414 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3414
T precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3414

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3414 precursor RNA is designated SEQ ID:5972, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5972 is located from position 50214299 to position 50214399 relative to chromosome 7 on the `+` strand.

GAM3414 precursor RNA folds onto itself, forming GAM3414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3414 precursor RNA, designated SEQ ID NO: 5972, and a schematic representation of a predicted secondary folding of GAM3414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3414 folded precursor RNA yielding a GAM3414 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3414 RNA, hereby incorporated herein.

GAM3414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3414 target RNA, herein designated GAM TARGET RNA. GAM3414 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3414 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3414 RNA, herein designated GAM RNA, to target binding sites on GAM3414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3414 target RNA into GAM3414 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3414 target genes. The mRNA of each one of this plurality of GAM3414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3414 RNA, herein designated GAM RNA, and which when bound by GAM3414 RNA causes inhibition of translation of the GAM3414 target mRNA into a corresponding GAM3414 target protein.

The mechanism of the translational inhibition exerted by GAM3414 RNA, herein designated GAM RNA, on one or more GAM3414 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3414 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3414 RNA, herein designated GAM RNA, of

GAM3414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3414 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3414 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3414 RNA correlate with, and may be deduced from, the identity of the GAM3414 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3422 6815 GGGGGACAGA GCGAGACTCC ATCTTTTCTG GGAGACTCCA TTGGGAGACT GTCTTTTTTG GGAGACGGAG TCGTGCCTTA GTTTCCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3422 (GAM3422) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM3422 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM3422 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM3422 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3422 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3422 precursor RNA is designated SEQ ID:6815, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6815 is located from position 122969346 to position 122969432 relative to chromosome 11 on the `-` strand.

GAM3422 precursor RNA folds onto itself, forming GAM3422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3422 precursor RNA, designated SEQ ID NO: 6815, and a schematic representation of a predicted secondary folding of GAM3422 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3422 folded precursor RNA yielding a GAM3422 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3422 RNA, hereby incorporated herein.

GAM3422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3422 target RNA, herein designated GAM TARGET RNA. GAM3422 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3422 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3422 RNA, herein designated GAM RNA, to target binding sites on GAM3422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3422 target RNA into GAM3422 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3422 target genes. The mRNA of each one of this plurality of GAM3422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3422 RNA, herein designated GAM RNA, and which when bound by GAM3422 RNA causes inhibition of translation of the GAM3422 target mRNA into a corresponding GAM3422 target protein.

The mechanism of the translational inhibition exerted by GAM3422 RNA, herein designated GAM RNA, on one or more GAM3422 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3422 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM3422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3422 RNA, herein designated GAM RNA, of GAM3422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3422 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3422 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3422 RNA correlate with, and may be deduced from, the identity of the GAM3422 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3426 5954 ATCAATCACA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGTGACC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTACTCCCT Messenger 3426 (GAM3426) oligonucleotides modulates expression of respective target genes

GTCAGGTCAG whose function and utility is known in the art.

TAAGAGTCAC GAM3426 is a novel bioinformatically detectable regulatory, non protein coding,

CCAGTGTAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3426 was detected is

CAGCATGAT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3426 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3426

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3426

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3426 precursor RNA is designated SEQ ID:5954, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5954 is located from position 98551385 to position 98551453 relative to chromosome 7 on the `+` strand.

GAM3426 precursor RNA folds onto itself, forming GAM3426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3426 precursor RNA, designated SEQ ID NO: 5954, and a schematic representation of a predicted secondary folding of GAM3426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3426 folded precursor RNA yielding a GAM3426 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3426 RNA, hereby incorporated herein.

GAM3426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3426 target RNA, herein designated GAM TARGET RNA. GAM3426 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3426 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3426 RNA, herein designated GAM RNA, to target binding sites on GAM3426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3426 target RNA into GAM3426 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3426 target genes. The mRNA of each one of this plurality of GAM3426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3426 RNA, herein designated GAM RNA, and which when bound by GAM3426 RNA causes inhibition of translation of the GAM3426 target mRNA into a corresponding GAM3426 target protein.

The mechanism of the translational inhibition exerted by GAM3426 RNA, herein designated GAM RNA, on one or more GAM3426 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3426 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3426 RNA, herein designated GAM RNA, of GAM3426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3426 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3426 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3426 RNA correlate with, and may be deduced from, the identity of the GAM3426 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3431 6804 GGGCGGGGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCGTCTTA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCAGCAGTG Messenger 3431 (GAM3431) oligonucleotides modulates expression of respective target genes

TTTGGGTGCG whose function and utility is known in the art.

GTTGGGAGTC GAM3431 is a novel bioinformatically detectable regulatory, non protein coding,

TCTAATACTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3431 was detected is

CCGGGTAATG described with additional reference to Figs. 9-15.

ATGGAGGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGTCC encoded by the human genome.

GAM3431 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3431

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3431

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3431 precursor RNA is designated SEQ ID:6804, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6804 is located from position 6952114 to position 6952199 relative to chromosome 12 on the `+` strand.

GAM3431 precursor RNA folds onto itself, forming GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3431 precursor RNA, designated SEQ ID NO: 6804, and a schematic representation of a predicted secondary folding of GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3431 folded precursor RNA yielding a GAM3431 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3431 RNA, hereby incorporated herein. Expression of GAM3431 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM3431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3431 target RNA, herein designated GAM TARGET RNA. GAM3431 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3431 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3431 RNA, herein designated GAM RNA, to target binding sites on GAM3431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3431 target RNA into GAM3431 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3431 target genes. The mRNA of each one of this

plurality of GAM3431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3431 RNA, herein designated GAM RNA, and which when bound by GAM3431 RNA causes inhibition of translation of the GAM3431 target mRNA into a corresponding GAM3431 target protein.

The mechanism of the translational inhibition exerted by GAM3431 RNA, herein designated GAM RNA, on one or more GAM3431 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3431 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3431 RNA, herein designated GAM RNA, of GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3431 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3431 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3431 RNA correlate with, and may be deduced from, the identity of the GAM3431 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3452 5703 ACTCCAGCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCCTCTGAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCAGTTCAA Messenger 3452 (GAM3452) oligonucleotides modulates expression of respective target genes

TCCGACCATG whose function and utility is known in the art.

CCCAAGCCCA GAM3452 is a novel bioinformatically detectable regulatory, non protein coding,

AGCGGGCCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3452 was detected is

TCCTCCAGAA described with additional reference to Figs. 9-15.

CTGCTCCGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCTGGCTGT encoded by the human genome.

GT GAM3452 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3452

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3452

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3452 precursor RNA is designated SEQ ID:5703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5703 is located from position 124136937 to position 124137028 relative to chromosome 9 on the `-` strand.

GAM3452 precursor RNA folds onto itself, forming GAM3452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3452 precursor RNA, designated SEQ ID NO: 5703, and a schematic representation of a predicted secondary folding of GAM3452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3452 folded precursor RNA yielding a GAM3452 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3452 RNA, hereby incorporated herein.

GAM3452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3452 target RNA, herein designated GAM TARGET RNA. GAM3452 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3452 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3452 RNA, herein designated GAM RNA, to target binding sites on GAM3452 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3452 target RNA

into GAM3452 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3452 target genes. The mRNA of each one of this plurality of GAM3452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3452 RNA, herein designated GAM RNA, and which when bound by GAM3452 RNA causes inhibition of translation of the GAM3452 target mRNA into a corresponding GAM3452 target protein.

The mechanism of the translational inhibition exerted by GAM3452 RNA, herein designated GAM RNA, on one or more GAM3452 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3452 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3452 RNA, herein designated GAM RNA, of GAM3452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3452 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3452 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3452 RNA correlate with, and may be deduced from, the identity of the GAM3452 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3461 5996 CACCTGCCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TATTACATTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTTGATGG Messenger 3461 (GAM3461) oligonucleotides modulates expression of respective target genes
TTTGTATCTC whose function and utility is known in the art.

AAAGGAGTAC GAM3461 is a novel bioinformatically detectable regulatory, non protein coding,
AGTGAACGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3461 was detected is

ACTTGTTTAA described with additional reference to Figs. 9-15.

AGATACACCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAAGAAAAA encoded by the human genome.

GAGAAGAGGC GAM3461 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3461
AGAGTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3461
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3461 precursor RNA is designated SEQ ID:5996, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5996 is located from position 88520252 to position 88520357 relative to chromosome 9 on the `+` strand.

GAM3461 precursor RNA folds onto itself, forming GAM3461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3461 precursor RNA, designated SEQ ID NO: 5996, and a schematic representation of a predicted secondary folding of GAM3461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3461 folded precursor RNA yielding a GAM3461 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3461 RNA, hereby incorporated herein.

GAM3461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3461 target RNA, herein designated GAM TARGET RNA. GAM3461 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3461 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3461 RNA, herein designated GAM RNA, to target binding sites on GAM3461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3461 target RNA into GAM3461 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3461 target genes. The mRNA of each one of this plurality of GAM3461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3461 RNA, herein designated GAM RNA, and which when bound by GAM3461 RNA causes inhibition of translation of the GAM3461 target mRNA into a corresponding GAM3461 target protein.

The mechanism of the translational inhibition exerted by GAM3461 RNA, herein designated GAM RNA, on one or more GAM3461 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3461 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3461 RNA, herein designated GAM RNA, of GAM3461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3461 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3461 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3461 RNA correlate with, and may be deduced from, the identity of the GAM3461 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3463 6798 GGGATGGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGCAGACAC detected oligonucleotides of the present invention, referred to here as Genomic Address
AATATAGCAA Messenger 3463 (GAM3463) oligonucleotides modulates expression of respective target genes
ATAGAGGGTC whose function and utility is known in the art.

TTTTCCTGTC GAM3463 is a novel bioinformatically detectable regulatory, non protein coding,
ATGGAAATCG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3463 was detected is

GTCAGCCCTG described with additional reference to Figs. 9-15.

ATGCTTCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTTCTTTCC encoded by the human genome.

C GAM3463 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3463 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3463 precursor RNA is designated SEQ ID:6798, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6798 is located from position 131571664 to position 131571754 relative to chromosome 7 on the `+` strand.

GAM3463 precursor RNA folds onto itself, forming GAM3463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3463 precursor RNA, designated SEQ ID NO: 6798, and a schematic representation of a predicted secondary folding of GAM3463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3463 folded precursor RNA yielding a GAM3463 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3463 RNA, hereby incorporated herein.

GAM3463 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3463 target RNA, herein designated GAM TARGET RNA. GAM3463 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3463 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3463 RNA, herein designated GAM RNA, to target binding sites on GAM3463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3463 target RNA into GAM3463 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3463 target genes. The mRNA of each one of this plurality of GAM3463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3463 RNA, herein designated GAM RNA, and which when bound by GAM3463 RNA causes inhibition of translation of the GAM3463 target mRNA into a corresponding GAM3463 target protein.

The mechanism of the translational inhibition exerted by GAM3463 RNA, herein designated GAM RNA, on one or more GAM3463 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3463 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3463 RNA, herein designated GAM RNA, of GAM3463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3463 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3463 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3463 RNA correlate with, and may be deduced from, the identity of the GAM3463 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3479 6877 GTCCATCTTC AGTGGCATTG GGCCTTGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3479 (GAM3479) oligonucleotides modulates expression of respective target genes

GGGATGCTGA whose function and utility is known in the art.

GTTATCCACT GAM3479 is a novel bioinformatically detectable regulatory, non protein coding,
GGAGCATCGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3479 was detected is

CAGTACAGGC described with additional reference to Figs. 9-15.

AGGCACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAGTGGATC encoded by the human genome.

CATCGGAGGT GAM3479 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3479
GGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3479

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3479 precursor RNA is designated SEQ ID:6877, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6877 is located from position 69762451 to position 69762553 relative to chromosome 16 on the `+` strand.

GAM3479 precursor RNA folds onto itself, forming GAM3479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3479 precursor RNA, designated SEQ ID NO: 6877, and a schematic representation of a predicted secondary folding of GAM3479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3479 folded precursor RNA yielding a GAM3479 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3479 RNA, hereby incorporated herein.

GAM3479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3479 target RNA, herein designated GAM TARGET RNA. GAM3479 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3479 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3479 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3479 RNA, herein designated GAM RNA, to target binding sites on GAM3479 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3479 target RNA into GAM3479 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3479 target genes. The mRNA of each one of this plurality of GAM3479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3479 RNA, herein designated GAM RNA, and which when bound by GAM3479 RNA causes inhibition of translation of the GAM3479 target mRNA into a corresponding GAM3479 target protein.

The mechanism of the translational inhibition exerted by GAM3479 RNA, herein designated GAM RNA, on one or more GAM3479 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3479 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3479 RNA, herein designated GAM RNA, of GAM3479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3479 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3479 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3479 RNA correlate with, and may be deduced from, the identity of the GAM3479 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3486 6058 CCAGTTCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTAGTGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTCAAAT Messenger 3486 (GAM3486) oligonucleotides modulates expression of respective target genes

GAAAGGCCAC whose function and utility is known in the art.

TTTCAGCAAG GAM3486 is a novel bioinformatically detectable regulatory, non protein coding,

TTTTCCTGAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3486 was detected is

ATTGTCGGAG described with additional reference to Figs. 9-15.

ACTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3486 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3486

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3486

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3486 precursor RNA is designated SEQ ID:6058, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6058 is located from position 59248137 to position 59248211 relative to chromosome 20 on the `+` strand.

GAM3486 precursor RNA folds onto itself, forming GAM3486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3486 precursor RNA, designated SEQ ID NO: 6058, and a schematic representation of a predicted secondary folding of GAM3486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3486 folded precursor RNA yielding a GAM3486 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3486 RNA, hereby incorporated herein.

GAM3486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3486 target RNA, herein designated GAM TARGET RNA. GAM3486 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3486 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3486 RNA, herein designated GAM RNA, to target binding sites on GAM3486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3486 target RNA into GAM3486 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3486 target genes. The mRNA of each one of this plurality of GAM3486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3486 RNA, herein designated GAM RNA, and which when bound by GAM3486 RNA causes inhibition of translation of the GAM3486 target mRNA into a corresponding GAM3486 target protein.

The mechanism of the translational inhibition exerted by GAM3486 RNA, herein designated GAM RNA, on one or more GAM3486 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3486 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3486 RNA, herein designated GAM RNA, of GAM3486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3486 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3486 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3486 RNA correlate with, and may be deduced from, the identity of the GAM3486 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3513 6284 GAAATGGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTGCTTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACCGAGGCT Messenger 3513 (GAM3513) oligonucleotides modulates expression of respective target genes
GGAGTGCAGT whose function and utility is known in the art.

GGCATGATCT GAM3513 is a novel bioinformatically detectable regulatory, non protein coding,
CTGCTCACTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3513 was detected is

CAAGCTCCAC described with additional reference to Figs. 9-15.

CTCCCGGGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CACGCCATTC encoded by the human genome.

TCCTGCCTC GAM3513 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3513
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3513
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3513 precursor RNA is designated SEQ ID:6284, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6284 is located from position 130044291 to position 130044389 relative to chromosome 11 on the `+` strand.

GAM3513 precursor RNA folds onto itself, forming GAM3513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3513 precursor RNA, designated SEQ ID NO: 6284, and a schematic representation of a predicted secondary folding of GAM3513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3513 folded precursor RNA yielding a GAM3513 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3513 RNA, hereby incorporated herein.

GAM3513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3513 target RNA, herein designated GAM TARGET RNA. GAM3513 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3513 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3513 RNA, herein designated GAM RNA, to target binding sites on GAM3513 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3513 target RNA into GAM3513 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3513 target genes. The mRNA of each one of this plurality of GAM3513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3513 RNA, herein designated GAM RNA, and which when bound by GAM3513 RNA causes inhibition of translation of the GAM3513 target mRNA into a corresponding GAM3513 target protein.

The mechanism of the translational inhibition exerted by GAM3513 RNA, herein designated GAM RNA, on one or more GAM3513 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3513 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3513 RNA, herein designated GAM RNA, of GAM3513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM3513 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3513 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3513 RNA correlate with, and may be deduced from, the identity of the GAM3513 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3535 6278 CTTTTTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCCTTCGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTATGCAGC Messenger 3535 (GAM3535) oligonucleotides modulates expression of respective target
genes
CTGTGAACAG whose function and utility is known in the art.

CGTCTGGGAA GAM3535 is a novel bioinformatically detectable regulatory, non protein coding,
AGTGGTGGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3535 was detected is

ATTGGTTGCA described with additional reference to Figs. 9-15.

TAATTTGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
TGAGGCTTAT encoded by the human genome.

GGAGGAAAGG GAM3535 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM3535
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM3535
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3535 precursor RNA is designated SEQ ID:6278, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6278 is located from position 22420611 to position 22420710 relative to chromosome 13 on the `+` strand.

GAM3535 precursor RNA folds onto itself, forming GAM3535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3535 precursor RNA, designated SEQ ID NO: 6278, and a schematic representation of a predicted secondary folding of GAM3535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3535 folded precursor RNA yielding a GAM3535 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3535 RNA, hereby incorporated herein.

GAM3535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3535 target RNA, herein designated GAM TARGET RNA. GAM3535 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3535 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3535 RNA, herein designated GAM RNA, to target binding sites on GAM3535 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3535 target RNA into GAM3535 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3535 target genes. The mRNA of each one of this plurality of GAM3535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3535 RNA, herein designated GAM RNA, and which when bound by GAM3535 RNA causes inhibition of translation of the GAM3535 target mRNA into a corresponding GAM3535 target protein.

The mechanism of the translational inhibition exerted by GAM3535 RNA, herein designated GAM RNA, on one or more GAM3535 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3535 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3535 RNA, herein designated GAM RNA, of

GAM3535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3535 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3535 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3535 RNA correlate with, and may be deduced from, the identity of the GAM3535 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3593 5825 AGTTCTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 3593 (GAM3593) oligonucleotides modulates expression of respective target genes
GTTTGTTACA whose function and utility is known in the art.

TAGGTATACA GAM3593 is a novel bioinformatically detectable regulatory, non protein coding,
TGTGCTATGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3593 was detected is

TGGTGTGCTG described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM3593 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3593

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3593

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3593 precursor RNA is designated SEQ ID:5825, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5825 is located from position 190505666 to position 190505747 relative to chromosome 3 on the `+` strand.

GAM3593 precursor RNA folds onto itself, forming GAM3593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3593 precursor RNA, designated SEQ ID NO: 5825, and a schematic representation of a predicted secondary folding of GAM3593 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3593 folded precursor RNA yielding a GAM3593 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3593 RNA, hereby incorporated herein.

GAM3593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3593 target RNA, herein designated GAM TARGET RNA. GAM3593 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3593 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3593 RNA, herein designated GAM RNA, to target binding sites on GAM3593 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3593 target RNA into GAM3593 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3593 target genes. The mRNA of each one of this plurality of GAM3593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3593 RNA, herein designated GAM RNA, and which when bound by GAM3593 RNA causes inhibition of translation of the GAM3593 target mRNA into a corresponding GAM3593 target protein.

The mechanism of the translational inhibition exerted by GAM3593 RNA, herein designated GAM RNA, on one or more GAM3593 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3593 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM3593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3593 RNA, herein designated GAM RNA, of GAM3593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3593 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3593 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3593 RNA correlate with, and may be deduced from, the identity of the GAM3593 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3595 5736 AGAGTCTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTGTCACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 3595 (GAM3595) oligonucleotides modulates expression of respective target genes

GTAGTGGCAT whose function and utility is known in the art.

GATCTCGGCT GAM3595 is a novel bioinformatically detectable regulatory, non protein coding,

CACTGCAACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3595 was detected is

CCCGCCTCCT described with additional reference to Figs. 9-15.

GGGTTCAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CATTCT encoded by the human genome.

GAM3595 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3595

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3595

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3595 precursor RNA is designated SEQ ID:5736, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5736 is located from position 79670251 to position 79670336 relative to chromosome 14 on the `+` strand.

GAM3595 precursor RNA folds onto itself, forming GAM3595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3595 precursor RNA, designated SEQ ID NO: 5736, and a schematic representation of a predicted secondary folding of GAM3595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3595 folded precursor RNA yielding a GAM3595 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3595 RNA, hereby incorporated herein.

GAM3595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3595 target RNA, herein designated GAM TARGET RNA. GAM3595 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3595 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3595 RNA, herein designated GAM RNA, to target binding sites on GAM3595 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3595 target RNA into GAM3595 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3595 target genes. The mRNA of each one of this plurality of GAM3595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3595 RNA, herein designated GAM RNA, and which when bound by GAM3595 RNA causes inhibition of translation of the GAM3595 target mRNA into a corresponding GAM3595 target protein.

The mechanism of the translational inhibition exerted by GAM3595 RNA, herein designated GAM RNA, on one or more GAM3595 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3595 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3595 RNA, herein designated GAM RNA, of GAM3595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3595 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3595 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3595 RNA correlate with, and may be deduced from, the identity of the GAM3595 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3605 6144 CGGACCCTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTGAGCAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCCTATTCC Messenger 3605 (GAM3605) oligonucleotides modulates expression of respective target genes

ATGACAGTGT whose function and utility is known in the art.

GTTGAGCTCT GAM3605 is a novel bioinformatically detectable regulatory, non protein coding,

CCATTGTCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3605 was detected is

AGGCTGGTAG described with additional reference to Figs. 9-15.

GGTGTTCAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGAGGTGCC encoded by the human genome.

G GAM3605 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3605

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3605

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3605 precursor RNA is designated SEQ ID:6144, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6144 is located from position 30275106 to position 30275196 relative to chromosome 8 on the `+` strand.

GAM3605 precursor RNA folds onto itself, forming GAM3605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3605 precursor RNA, designated SEQ ID NO: 6144, and a schematic representation of a predicted secondary folding of GAM3605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3605 folded precursor RNA yielding a GAM3605 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3605 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3605 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3605 target RNA, herein designated GAM TARGET RNA. GAM3605 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3605 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3605 RNA, herein designated GAM RNA, to target binding sites on GAM3605 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3605 target RNA into GAM3605 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3605 target genes. The mRNA of each one of this plurality of GAM3605 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM3605 RNA, herein designated GAM RNA, and which when bound by GAM3605 RNA causes inhibition of translation of the GAM3605 target mRNA into a corresponding GAM3605 target protein.

The mechanism of the translational inhibition exerted by GAM3605 RNA, herein designated GAM RNA, on one or more GAM3605 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3605 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3605 RNA, herein designated GAM RNA, of GAM3605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3605 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3605 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3605 RNA correlate with, and may be deduced from, the identity of the GAM3605 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3630 6886 GTCTATTATG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTCTGACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCACAGACAT Messenger 3630 (GAM3630) oligonucleotides modulates expression of respective target genes

CTGTCAAGGA whose function and utility is known in the art.

AGAAGGATTC GAM3630 is a novel bioinformatically detectable regulatory, non protein coding,

TTTGAGCGTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3630 was detected is

TTTGTGTCAG described with additional reference to Figs. 9-15.

TCAACTGCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATATGGAC encoded by the human genome.

GAM3630 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3630

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3630

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3630 precursor RNA is designated SEQ ID:6886, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6886 is located from position 78654898 to position 78654985 relative to chromosome 11 on the `-` strand.

GAM3630 precursor RNA folds onto itself, forming GAM3630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3630 precursor RNA, designated SEQ ID NO: 6886, and a schematic representation of a predicted secondary folding of GAM3630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3630 folded precursor RNA yielding a GAM3630 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3630 RNA, hereby incorporated herein.

GAM3630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3630 target RNA, herein designated GAM TARGET RNA. GAM3630 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3630 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3630 RNA, herein designated GAM RNA, to target binding sites on GAM3630 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3630 target RNA into GAM3630 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3630 target genes. The mRNA of each one of this plurality of GAM3630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3630 RNA, herein designated GAM RNA, and which when bound by GAM3630 RNA causes inhibition of translation of the GAM3630 target mRNA into a corresponding GAM3630 target protein.

The mechanism of the translational inhibition exerted by GAM3630 RNA, herein designated GAM RNA, on one or more GAM3630 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3630 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3630 RNA, herein designated GAM RNA, of GAM3630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3630 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3630 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3630 RNA correlate with, and may be deduced from, the identity of the GAM3630 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3640 6858 GGTTTCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AACTTTGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GATCATTATA Messenger 3640 (GAM3640) oligonucleotides modulates expression of respective target genes

AAAATACTAG whose function and utility is known in the art.

GGTAAAAAAG GAM3640 is a novel bioinformatically detectable regulatory, non protein coding,

CAACCTTAGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3640 was detected is

AATCCCAGCA described with additional reference to Figs. 9-15.

ATTTGGGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CC encoded by the human genome.

GAM3640 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3640 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3640 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3640 precursor RNA is designated SEQ ID:6858, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6858 is located from position 47669037 to position 47669118 relative to chromosome 11 on the `-` strand.

GAM3640 precursor RNA folds onto itself, forming GAM3640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3640 precursor RNA, designated SEQ ID NO: 6858, and a schematic representation of a predicted secondary folding of GAM3640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3640 folded precursor RNA yielding a GAM3640 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3640 RNA, hereby incorporated herein.

GAM3640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3640 target RNA, herein designated GAM TARGET RNA. GAM3640 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3640 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3640 RNA, herein designated GAM RNA, to target binding sites on GAM3640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3640 target RNA into GAM3640 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3640 target genes. The mRNA of each one of this plurality of GAM3640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3640 RNA, herein designated GAM RNA, and which when bound by GAM3640 RNA causes inhibition of translation of the GAM3640 target mRNA into a corresponding GAM3640 target protein.

The mechanism of the translational inhibition exerted by GAM3640 RNA, herein designated GAM RNA, on one or more GAM3640 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3640 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3640 RNA, herein designated GAM RNA, of GAM3640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3640 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3640 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3640 RNA correlate with, and may be deduced from, the identity of the GAM3640 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3666 6531 GCTCACAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTAGGTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGAAAGCT Messenger 3666 (GAM3666) oligonucleotides modulates expression of respective target genes

GAGAAAGCGA whose function and utility is known in the art.

AGAGGTGGTT GAM3666 is a novel bioinformatically detectable regulatory, non protein coding,

CAGGGGATCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3666 was detected is

CTCTTTCCTA described with additional reference to Figs. 9-15.

CTTGTTCCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCACCTCAAA encoded by the human genome.

CTCACCTTCT GAM3666 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3666

ACTGCACAGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3666

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3666 precursor RNA is designated SEQ ID:6531, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6531 is located from position 143019237 to position 143019346 relative to chromosome 1 on the `+` strand.

GAM3666 precursor RNA folds onto itself, forming GAM3666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3666 precursor RNA, designated SEQ ID NO: 6531, and a schematic representation of a predicted secondary folding of GAM3666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3666 folded precursor RNA yielding a GAM3666 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3666 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3666 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3666 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3666 target RNA, herein designated GAM TARGET RNA. GAM3666 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3666 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3666 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3666 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3666 RNA, herein designated GAM RNA, to target binding sites on GAM3666 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3666 target RNA into GAM3666 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3666 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3666 target genes. The mRNA of each one of this plurality of GAM3666 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3666 RNA, herein designated GAM RNA, and which when bound by GAM3666 RNA causes inhibition of translation of the GAM3666 target mRNA into a corresponding GAM3666 target protein.

The mechanism of the translational inhibition exerted by GAM3666 RNA, herein designated GAM RNA, on one or more GAM3666 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3666 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3666 RNA, herein designated GAM RNA, of GAM3666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3666 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3666 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3666 RNA correlate with, and may be deduced from, the identity of the GAM3666 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3691 6194 CTGAATGACC TGCAGTCAGG GCCCAGAGTT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3691 (GAM3691) oligonucleotides modulates expression of respective target genes

GGGACTCTAT whose function and utility is known in the art.

ACTACCCTGG GAM3691 is a novel bioinformatically detectable regulatory, non protein coding,
GCTCTGGTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3691 was detected is

GTAGGTTTGT described with additional reference to Figs. 9-15.

AG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3691 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3691

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3691

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3691 precursor RNA is designated SEQ ID:6194, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6194 is located from position 8085889 to position 8085960 relative to chromosome 11 on the `+` strand.

GAM3691 precursor RNA folds onto itself, forming GAM3691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3691 precursor RNA, designated SEQ ID NO: 6194, and a schematic representation of a predicted secondary folding of GAM3691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3691 folded precursor RNA yielding a GAM3691 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3691 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3691 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3691 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3691 target RNA, herein designated GAM TARGET RNA. GAM3691 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3691 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM3691 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3691 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3691 RNA, herein designated GAM RNA, to target binding sites on GAM3691 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3691 target RNA into GAM3691 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3691 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3691 target genes. The mRNA of each one of this plurality of GAM3691 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3691 RNA, herein designated GAM RNA, and which when bound by GAM3691 RNA causes inhibition of translation of the GAM3691 target mRNA into a corresponding GAM3691 target protein.

The mechanism of the translational inhibition exerted by GAM3691 RNA, herein designated GAM RNA, on one or more GAM3691 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3691 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3691 RNA, herein designated GAM RNA, of GAM3691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3691 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3691 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3691 RNA correlate with, and may be deduced from, the identity of the GAM3691 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3747 5731 AGAGGGTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CATTAGGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTGAGATGA Messenger 3747 (GAM3747) oligonucleotides modulates expression of respective target genes

GTTGCTTGGC whose function and utility is known in the art.

ACAGATCAGC GAM3747 is a novel bioinformatically detectable regulatory, non protein coding,

AGAACAGGAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3747 was detected is

CCTGGTGATA described with additional reference to Figs. 9-15.

AGGCATCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTTGCTAAC encoded by the human genome.

CACTTATCAT GAM3747 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3747

CTTCCATTAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3747

TCTCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3747 precursor RNA is designated SEQ ID:5731, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5731 is located from position 117953553 to position 117953667 relative to chromosome 10 on the `-` strand.

GAM3747 precursor RNA folds onto itself, forming GAM3747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3747 precursor RNA, designated SEQ ID NO: 5731, and a schematic representation of a predicted secondary folding of GAM3747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3747 folded precursor RNA yielding a GAM3747 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3747 RNA, hereby incorporated herein.

GAM3747 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3747 target RNA, herein designated GAM TARGET RNA. GAM3747 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3747 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3747 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3747 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3747 RNA, herein designated GAM RNA, to target binding sites on GAM3747 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3747 target RNA into GAM3747 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3747 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3747 target genes. The mRNA of each one of this plurality of GAM3747 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3747 RNA, herein designated GAM RNA, and which when bound by GAM3747 RNA causes inhibition of translation of the GAM3747 target mRNA into a corresponding GAM3747 target protein.

The mechanism of the translational inhibition exerted by GAM3747 RNA, herein designated GAM RNA, on one or more GAM3747 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3747 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3747 RNA, herein designated GAM RNA, of GAM3747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3747 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3747 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3747 RNA correlate with, and may be deduced from, the identity of the GAM3747 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3768 6947 GTTTGTGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAGGACTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAAAAATATG Messenger 3768 (GAM3768) oligonucleotides modulates expression of respective target genes
AGAGTAGGAG whose function and utility is known in the art.

TTTGGGCTCT GAM3768 is a novel bioinformatically detectable regulatory, non protein coding,
TGAGCTTGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3768 was detected is

CCTGGCCTTC described with additional reference to Figs. 9-15.

AAATTTCCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTTCACTC encoded by the human genome.

ACTAGC GAM3768 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3768
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3768
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3768 precursor RNA is designated SEQ ID:6947, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6947 is located from position 47243042 to position 47243137 relative to chromosome X on the `+` strand.

GAM3768 precursor RNA folds onto itself, forming GAM3768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3768 precursor RNA, designated SEQ ID NO: 6947, and a schematic representation of a predicted secondary folding of GAM3768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3768 folded precursor RNA yielding a GAM3768 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM3768 RNA, hereby incorporated herein.

GAM3768 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3768 target RNA, herein designated GAM TARGET RNA. GAM3768 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3768 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3768 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3768 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3768 RNA, herein designated GAM RNA, to target binding sites on GAM3768 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3768 target RNA into GAM3768 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3768 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3768 target genes. The mRNA of each one of this plurality of GAM3768 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3768 RNA, herein designated GAM RNA, and which when bound by GAM3768 RNA causes inhibition of translation of the GAM3768 target mRNA into a corresponding GAM3768 target protein.

The mechanism of the translational inhibition exerted by GAM3768 RNA, herein designated GAM RNA, on one or more GAM3768 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3768 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3768 RNA, herein designated GAM RNA, of GAM3768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3768 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3768 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3768 RNA correlate with, and may be deduced from, the identity of the GAM3768 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3781 6482 GCAAGGTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAATAAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGATAGTAAA Messenger 3781 (GAM3781) oligonucleotides modulates expression of respective target genes

GTCATGTAAC whose function and utility is known in the art.

ACTTTCTGTG GAM3781 is a novel bioinformatically detectable regulatory, non protein coding,

CAGGTTAACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3781 was detected is

TTTCTGGACC described with additional reference to Figs. 9-15.

TTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3781 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3781

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3781

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3781 precursor RNA is designated SEQ ID:6482, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6482 is located from position 23264656 to position 23264729 relative to chromosome 19 on the `-` strand.

GAM3781 precursor RNA folds onto itself, forming GAM3781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3781 precursor RNA, designated SEQ ID NO: 6482, and a schematic representation of a predicted secondary folding of GAM3781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3781 folded precursor RNA

yielding a GAM3781 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3781 RNA, hereby incorporated herein.

GAM3781 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3781 target RNA, herein designated GAM TARGET RNA. GAM3781 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3781 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3781 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3781 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3781 RNA, herein designated GAM RNA, to target binding sites on GAM3781 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3781 target RNA into GAM3781 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3781 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3781 target genes. The mRNA of each one of this plurality of GAM3781 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3781 RNA, herein designated GAM RNA, and which when bound by GAM3781 RNA causes inhibition of translation of the GAM3781 target mRNA into a corresponding GAM3781 target protein.

The mechanism of the translational inhibition exerted by GAM3781 RNA, herein designated GAM RNA, on one or more GAM3781 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3781 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3781 RNA, herein designated GAM RNA, of GAM3781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3781 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3781 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3781 RNA correlate with, and may be deduced from, the identity of the GAM3781 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3788 6006 CACTGTGTGA TTTGATTCCA AGCTACCCAT GAAGAAACCC AGACTCAGAG GTCACTTGCC TAGGGTCACA CAGTG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3788 (GAM3788) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM3788 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM3788 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM3788 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3788 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3788 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3788 precursor RNA is designated SEQ ID:6006, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6006 is located from position 50069896 to position 50069970 relative to chromosome 12 on the `-` strand.

GAM3788 precursor RNA folds onto itself, forming GAM3788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3788 precursor RNA, designated SEQ ID NO: 6006, and a

schematic representation of a predicted secondary folding of GAM3788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3788 folded precursor RNA yielding a GAM3788 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3788 RNA, hereby incorporated herein.

GAM3788 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3788 target RNA, herein designated GAM TARGET RNA. GAM3788 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3788 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3788 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3788 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3788 RNA, herein designated GAM RNA, to target binding sites on GAM3788 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3788 target RNA into GAM3788 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3788 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3788 target genes. The mRNA of each one of this plurality of GAM3788 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3788 RNA, herein designated GAM RNA, and which when bound by GAM3788 RNA causes inhibition of translation of the GAM3788 target mRNA into a corresponding GAM3788 target protein.

The mechanism of the translational inhibition exerted by GAM3788 RNA, herein designated GAM RNA, on one or more GAM3788 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3788 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3788 RNA, herein designated GAM RNA, of GAM3788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3788 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3788 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3788 RNA correlate with, and may be deduced from, the identity of the GAM3788 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3810 6494 GCAGGGAGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGAGAGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCGAAGATGT Messenger 3810 (GAM3810) oligonucleotides modulates expression of respective target genes

AGCCCAAAGC whose function and utility is known in the art.

CATAGTGCTT GAM3810 is a novel bioinformatically detectable regulatory, non protein coding,

TGTGTGCCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3810 was detected is

GCAACTGAGC described with additional reference to Figs. 9-15.

TTTCCCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTTTCTGT encoded by the human genome.

GAM3810 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3810

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3810

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3810 precursor RNA is designated SEQ ID:6494, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6494 is located from position 119579263 to position 119579351 relative to chromosome 11 on the `-` strand.

GAM3810 precursor RNA folds onto itself, forming GAM3810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3810 precursor RNA, designated SEQ ID NO: 6494, and a schematic representation of a predicted secondary folding of GAM3810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3810 folded precursor RNA yielding a GAM3810 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3810 RNA, hereby incorporated herein.

GAM3810 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3810 target RNA, herein designated GAM TARGET RNA. GAM3810 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3810 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3810 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3810 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3810 RNA, herein designated GAM RNA, to target binding sites on GAM3810 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3810 target RNA into GAM3810 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3810 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3810 target genes. The mRNA of each one of this plurality of GAM3810 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3810 RNA, herein designated GAM RNA, and which when bound by GAM3810 RNA causes inhibition of translation of the GAM3810 target mRNA into a corresponding GAM3810 target protein.

The mechanism of the translational inhibition exerted by GAM3810 RNA, herein

designated GAM RNA, on one or more GAM3810 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3810 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3810 RNA, herein designated GAM RNA, of GAM3810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3810 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3810 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3810 RNA correlate with, and may be deduced from, the identity of the GAM3810 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3890 7277 TGTGGTCCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGGGAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGGGGACAC Messenger 3890 (GAM3890) oligonucleotides modulates expression of respective target genes

AGCATTGGCA whose function and utility is known in the art.

GGAACCTCAA GAM3890 is a novel bioinformatically detectable regulatory, non protein coding,

ATTCCTGACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3890 was detected is

AAACCCTCTT described with additional reference to Figs. 9-15.

CCACACAATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTCCCGAAA encoded by the human genome.

GAAAGGAACC GAM3890 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3890

CA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3890

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3890 precursor RNA is designated SEQ ID:7277, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7277 is located from position 92752551 to position 92752652 relative to chromosome 8 on

the `+` strand.

GAM3890 precursor RNA folds onto itself, forming GAM3890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3890 precursor RNA, designated SEQ ID NO: 7277, and a schematic representation of a predicted secondary folding of GAM3890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3890 folded precursor RNA yielding a GAM3890 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3890 RNA, hereby incorporated herein.

GAM3890 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3890 target RNA, herein designated GAM TARGET RNA. GAM3890 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3890 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3890 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3890 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3890 RNA, herein designated GAM RNA, to target binding sites on GAM3890 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3890 target RNA into GAM3890 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3890 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3890 target genes. The mRNA of each one of this plurality of GAM3890 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM3890 RNA, herein designated GAM RNA, and which when bound by GAM3890 RNA causes inhibition of translation of the GAM3890 target mRNA into a corresponding GAM3890 target protein.

The mechanism of the translational inhibition exerted by GAM3890 RNA, herein designated GAM RNA, on one or more GAM3890 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3890 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3890 RNA, herein designated GAM RNA, of GAM3890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3890 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3890 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3890 RNA correlate with, and may be deduced from, the identity of the GAM3890 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3892 6543 GCTGCTGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGTCACCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAACTCAAC Messenger 3892 (GAM3892) oligonucleotides modulates expression of respective target genes

TAAGCTAAAG whose function and utility is known in the art.

AGCCTAGATG GAM3892 is a novel bioinformatically detectable regulatory, non protein coding,

GGTTACTCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM3892 was detected is

ATGACTGGCA described with additional reference to Figs. 9-15.

GTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3892 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3892

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3892

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3892 precursor RNA is designated SEQ ID:6543, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6543 is located from position 34242096 to position 34242169 relative to chromosome 12 on the `-` strand.

GAM3892 precursor RNA folds onto itself, forming GAM3892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3892 precursor RNA, designated SEQ ID NO: 6543, and a schematic representation of a predicted secondary folding of GAM3892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3892 folded precursor RNA yielding a GAM3892 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3892 RNA, hereby incorporated herein.

GAM3892 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3892 target RNA, herein designated GAM TARGET RNA. GAM3892 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3892 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3892 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3892 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3892 RNA, herein designated GAM RNA, to target binding sites on GAM3892 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3892 target RNA into GAM3892 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3892 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3892 target genes. The mRNA of each one of this plurality of GAM3892 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3892 RNA, herein designated GAM RNA, and which when bound by GAM3892 RNA causes inhibition of translation of the GAM3892 target mRNA into a corresponding GAM3892 target protein.

The mechanism of the translational inhibition exerted by GAM3892 RNA, herein designated GAM RNA, on one or more GAM3892 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3892 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3892 RNA, herein designated GAM RNA, of GAM3892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3892 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3892 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3892 RNA correlate with, and may be deduced from, the identity of the GAM3892 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3946 6888 GTCTCTGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCAGGCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGCAGTGG Messenger 3946 (GAM3946) oligonucleotides modulates expression of respective target genes

CGCAATCTCA whose function and utility is known in the art.

GCTCACTGCA GAM3946 is a novel bioinformatically detectable regulatory, non protein coding,

ACCTCCACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM3946 was detected is

CCTGGGTTCA described with additional reference to Figs. 9-15.

AGCGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM3946 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3946 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3946 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3946 precursor RNA is designated SEQ ID:6888, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6888 is located from position 44652554 to position 44652629 relative to chromosome 11 on the `+` strand.

GAM3946 precursor RNA folds onto itself, forming GAM3946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3946 precursor RNA, designated SEQ ID NO: 6888, and a schematic representation of a predicted secondary folding of GAM3946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3946 folded precursor RNA yielding a GAM3946 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM3946 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3946 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM3946 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3946 target RNA, herein designated GAM TARGET RNA. GAM3946 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3946 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3946 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3946 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3946 RNA, herein designated GAM RNA, to target binding sites on GAM3946 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3946 target RNA into GAM3946 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3946 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3946 target genes. The mRNA of each one of this plurality of GAM3946 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3946 RNA, herein designated GAM RNA, and which when bound by GAM3946 RNA causes inhibition of translation of the GAM3946 target mRNA into a corresponding GAM3946 target protein.

The mechanism of the translational inhibition exerted by GAM3946 RNA, herein designated GAM RNA, on one or more GAM3946 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3946 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3946 RNA, herein designated GAM RNA, of GAM3946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3946 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3946 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3946 RNA correlate with, and may be deduced from, the identity of the GAM3946 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3978 6807 GGGCTTGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTTTACAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGCAAAGAT Messenger 3978 (GAM3978) oligonucleotides modulates expression of respective target genes

CTGGCAAATT whose function and utility is known in the art.

AAAAATAGCC GAM3978 is a novel bioinformatically detectable regulatory, non protein coding,

TTAGGCCAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM3978 was detected is

GATCAAACCC described with additional reference to Figs. 9-15.

AAGGTGGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

T encoded by the human genome.

GAM3978 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3978 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3978 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3978 precursor RNA is designated SEQ ID:6807, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6807 is located from position 118768041 to position 118768121 relative to chromosome 12 on the `+` strand.

GAM3978 precursor RNA folds onto itself, forming GAM3978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3978 precursor RNA, designated SEQ ID NO: 6807, and a schematic representation of a predicted secondary folding of GAM3978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3978 folded precursor RNA yielding a GAM3978 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3978 RNA, hereby incorporated herein.

GAM3978 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3978 target RNA, herein designated GAM TARGET RNA. GAM3978 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3978 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3978 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3978 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3978 RNA, herein designated GAM RNA, to target binding sites on GAM3978 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3978 target RNA into GAM3978 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3978 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3978 target genes. The mRNA of each one of this plurality of GAM3978 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3978 RNA, herein designated GAM RNA, and which when bound by GAM3978 RNA causes inhibition of translation of the GAM3978 target mRNA into a corresponding GAM3978 target protein.

The mechanism of the translational inhibition exerted by GAM3978 RNA, herein designated GAM RNA, on one or more GAM3978 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3978 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3978 RNA, herein designated GAM RNA, of GAM3978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3978 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3978 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3978 RNA correlate with, and may be deduced from, the identity of the GAM3978 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM3990 5813 AGTCTTGCTC TGTTGCCTAG GCTGGAGTGC Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 3990 (GAM3990) oligonucleotides modulates expression of respective target genes

AGTGATGCAA whose function and utility is known in the art.

TTTTGGCTCA GAM3990 is a novel bioinformatically detectable regulatory, non protein coding, CTGCAACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM3990 was detected is

CACCTCCTGG described with additional reference to Figs. 9-15.

GTTCAAGCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCT encoded by the human genome.

GAM3990 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM3990

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM3990

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3990 precursor RNA is designated SEQ ID:5813, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5813 is located from position 44650568 to position 44650651 relative to chromosome 19 on the `+` strand.

GAM3990 precursor RNA folds onto itself, forming GAM3990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM3990 precursor RNA, designated SEQ ID NO: 5813, and a schematic representation of a predicted secondary folding of GAM3990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM3990 folded precursor RNA yielding a GAM3990 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM3990 RNA, hereby incorporated herein.

GAM3990 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM3990 target RNA, herein designated GAM TARGET RNA. GAM3990 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM3990 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3990 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3990 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM3990 RNA, herein designated GAM RNA, to target binding sites on GAM3990 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3990 target RNA into GAM3990 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM3990 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM3990 target genes. The mRNA of each one of this plurality of GAM3990 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3990 RNA, herein designated GAM RNA, and which when bound by GAM3990 RNA causes inhibition of translation of the GAM3990 target mRNA into a corresponding GAM3990 target protein.

The mechanism of the translational inhibition exerted by GAM3990 RNA, herein designated GAM RNA, on one or more GAM3990 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM3990 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM3990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM3990 RNA, herein designated GAM RNA, of GAM3990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM3990 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM3990 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM3990 RNA correlate with, and may be deduced from, the identity of the GAM3990 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4008 7007 TCAGAGACAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCTCATTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCTCAATGC Messenger 4008 (GAM4008) oligonucleotides modulates expression of respective target genes

CACTGCACTG whose function and utility is known in the art.

ATGTCAACTG GAM4008 is a novel bioinformatically detectable regulatory, non protein coding,

ACTTAGGGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4008 was detected is

GGCATGAGAG described with additional reference to Figs. 9-15.

AACTGAGGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TACATGG encoded by the human genome.

GAM4008 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4008 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4008 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4008 precursor RNA is designated SEQ ID:7007, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7007 is located from position 86637061 to position 86637147 relative to chromosome 14 on the `+` strand.

GAM4008 precursor RNA folds onto itself, forming GAM4008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4008 precursor RNA, designated SEQ ID NO: 7007, and a schematic representation of a predicted secondary folding of GAM4008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4008 folded precursor RNA yielding a GAM4008 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4008 RNA, hereby incorporated herein.

GAM4008 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4008 target RNA, herein designated GAM TARGET RNA. GAM4008 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4008 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4008 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4008 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4008 RNA, herein designated GAM RNA, to target binding sites on GAM4008 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4008 target RNA into GAM4008 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4008 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4008 target genes. The mRNA of each one of this plurality of GAM4008 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4008 RNA, herein designated GAM RNA, and which when bound by GAM4008 RNA causes inhibition of translation of the GAM4008 target mRNA into a corresponding GAM4008 target protein.

The mechanism of the translational inhibition exerted by GAM4008 RNA, herein designated GAM RNA, on one or more GAM4008 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4008 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4008 RNA, herein designated GAM RNA, of GAM4008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4008 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4008 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4008 RNA correlate with, and may be deduced from, the identity of the GAM4008 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4011 5820 AGTTCAAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCCTCCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTCTTCAT Messenger 4011 (GAM4011) oligonucleotides modulates expression of respective target genes

TATGTGAATT whose function and utility is known in the art.

GAATGTGGTC GAM4011 is a novel bioinformatically detectable regulatory, non protein coding,

ACACATCTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4011 was detected is

GTTGGAGCAG described with additional reference to Figs. 9-15.

AGGCAGGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCAGCTTTC encoded by the human genome.

AGCT GAM4011 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4011

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4011

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4011 precursor RNA is designated SEQ ID:5820, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5820 is located from position 45149119 to position 45149212 relative to chromosome 22 on the `+` strand.

GAM4011 precursor RNA folds onto itself, forming GAM4011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4011 precursor RNA, designated SEQ ID NO: 5820, and a schematic representation of a predicted secondary folding of GAM4011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4011 folded precursor RNA yielding a GAM4011 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4011 RNA, hereby incorporated herein.

GAM4011 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4011 target RNA, herein designated GAM TARGET RNA. GAM4011 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4011 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4011 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4011 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4011 RNA, herein designated GAM RNA, to target binding sites on GAM4011 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4011 target RNA into GAM4011 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4011 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4011 target genes. The mRNA of each one of this plurality of GAM4011 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4011 RNA, herein designated GAM RNA, and which when bound by GAM4011 RNA causes inhibition of translation of the GAM4011 target mRNA into a corresponding GAM4011 target protein.

The mechanism of the translational inhibition exerted by GAM4011 RNA, herein designated GAM RNA, on one or more GAM4011 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4011 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4011 RNA, herein designated GAM RNA, of GAM4011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM4011 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4011 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4011 RNA correlate with, and may be deduced from, the identity of the GAM4011 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4020 5670 AAGGTATTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGAGCTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCCTGCCTT Messenger 4020 (GAM4020) oligonucleotides modulates expression of respective target genes
CCAGTGACAT whose function and utility is known in the art.

GTTCTAAAAA GAM4020 is a novel bioinformatically detectable regulatory, non protein coding,
TTGCAAGTTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4020 was detected is

TTTGAGGAGG described with additional reference to Figs. 9-15.

CTTTACAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATAGGAAGT encoded by the human genome.

TCTT GAM4020 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4020
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4020
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4020 precursor RNA is designated SEQ ID:5670, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5670 is located from position 62871608 to position 62871701 relative to chromosome 11 on the `-` strand.

GAM4020 precursor RNA folds onto itself, forming GAM4020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4020 precursor RNA, designated SEQ ID NO: 5670, and a schematic representation of a predicted secondary folding of GAM4020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4020 folded precursor RNA yielding a GAM4020 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4020 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4020 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4020 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4020 target RNA, herein designated GAM TARGET RNA. GAM4020 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4020 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4020 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4020 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4020 RNA, herein designated GAM RNA, to target binding sites on GAM4020 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4020 target RNA into GAM4020 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4020 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4020 target genes. The mRNA of each one of this plurality of GAM4020 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4020 RNA, herein designated GAM RNA, and which when bound by GAM4020 RNA causes inhibition of translation of the GAM4020 target mRNA into a corresponding GAM4020 target protein.

The mechanism of the translational inhibition exerted by GAM4020 RNA, herein designated GAM RNA, on one or more GAM4020 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4020 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4020 RNA, herein designated GAM RNA, of GAM4020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4020 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4020 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4020 RNA correlate with, and may be deduced from, the identity of the GAM4020 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4027 7246 TGGGTCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTCTTCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGGAGGCAT Messenger 4027 (GAM4027) oligonucleotides modulates expression of respective target genes

TCGGAGAGCA whose function and utility is known in the art.

ACACCCTGGC GAM4027 is a novel bioinformatically detectable regulatory, non protein coding,

CTTAACACAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4027 was detected is

TACATATCTT described with additional reference to Figs. 9-15.

TGAATTTCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACGGGGGCAG encoded by the human genome.

CCTTCTGGGA GAM4027 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4027

AAACCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4027

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4027 precursor RNA is designated SEQ ID:7246, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7246 is located from position 6197075 to position 6197180 relative to chromosome 17 on the `-` strand.

GAM4027 precursor RNA folds onto itself, forming GAM4027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4027 precursor RNA, designated SEQ ID NO: 7246, and a

schematic representation of a predicted secondary folding of GAM4027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4027 folded precursor RNA yielding a GAM4027 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4027 RNA, hereby incorporated herein.

GAM4027 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4027 target RNA, herein designated GAM TARGET RNA. GAM4027 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4027 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4027 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4027 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4027 RNA, herein designated GAM RNA, to target binding sites on GAM4027 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4027 target RNA into GAM4027 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4027 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4027 target genes. The mRNA of each one of this plurality of GAM4027 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4027 RNA, herein designated GAM RNA, and which when bound by GAM4027 RNA causes inhibition of translation of the GAM4027 target mRNA into a corresponding GAM4027 target protein.

The mechanism of the translational inhibition exerted by GAM4027 RNA, herein designated GAM RNA, on one or more GAM4027 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4027 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4027 RNA, herein designated GAM RNA, of GAM4027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4027 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4027 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4027 RNA correlate with, and may be deduced from, the identity of the GAM4027 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4064 6077 CCCCAGCCCG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAGCCTCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTATCTCCAG Messenger 4064 (GAM4064) oligonucleotides modulates expression of respective target genes

CCCAGACAAA whose function and utility is known in the art.

CCCTGTGGTC GAM4064 is a novel bioinformatically detectable regulatory, non protein coding,

CAGAGGAGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4064 was detected is

ATGAGGGTGC described with additional reference to Figs. 9-15.

AGGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4064 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4064

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4064

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4064 precursor RNA is designated SEQ ID:6077, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6077 is located from position 1197566 to position 1197640 relative to chromosome 7 on the `-` strand.

GAM4064 precursor RNA folds onto itself, forming GAM4064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4064 precursor RNA, designated SEQ ID NO: 6077, and a schematic representation of a predicted secondary folding of GAM4064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4064 folded precursor RNA yielding a GAM4064 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4064 RNA, hereby incorporated herein.

GAM4064 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4064 target RNA, herein designated GAM TARGET RNA. GAM4064 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4064 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4064 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4064 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4064 RNA, herein designated GAM RNA, to target binding sites on GAM4064 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4064 target RNA into GAM4064 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4064 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4064 target genes. The mRNA of each one of this plurality of GAM4064 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4064 RNA, herein designated GAM RNA, and which when bound by GAM4064 RNA causes inhibition of translation of the GAM4064 target mRNA into a corresponding GAM4064 target protein.

The mechanism of the translational inhibition exerted by GAM4064 RNA, herein

designated GAM RNA, on one or more GAM4064 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4064 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4064 RNA, herein designated GAM RNA, of GAM4064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4064 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4064 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4064 RNA correlate with, and may be deduced from, the identity of the GAM4064 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4074 6195 CTGACATGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CATTATCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTCATTTTAA Messenger 4074 (GAM4074) oligonucleotides modulates expression of respective target genes
ACAAAGTGAC whose function and utility is known in the art.

CTATGGAAGG GAM4074 is a novel bioinformatically detectable regulatory, non protein coding,
GTACGCTGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4074 was detected is

CTGTGACATG described with additional reference to Figs. 9-15.

GTAATGGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTGG encoded by the human genome.

GAM4074 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4074

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4074

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4074 precursor RNA is designated SEQ ID:6195, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6195 is located from position 69300375 to position 69300459 relative to chromosome 7 on

the `+` strand.

GAM4074 precursor RNA folds onto itself, forming GAM4074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4074 precursor RNA, designated SEQ ID NO: 6195, and a schematic representation of a predicted secondary folding of GAM4074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4074 folded precursor RNA yielding a GAM4074 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4074 RNA, hereby incorporated herein.

GAM4074 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4074 target RNA, herein designated GAM TARGET RNA. GAM4074 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4074 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4074 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4074 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4074 RNA, herein designated GAM RNA, to target binding sites on GAM4074 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4074 target RNA into GAM4074 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4074 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4074 target genes. The mRNA of each one of this plurality of GAM4074 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM4074 RNA, herein designated GAM RNA, and which when bound by GAM4074 RNA causes inhibition of translation of the GAM4074 target mRNA into a corresponding GAM4074 target protein.

The mechanism of the translational inhibition exerted by GAM4074 RNA, herein designated GAM RNA, on one or more GAM4074 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4074 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4074 RNA, herein designated GAM RNA, of GAM4074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4074 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4074 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4074 RNA correlate with, and may be deduced from, the identity of the GAM4074 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4085 5766 AGGCACCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGTGTAGAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGGGGTGGAG Messenger 4085 (GAM4085) oligonucleotides modulates expression of respective target genes

CCGCATGGGC whose function and utility is known in the art.

ACCTGGGGGT GAM4085 is a novel bioinformatically detectable regulatory, non protein coding,

GTAGACCGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4085 was detected is

GTGGAACTAT described with additional reference to Figs. 9-15.

GTAAACATCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CACACACTCA encoded by the human genome.

GGTGACTT GAM4085 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4085

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4085

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4085 precursor RNA is designated SEQ ID:5766, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5766 is located from position 71416467 to position 71416564 relative to chromosome 11 on the `+` strand.

GAM4085 precursor RNA folds onto itself, forming GAM4085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4085 precursor RNA, designated SEQ ID NO: 5766, and a schematic representation of a predicted secondary folding of GAM4085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4085 folded precursor RNA yielding a GAM4085 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4085 RNA, hereby incorporated herein.

GAM4085 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4085 target RNA, herein designated GAM TARGET RNA. GAM4085 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4085 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4085 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4085 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4085 RNA, herein designated GAM RNA, to target binding sites on GAM4085 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4085 target RNA into GAM4085 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4085 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4085 target genes. The mRNA of each one of this plurality of GAM4085 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4085 RNA, herein designated GAM RNA, and which when bound by GAM4085 RNA causes inhibition of translation of the GAM4085 target mRNA into a corresponding GAM4085 target protein.

The mechanism of the translational inhibition exerted by GAM4085 RNA, herein designated GAM RNA, on one or more GAM4085 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4085 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4085 RNA, herein designated GAM RNA, of GAM4085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4085 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4085 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4085 RNA correlate with, and may be deduced from, the identity of the GAM4085 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4130 6254 CTTCCATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGGGCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GACAGGGAGA Messenger 4130 (GAM4130) oligonucleotides modulates expression of respective target genes
TAGGCCACAC whose function and utility is known in the art.

CTTTCCCAGG GAM4130 is a novel bioinformatically detectable regulatory, non protein coding,
TGGAACCTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4130 was detected is

AGATGGAGG described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM4130 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4130 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4130 precursor RNA is designated SEQ ID:6254, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6254 is located from position 77528890 to position 77528958 relative to chromosome X on the `+` strand.

GAM4130 precursor RNA folds onto itself, forming GAM4130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4130 precursor RNA, designated SEQ ID NO: 6254, and a schematic representation of a predicted secondary folding of GAM4130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4130 folded precursor RNA yielding a GAM4130 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4130 RNA, hereby incorporated herein.

GAM4130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4130 target RNA, herein designated GAM TARGET RNA. GAM4130 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4130 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4130 RNA, herein designated GAM RNA, to target binding sites on GAM4130 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4130 target RNA into GAM4130 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4130 target genes. The mRNA of each one of this plurality of GAM4130 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4130 RNA, herein designated GAM RNA, and which when bound by GAM4130 RNA causes inhibition of translation of the GAM4130 target mRNA into a corresponding GAM4130 target protein.

The mechanism of the translational inhibition exerted by GAM4130 RNA, herein designated GAM RNA, on one or more GAM4130 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4130 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4130 RNA, herein designated GAM RNA, of GAM4130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4130 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4130 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4130 RNA correlate with, and may be deduced from, the identity of the GAM4130 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4136 5723 AGACGTGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTCGCTATG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGGCCAGGT Messenger 4136 (GAM4136) oligonucleotides modulates expression of respective target genes
TGGTCTTGAA whose function and utility is known in the art.

CTCTTGGCCT GAM4136 is a novel bioinformatically detectable regulatory, non protein coding,
CAAGCATTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4136 was detected is

TCCTGCCTCA described with additional reference to Figs. 9-15.

GCTTCCCAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGCTAGGAT encoded by the human genome.

TACAGCCATG GAM4136 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4136

AGCCAATAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4136

AGTAAAATGA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

CTTTTTGTTT to the nucleotide sequence of GAM4136 precursor RNA is designated SEQ ID:5723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5723 is located from position 58315712 to position 58315841 relative to chromosome 19 on the `-` strand.

GAM4136 precursor RNA folds onto itself, forming GAM4136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4136 precursor RNA, designated SEQ ID NO: 5723, and a schematic representation of a predicted secondary folding of GAM4136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4136 folded precursor RNA yielding a GAM4136 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4136 RNA, hereby incorporated herein.

GAM4136 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4136 target RNA, herein designated GAM TARGET RNA. GAM4136 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4136 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4136 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4136 RNA, herein designated GAM RNA, to target binding sites on GAM4136 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4136 target RNA into GAM4136 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4136 target genes. The mRNA of each one of this plurality of GAM4136 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4136 RNA, herein designated GAM RNA, and which when bound by GAM4136 RNA causes inhibition of translation of the GAM4136 target mRNA into a corresponding GAM4136 target protein.

The mechanism of the translational inhibition exerted by GAM4136 RNA, herein designated GAM RNA, on one or more GAM4136 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4136 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4136 RNA, herein designated GAM RNA, of GAM4136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4136 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4136 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4136 RNA correlate with, and may be deduced from, the identity of the GAM4136 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4142 6136 CGAATGGACC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCAAAGATT Messenger 4142 (GAM4142) oligonucleotides modulates expression of respective target genes

CCAGTTCTAA whose function and utility is known in the art.

TATGGGAATG AGCCTCTTTG ATCTCTTCCG GGGCTTTTTC G GAM4142 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM4142 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM4142 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4142 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4142 precursor RNA is designated SEQ ID:6136, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6136 is located from position 145175426 to position 145175506 relative to chromosome X on the `-` strand.

GAM4142 precursor RNA folds onto itself, forming GAM4142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4142 precursor RNA, designated SEQ ID NO: 6136, and a schematic representation of a predicted secondary folding of GAM4142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4142 folded precursor RNA yielding a GAM4142 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4142 RNA, hereby incorporated herein.

GAM4142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4142 target RNA, herein designated GAM TARGET RNA. GAM4142 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4142 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4142 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4142 RNA, herein designated GAM RNA, to target binding sites on GAM4142 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4142 target RNA into GAM4142 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4142 target genes. The mRNA of each one of this plurality of GAM4142 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4142 RNA, herein designated GAM RNA, and which when bound by GAM4142 RNA causes inhibition of translation of the GAM4142 target mRNA into a corresponding GAM4142 target protein.

The mechanism of the translational inhibition exerted by GAM4142 RNA, herein designated GAM RNA, on one or more GAM4142 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4142 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4142 RNA, herein designated GAM RNA, of GAM4142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4142 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4142 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4142 RNA correlate with, and may be deduced from, the identity of the GAM4142 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4147 7262 TGTATTGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGTTGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCTCAGTAA Messenger 4147 (GAM4147) oligonucleotides modulates expression of respective target genes
ATCTCCATTT whose function and utility is known in the art.

GTAAATGTGA GAM4147 is a novel bioinformatically detectable regulatory, non protein coding,
CAGTCAGCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4147 was detected is

AATCTCCAGT described with additional reference to Figs. 9-15.

TACAGTCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAAAGCAAG encoded by the human genome.

CAGGGGCATG GAM4147 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4147
CCACATACAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4147
GTTCATATAT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
A to the nucleotide sequence of GAM4147 precursor RNA is designated SEQ ID:7262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7262 is located from position 79828332 to position 79828452 relative to chromosome 14 on the `-` strand.

GAM4147 precursor RNA folds onto itself, forming GAM4147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4147 precursor RNA, designated SEQ ID NO: 7262, and a schematic representation of a predicted secondary folding of GAM4147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4147 folded precursor RNA yielding a GAM4147 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4147 RNA, hereby incorporated herein.

GAM4147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4147 target RNA, herein designated GAM TARGET RNA. GAM4147 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4147 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4147 RNA, herein designated GAM RNA, to target binding sites on GAM4147 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4147 target RNA into GAM4147 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4147 target genes. The mRNA of each one of this plurality of GAM4147 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4147 RNA, herein designated GAM RNA, and which when bound by GAM4147 RNA causes inhibition of translation of the GAM4147 target mRNA into a corresponding GAM4147 target protein.

The mechanism of the translational inhibition exerted by GAM4147 RNA, herein designated GAM RNA, on one or more GAM4147 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4147 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4147 RNA, herein designated GAM RNA, of GAM4147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4147 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4147 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4147 RNA correlate with, and may be deduced from, the identity of the GAM4147 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4152 6209 CTGCAGCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCAAAATGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AAATACAAGC Messenger 4152 (GAM4152) oligonucleotides modulates expression of respective target genes
AATCATGTAG whose function and utility is known in the art.

TTCACTGTGT GAM4152 is a novel bioinformatically detectable regulatory, non protein coding,
CCATCAGACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4152 was detected is

GGAACAAATC described with additional reference to Figs. 9-15.

AGATGACCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAATTGAGAG encoded by the human genome.

ACTGAACATT GAM4152 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4152
TCCTCAGGTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4152
GCTGGAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4152 precursor RNA is designated SEQ ID:6209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6209 is located from position 25256625 to position 25256741 relative to chromosome 22 on the `+` strand.

GAM4152 precursor RNA folds onto itself, forming GAM4152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4152 precursor RNA, designated SEQ ID NO: 6209, and a schematic representation of a predicted secondary folding of GAM4152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4152 folded precursor RNA yielding a GAM4152 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4152 RNA, hereby incorporated herein.

GAM4152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4152 target RNA, herein designated GAM TARGET RNA. GAM4152 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4152 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4152 RNA, herein designated GAM RNA, to target binding sites on GAM4152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4152 target RNA into GAM4152 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4152 target genes. The mRNA of each one of this plurality of GAM4152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4152 RNA, herein designated GAM RNA, and which when bound by GAM4152 RNA causes inhibition of translation of the GAM4152 target mRNA into a corresponding GAM4152 target protein.

The mechanism of the translational inhibition exerted by GAM4152 RNA, herein designated GAM RNA, on one or more GAM4152 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4152 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4152 RNA, herein designated GAM RNA, of GAM4152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM4152 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4152 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4152 RNA correlate with, and may be deduced from, the identity of the GAM4152 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4188 5964 ATGACAGCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GACACTGGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGAATCCT Messenger 4188 (GAM4188) oligonucleotides modulates expression of respective target genes
CCGTGTCACA whose function and utility is known in the art.

TGTGGGCTGC GAM4188 is a novel bioinformatically detectable regulatory, non protein coding,
TGACAGGAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4188 was detected is

AATGTGCTTT described with additional reference to Figs. 9-15.

TGTTGTTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM4188 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4188

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4188
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4188 precursor RNA is designated SEQ ID:5964, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5964 is located from position 113971971 to position 113972049 relative to chromosome 11 on the `+` strand.

GAM4188 precursor RNA folds onto itself, forming GAM4188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4188 precursor RNA, designated SEQ ID NO: 5964, and a schematic representation of a predicted secondary folding of GAM4188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4188 folded precursor RNA yielding a GAM4188 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4188 RNA, hereby incorporated herein.

GAM4188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4188 target RNA, herein designated GAM TARGET RNA. GAM4188 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4188 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4188 RNA, herein designated GAM RNA, to target binding sites on GAM4188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4188 target RNA into GAM4188 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4188 target genes. The mRNA of each one of this plurality of GAM4188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4188 RNA, herein designated GAM RNA, and which when bound by GAM4188 RNA causes inhibition of translation of the GAM4188 target mRNA into a corresponding GAM4188 target protein.

The mechanism of the translational inhibition exerted by GAM4188 RNA, herein designated GAM RNA, on one or more GAM4188 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4188 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4188 RNA, herein designated GAM RNA, of

GAM4188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4188 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4188 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4188 RNA correlate with, and may be deduced from, the identity of the GAM4188 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4189 5721 AGACATGTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGCAGGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CATCTGATCG Messenger 4189 (GAM4189) oligonucleotides modulates expression of respective target genes

ACCTTAGACT whose function and utility is known in the art.

TGGCAAGCTG GAM4189 is a novel bioinformatically detectable regulatory, non protein coding,

GTGGCTAAGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4189 was detected is

CCAGTGCTCA described with additional reference to Figs. 9-15.

CTGCCGACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGTCT encoded by the human genome.

GAM4189 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4189

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4189

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4189 precursor RNA is designated SEQ ID:5721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5721 is located from position 32944216 to position 32944301 relative to chromosome 19 on the `-` strand.

GAM4189 precursor RNA folds onto itself, forming GAM4189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4189 precursor RNA, designated SEQ ID NO: 5721, and a schematic representation of a predicted secondary folding of GAM4189 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4189 folded precursor RNA yielding a GAM4189 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4189 RNA, hereby incorporated herein.

GAM4189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4189 target RNA, herein designated GAM TARGET RNA. GAM4189 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4189 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4189 RNA, herein designated GAM RNA, to target binding sites on GAM4189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4189 target RNA into GAM4189 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4189 target genes. The mRNA of each one of this plurality of GAM4189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4189 RNA, herein designated GAM RNA, and which when bound by GAM4189 RNA causes inhibition of translation of the GAM4189 target mRNA into a corresponding GAM4189 target protein.

The mechanism of the translational inhibition exerted by GAM4189 RNA, herein designated GAM RNA, on one or more GAM4189 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4189 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM4189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4189 RNA, herein designated GAM RNA, of GAM4189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4189 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4189 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4189 RNA correlate with, and may be deduced from, the identity of the GAM4189 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4199 6228 CTGGCTGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCTCCATGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCATTCCC Messenger 4199 (GAM4199) oligonucleotides modulates expression of respective target genes

CTTGGGGTGC whose function and utility is known in the art.

AAGCCACACC GAM4199 is a novel bioinformatically detectable regulatory, non protein coding,

ACCCTTCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4199 was detected is

TGGGGGATGA described with additional reference to Figs. 9-15.

TAGCAGCCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4199 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4199

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4199

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4199 precursor RNA is designated SEQ ID:6228, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6228 is located from position 35997845 to position 35997924 relative to chromosome 22 on the `-` strand.

GAM4199 precursor RNA folds onto itself, forming GAM4199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4199 precursor RNA, designated SEQ ID NO: 6228, and a schematic representation of a predicted secondary folding of GAM4199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4199 folded precursor RNA yielding a GAM4199 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4199 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4199 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4199 target RNA, herein designated GAM TARGET RNA. GAM4199 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4199 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4199 RNA, herein designated GAM RNA, to target binding sites on GAM4199 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4199 target RNA into GAM4199 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4199 target genes. The mRNA of each one of this plurality of GAM4199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4199 RNA, herein designated GAM RNA, and which when bound by GAM4199 RNA causes inhibition of translation of the GAM4199 target mRNA into a corresponding GAM4199 target protein.

The mechanism of the translational inhibition exerted by GAM4199 RNA, herein

designated GAM RNA, on one or more GAM4199 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4199 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4199 RNA, herein designated GAM RNA, of GAM4199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4199 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4199 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4199 RNA correlate with, and may be deduced from, the identity of the GAM4199 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4205 6549 GCTGTCAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGTTCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGGAGTTC Messenger 4205 (GAM4205) oligonucleotides modulates expression of respective target genes

TCTTATCTGC whose function and utility is known in the art.

TCTGGTTTGG GAM4205 is a novel bioinformatically detectable regulatory, non protein coding,

AGGGCTGCCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4205 was detected is

CATTCGGGAA described with additional reference to Figs. 9-15.

TCTGTTTTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGC encoded by the human genome.

GAM4205 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4205

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4205

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4205 precursor RNA is designated SEQ ID:6549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6549 is located from position 110102091 to position 110102175 relative to chromosome 13

on the `-` strand.

GAM4205 precursor RNA folds onto itself, forming GAM4205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4205 precursor RNA, designated SEQ ID NO: 6549, and a schematic representation of a predicted secondary folding of GAM4205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4205 folded precursor RNA yielding a GAM4205 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4205 RNA, hereby incorporated herein.

GAM4205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4205 target RNA, herein designated GAM TARGET RNA. GAM4205 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4205 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4205 RNA, herein designated GAM RNA, to target binding sites on GAM4205 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4205 target RNA into GAM4205 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4205 target genes. The mRNA of each one of this plurality of GAM4205 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM4205 RNA, herein designated GAM RNA, and which when bound by GAM4205 RNA causes inhibition of translation of the GAM4205 target mRNA into a corresponding GAM4205 target protein.

The mechanism of the translational inhibition exerted by GAM4205 RNA, herein designated GAM RNA, on one or more GAM4205 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4205 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4205 RNA, herein designated GAM RNA, of GAM4205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4205 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4205 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4205 RNA correlate with, and may be deduced from, the identity of the GAM4205 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4238 6167 CTCCTGTAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTAGAGCGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCTCTTGAA Messenger 4238 (GAM4238) oligonucleotides modulates expression of respective target genes

CCCTAATTTT whose function and utility is known in the art.

TAGGTCTCAA GAM4238 is a novel bioinformatically detectable regulatory, non protein coding,

AGAGTGGGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4238 was detected is

TCAGAGATAA described with additional reference to Figs. 9-15.

AGAGGTTTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAGGGACAG encoded by the human genome.

GGCGAGGAG GAM4238 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4238

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4238

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4238 precursor RNA is designated SEQ ID:6167, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6167 is located from position 42216969 to position 42217067 relative to chromosome 9 on the `-` strand.

GAM4238 precursor RNA folds onto itself, forming GAM4238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4238 precursor RNA, designated SEQ ID NO: 6167, and a schematic representation of a predicted secondary folding of GAM4238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4238 folded precursor RNA yielding a GAM4238 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4238 RNA, hereby incorporated herein.

GAM4238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4238 target RNA, herein designated GAM TARGET RNA. GAM4238 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4238 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4238 RNA, herein designated GAM RNA, to target binding sites on GAM4238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4238 target RNA into GAM4238 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4238 target genes. The mRNA of each one of this plurality of GAM4238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4238 RNA, herein designated GAM RNA, and which when bound by GAM4238 RNA causes inhibition of translation of the GAM4238 target mRNA into a corresponding GAM4238 target protein.

The mechanism of the translational inhibition exerted by GAM4238 RNA, herein designated GAM RNA, on one or more GAM4238 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4238 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4238 RNA, herein designated GAM RNA, of GAM4238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4238 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4238 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4238 RNA correlate with, and may be deduced from, the identity of the GAM4238 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4243 5650 AAAGGCAGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGAATGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGAGAAATT Messenger 4243 (GAM4243) oligonucleotides modulates expression of respective target genes

GTTCAGATTC whose function and utility is known in the art.

AAGGACAAGC GAM4243 is a novel bioinformatically detectable regulatory, non protein coding,

ATTTGTTGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4243 was detected is

TTT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4243 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4243 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4243 precursor RNA is designated SEQ ID:5650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5650 is located from position 62347057 to position 62347119 relative to chromosome 15 on the `+` strand.

GAM4243 precursor RNA folds onto itself, forming GAM4243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4243 precursor RNA, designated SEQ ID NO: 5650, and a schematic representation of a predicted secondary folding of GAM4243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4243 folded precursor RNA yielding a GAM4243 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4243 RNA, hereby incorporated herein.

GAM4243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4243 target RNA, herein designated GAM TARGET RNA. GAM4243 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4243 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4243 RNA, herein designated GAM RNA, to target binding sites on GAM4243 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4243 target RNA into GAM4243 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4243 target genes. The mRNA of each one of this plurality of GAM4243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4243 RNA, herein designated GAM RNA, and which when bound by GAM4243 RNA causes inhibition of translation of the GAM4243 target mRNA into a corresponding GAM4243 target protein.

The mechanism of the translational inhibition exerted by GAM4243 RNA, herein designated GAM RNA, on one or more GAM4243 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4243 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4243 RNA, herein designated GAM RNA, of GAM4243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4243 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4243 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4243 RNA correlate with, and may be deduced from, the identity of the GAM4243 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4298 6898 GTGAGGCTCT GGCAAGGTGT GGGCTAGAGA TGCGACTCAG TTGGATCTAT CTCTCAGAAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 4298 (GAM4298) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM4298 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM4298 was detected is

GCTACCTTGT described with additional reference to Figs. 9-15.

AAGTAGAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCAC encoded by the human genome.

GAM4298 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4298 precursor RNA is designated SEQ ID:6898, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6898 is located from position 111675686 to position 111675769 relative to chromosome 12 on the `-` strand.

GAM4298 precursor RNA folds onto itself, forming GAM4298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4298 precursor RNA, designated SEQ ID NO: 6898, and a schematic representation of a predicted secondary folding of GAM4298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4298 folded precursor RNA yielding a GAM4298 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4298 RNA, hereby incorporated herein.

GAM4298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4298 target RNA, herein designated GAM TARGET RNA. GAM4298 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4298 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4298 RNA, herein designated GAM RNA, to target binding sites on GAM4298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4298 target RNA into GAM4298 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4298 target genes. The mRNA of each one of this plurality of GAM4298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4298 RNA, herein designated GAM RNA, and which when bound by GAM4298 RNA causes inhibition of translation of the GAM4298 target mRNA into a corresponding GAM4298 target protein.

The mechanism of the translational inhibition exerted by GAM4298 RNA, herein designated GAM RNA, on one or more GAM4298 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4298 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4298 RNA, herein designated GAM RNA, of GAM4298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4298 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4298 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4298 RNA correlate with, and may be deduced from, the identity of the GAM4298 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4315 6015 CAGATTGCAC GAACATTTCA TTTTTCACAC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 4315 (GAM4315) oligonucleotides modulates expression of respective target genes

AGGGTCACCA whose function and utility is known in the art.

GAATACCATC GAM4315 is a novel bioinformatically detectable regulatory, non protein coding,
AATTTTTTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4315 was detected is

TATCACTGTC described with additional reference to Figs. 9-15.

AAAAGTGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAGCACCTT encoded by the human genome.

CTGAAATAAC GAM4315 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4315
GTGAGCTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4315
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4315 precursor RNA is designated SEQ ID:6015, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6015 is located from position 75288703 to position 75288810 relative to chromosome 16 on the `+` strand.

GAM4315 precursor RNA folds onto itself, forming GAM4315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4315 precursor RNA, designated SEQ ID NO: 6015, and a schematic representation of a predicted secondary folding of GAM4315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4315 folded precursor RNA yielding a GAM4315 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4315 RNA, hereby incorporated herein.

GAM4315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4315 target RNA, herein designated GAM TARGET RNA. GAM4315 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4315 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4315 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4315 RNA, herein designated GAM RNA, to target binding sites on GAM4315 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4315 target RNA into GAM4315 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4315 target genes. The mRNA of each one of this plurality of GAM4315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4315 RNA, herein designated GAM RNA, and which when bound by GAM4315 RNA causes inhibition of translation of the GAM4315 target mRNA into a corresponding GAM4315 target protein.

The mechanism of the translational inhibition exerted by GAM4315 RNA, herein designated GAM RNA, on one or more GAM4315 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4315 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4315 RNA, herein designated GAM RNA, of GAM4315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4315 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4315 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4315 RNA correlate with, and may be deduced from, the identity of the GAM4315 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4364 5678 AATGTTCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACATAGTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTAATTAAGA Messenger 4364 (GAM4364) oligonucleotides modulates expression of respective target genes

AAATCGAGCA whose function and utility is known in the art.

CCCTTAATTA GAM4364 is a novel bioinformatically detectable regulatory, non protein coding,

CCTAGAATGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4364 was detected is

AGGGTTGTTA described with additional reference to Figs. 9-15.

GTTTTTTGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGACTTTTGT encoded by the human genome.

TTTGCTGGGG GAM4364 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4364

CATT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4364

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4364 precursor RNA is designated SEQ ID:5678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5678 is located from position 98918395 to position 98918498 relative to chromosome X on the `+` strand.

GAM4364 precursor RNA folds onto itself, forming GAM4364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4364 precursor RNA, designated SEQ ID NO: 5678, and a schematic representation of a predicted secondary folding of GAM4364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4364 folded precursor RNA yielding a GAM4364 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4364 RNA, hereby incorporated herein.

GAM4364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4364 target RNA, herein designated GAM TARGET RNA. GAM4364 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4364 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4364 RNA, herein designated GAM RNA, to target binding sites on GAM4364 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4364 target RNA into GAM4364 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4364 target genes. The mRNA of each one of this plurality of GAM4364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4364 RNA, herein designated GAM RNA, and which when bound by GAM4364 RNA causes inhibition of translation of the GAM4364 target mRNA into a corresponding GAM4364 target protein.

The mechanism of the translational inhibition exerted by GAM4364 RNA, herein designated GAM RNA, on one or more GAM4364 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4364 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4364 RNA, herein designated GAM RNA, of GAM4364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4364 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4364 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4364 RNA correlate with, and may be deduced from, the identity of the GAM4364 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4376 6380 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 4376 (GAM4376) oligonucleotides modulates expression of respective target genes

GTAGAGGTTG whose function and utility is known in the art.

CAGTGAGTCA GAM4376 is a novel bioinformatically detectable regulatory, non protein coding,

AGATCATGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4376 was detected is

ATTGCACTCC described with additional reference to Figs. 9-15.

AACCTGGGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCAA encoded by the human genome.

AACTCTGTCT GAM4376 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4376

C precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4376

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4376 precursor RNA is designated SEQ ID:6380, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6380 is located from position 182465 to position 182565 relative to chromosome 18 on the `+` strand.

GAM4376 precursor RNA folds onto itself, forming GAM4376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4376 precursor RNA, designated SEQ ID NO: 6380, and a schematic representation of a predicted secondary folding of GAM4376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4376 folded precursor RNA yielding a GAM4376 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4376 RNA, hereby incorporated herein.

GAM4376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4376 target RNA, herein designated GAM TARGET RNA. GAM4376 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4376 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4376 RNA, herein designated GAM RNA, to target binding sites on GAM4376 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4376 target RNA into GAM4376 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4376 target genes. The mRNA of each one of this plurality of GAM4376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4376 RNA, herein designated GAM RNA, and which when bound by GAM4376 RNA causes inhibition of translation of the GAM4376 target mRNA into a corresponding GAM4376 target protein.

The mechanism of the translational inhibition exerted by GAM4376 RNA, herein designated GAM RNA, on one or more GAM4376 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4376 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4376 RNA, herein designated GAM RNA, of GAM4376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM4376 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4376 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4376 RNA correlate with, and may be deduced from, the identity of the GAM4376 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4377 7031 TCCCTCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTGAGTACA detected oligonucleotides of the present invention, referred to here as Genomic Address
AATGAAGTCT Messenger 4377 (GAM4377) oligonucleotides modulates expression of respective target genes
GTGGGCCAAC whose function and utility is known in the art.

AAGGAGCGAG GAM4377 is a novel bioinformatically detectable regulatory, non protein coding,
GAGCAGTTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4377 was detected is

CTGGAAGCCC described with additional reference to Figs. 9-15.

TGGGCTGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTGACTTGC encoded by the human genome.

TTTGAGATAG GAM4377 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4377
AATAAATGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4377
A precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4377 precursor RNA is designated SEQ ID:7031, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7031 is located from position 49418894 to position 49419004 relative to chromosome 20 on the `-` strand.

GAM4377 precursor RNA folds onto itself, forming GAM4377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4377 precursor RNA, designated SEQ ID NO: 7031, and a schematic representation of a predicted secondary folding of GAM4377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4377 folded precursor RNA yielding a GAM4377 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4377 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4377 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4377 target RNA, herein designated GAM TARGET RNA. GAM4377 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4377 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4377 RNA, herein designated GAM RNA, to target binding sites on GAM4377 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4377 target RNA into GAM4377 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4377 target genes. The mRNA of each one of this plurality of GAM4377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4377 RNA, herein designated GAM RNA, and which when bound by GAM4377 RNA causes inhibition of translation of the GAM4377 target mRNA into a corresponding GAM4377 target protein.

The mechanism of the translational inhibition exerted by GAM4377 RNA, herein designated GAM RNA, on one or more GAM4377 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4377 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4377 RNA, herein designated GAM RNA, of GAM4377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4377 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4377 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4377 RNA correlate with, and may be deduced from, the identity of the GAM4377 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4382 6038 CATCAGCTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCTGTTCTA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAAGGGCAC Messenger 4382 (GAM4382) oligonucleotides modulates expression of respective target genes

TCTGGCTGCA whose function and utility is known in the art.

ATGTGGAGGA GAM4382 is a novel bioinformatically detectable regulatory, non protein coding,

GGGAGTGACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4382 was detected is

GGAGGAAGGG described with additional reference to Figs. 9-15.

AGGTAAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4382 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4382

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4382

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4382 precursor RNA is designated SEQ ID:6038, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6038 is located from position 98489976 to position 98490054 relative to chromosome 10 on the `+` strand.

GAM4382 precursor RNA folds onto itself, forming GAM4382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4382 precursor RNA, designated SEQ ID NO: 6038, and a

schematic representation of a predicted secondary folding of GAM4382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4382 folded precursor RNA yielding a GAM4382 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4382 RNA, hereby incorporated herein.

GAM4382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4382 target RNA, herein designated GAM TARGET RNA. GAM4382 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4382 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4382 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4382 RNA, herein designated GAM RNA, to target binding sites on GAM4382 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4382 target RNA into GAM4382 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4382 target genes. The mRNA of each one of this plurality of GAM4382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4382 RNA, herein designated GAM RNA, and which when bound by GAM4382 RNA causes inhibition of translation of the GAM4382 target mRNA into a corresponding GAM4382 target protein.

The mechanism of the translational inhibition exerted by GAM4382 RNA, herein designated GAM RNA, on one or more GAM4382 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4382 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4382 RNA, herein designated GAM RNA, of GAM4382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4382 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4382 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4382 RNA correlate with, and may be deduced from, the identity of the GAM4382 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4398 7254 TGGTGGGACA Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGAGCCAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GACTGACATA Messenger 4398 (GAM4398) oligonucleotides modulates expression of respective target genes

GAAGAGCAGT whose function and utility is known in the art.

GGGGTAGAAT GAM4398 is a novel bioinformatically detectable regulatory, non protein coding,

TACAGTTCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4398 was detected is

TCTGGTGCCT described with additional reference to Figs. 9-15.

TTTCTCTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAGCTGTA encoded by the human genome.

TCCATCACCA GAM4398 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4398

CCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4398

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4398 precursor RNA is designated SEQ ID:7254, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7254 is located from position 50452834 to position 50452936 relative to chromosome 16 on the `+` strand.

GAM4398 precursor RNA folds onto itself, forming GAM4398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4398 precursor RNA, designated SEQ ID NO: 7254, and a schematic representation of a predicted secondary folding of GAM4398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4398 folded precursor RNA yielding a GAM4398 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4398 RNA, hereby incorporated herein.

GAM4398 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4398 target RNA, herein designated GAM TARGET RNA. GAM4398 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4398 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4398 RNA, herein designated GAM RNA, to target binding sites on GAM4398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4398 target RNA into GAM4398 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4398 target genes. The mRNA of each one of this plurality of GAM4398 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4398 RNA, herein designated GAM RNA, and which when bound by GAM4398 RNA causes inhibition of translation of the GAM4398 target mRNA into a corresponding GAM4398 target protein.

The mechanism of the translational inhibition exerted by GAM4398 RNA, herein

designated GAM RNA, on one or more GAM4398 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4398 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4398 RNA, herein designated GAM RNA, of GAM4398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4398 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4398 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4398 RNA correlate with, and may be deduced from, the identity of the GAM4398 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4408 5801 AGTATCTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCTATTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGTGAGTCT Messenger 4408 (GAM4408) oligonucleotides modulates expression of respective target genes
GTGCAGGAAC whose function and utility is known in the art.

ACAATGAGTC GAM4408 is a novel bioinformatically detectable regulatory, non protein coding,
TCAAAGTGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4408 was detected is

AAAAACTTTG described with additional reference to Figs. 9-15.

GATTCCTGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCTACAGCA encoded by the human genome.

CTTTTGTTCA GAM4408 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4408
GATACT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4408
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4408 precursor RNA is designated SEQ ID:5801, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5801 is located from position 138777302 to position 138777407 relative to chromosome 8

on the `-` strand.

GAM4408 precursor RNA folds onto itself, forming GAM4408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4408 precursor RNA, designated SEQ ID NO: 5801, and a schematic representation of a predicted secondary folding of GAM4408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4408 folded precursor RNA yielding a GAM4408 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4408 RNA, hereby incorporated herein.

GAM4408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4408 target RNA, herein designated GAM TARGET RNA. GAM4408 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4408 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4408 RNA, herein designated GAM RNA, to target binding sites on GAM4408 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4408 target RNA into GAM4408 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4408 target genes. The mRNA of each one of this plurality of GAM4408 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM4408 RNA, herein designated GAM RNA, and which when bound by GAM4408 RNA causes inhibition of translation of the GAM4408 target mRNA into a corresponding GAM4408 target protein.

The mechanism of the translational inhibition exerted by GAM4408 RNA, herein designated GAM RNA, on one or more GAM4408 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4408 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4408 RNA, herein designated GAM RNA, of GAM4408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4408 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4408 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4408 RNA correlate with, and may be deduced from, the identity of the GAM4408 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4423 6541 GCTGCAGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGGAGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGACATTGA Messenger 4423 (GAM4423) oligonucleotides modulates expression of respective target genes
CATTGACAGC whose function and utility is known in the art.

ATGAAAATGG GAM4423 is a novel bioinformatically detectable regulatory, non protein coding,
GTCTTGCCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4423 was detected is

TGCATGTGAG described with additional reference to Figs. 9-15.

ACTGCCTCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACACTCAGC encoded by the human genome.

GAM4423 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4423

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4423

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4423 precursor RNA is designated SEQ ID:6541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6541 is located from position 40086542 to position 40086631 relative to chromosome 17 on the `+` strand.

GAM4423 precursor RNA folds onto itself, forming GAM4423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4423 precursor RNA, designated SEQ ID NO: 6541, and a schematic representation of a predicted secondary folding of GAM4423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4423 folded precursor RNA yielding a GAM4423 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4423 RNA, hereby incorporated herein.

GAM4423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4423 target RNA, herein designated GAM TARGET RNA. GAM4423 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4423 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4423 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4423 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4423 RNA, herein designated GAM RNA, to target binding sites on GAM4423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4423 target RNA into GAM4423 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4423 target genes. The mRNA of each one of this plurality of GAM4423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4423 RNA, herein designated GAM RNA, and which when bound by GAM4423 RNA causes inhibition of translation of the GAM4423 target mRNA into a corresponding GAM4423 target protein.

The mechanism of the translational inhibition exerted by GAM4423 RNA, herein designated GAM RNA, on one or more GAM4423 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4423 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4423 RNA, herein designated GAM RNA, of GAM4423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4423 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4423 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4423 RNA correlate with, and may be deduced from, the identity of the GAM4423 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4426 7338 TTGTGGATAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAAGTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCCTGTTGT Messenger 4426 (GAM4426) oligonucleotides modulates expression of respective target genes

TCATCTATAG whose function and utility is known in the art.

ATGCACTGGA GAM4426 is a novel bioinformatically detectable regulatory, non protein coding,

TGGGATTGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4426 was detected is

AGTCTTCAGA described with additional reference to Figs. 9-15.

TTTCAGTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTTTTCCACA encoded by the human genome.

A GAM4426 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4426 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4426 precursor RNA is designated SEQ ID:7338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7338 is located from position 77432988 to position 77433078 relative to chromosome 1 on the `-` strand.

GAM4426 precursor RNA folds onto itself, forming GAM4426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4426 precursor RNA, designated SEQ ID NO: 7338, and a schematic representation of a predicted secondary folding of GAM4426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4426 folded precursor RNA yielding a GAM4426 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4426 RNA, hereby incorporated herein. Expression of GAM4426 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM4426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4426 target RNA, herein designated GAM TARGET RNA. GAM4426 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4426 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4426 RNA, herein designated GAM RNA, to target binding sites on GAM4426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4426 target RNA into GAM4426 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4426 target genes. The mRNA of each one of this plurality of GAM4426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4426 RNA, herein designated GAM RNA, and which when bound by GAM4426 RNA causes inhibition of translation of the GAM4426 target mRNA into a corresponding GAM4426 target protein.

The mechanism of the translational inhibition exerted by GAM4426 RNA, herein designated GAM RNA, on one or more GAM4426 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4426 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4426 RNA, herein designated GAM RNA, of GAM4426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4426 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4426 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4426 RNA correlate with, and may be deduced from, the identity of the GAM4426 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4429 6914 GTGGCTCGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTTGACCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTGGGGTT Messenger 4429 (GAM4429) oligonucleotides modulates expression of respective target genes
CCTGAGGATG whose function and utility is known in the art.

AGCTAAACCC GAM4429 is a novel bioinformatically detectable regulatory, non protein coding,

TTTCCATGTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4429 was detected is

CTGGGGGTTG described with additional reference to Figs. 9-15.

AGGCCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4429 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4429

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4429

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4429 precursor RNA is designated SEQ ID:6914, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6914 is located from position 55937832 to position 55937908 relative to chromosome 12 on the `-` strand.

GAM4429 precursor RNA folds onto itself, forming GAM4429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4429 precursor RNA, designated SEQ ID NO: 6914, and a schematic representation of a predicted secondary folding of GAM4429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4429 folded precursor RNA yielding a GAM4429 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4429 RNA, hereby incorporated herein.

GAM4429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4429 target RNA, herein designated GAM TARGET RNA. GAM4429 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4429 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4429 RNA, herein designated GAM RNA, to target binding sites on GAM4429 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4429 target RNA into GAM4429 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4429 target genes. The mRNA of each one of this plurality of GAM4429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4429 RNA, herein designated GAM RNA, and which when bound by GAM4429 RNA causes inhibition of translation of the GAM4429 target mRNA into a corresponding GAM4429 target protein.

The mechanism of the translational inhibition exerted by GAM4429 RNA, herein designated GAM RNA, on one or more GAM4429 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4429 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4429 RNA, herein designated GAM RNA, of GAM4429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4429 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4429 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4429 RNA correlate with, and may be deduced from, the identity of the GAM4429 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4432 5986 CAACAGGTGC AAGTGTTAAA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGTATGATC Messenger 4432 (GAM4432) oligonucleotides modulates expression of respective target genes

CTTCAGTGGA whose function and utility is known in the art.

ACAAAGCCTC GAM4432 is a novel bioinformatically detectable regulatory, non protein coding, CGTGTCACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4432 was detected is

GAGGGATAGC described with additional reference to Figs. 9-15.

AACATGCCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGCACTGC encoded by the human genome.

AAGAGTTG GAM4432 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4432 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4432 precursor RNA is designated SEQ ID:5986, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5986 is located from position 27028798 to position 27028895 relative to chromosome 9 on the `+` strand.

GAM4432 precursor RNA folds onto itself, forming GAM4432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4432 precursor RNA, designated SEQ ID NO: 5986, and a schematic representation of a predicted secondary folding of GAM4432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4432 folded precursor RNA yielding a GAM4432 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4432 RNA, hereby incorporated herein.

GAM4432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4432 target RNA, herein designated GAM TARGET RNA. GAM4432 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4432 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4432 RNA, herein designated GAM RNA, to target binding sites on GAM4432 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4432 target RNA into GAM4432 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4432 target genes. The mRNA of each one of this plurality of GAM4432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4432 RNA, herein designated GAM RNA, and which when bound by GAM4432 RNA causes inhibition of translation of the GAM4432 target mRNA into a corresponding GAM4432 target protein.

The mechanism of the translational inhibition exerted by GAM4432 RNA, herein designated GAM RNA, on one or more GAM4432 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4432 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4432 RNA, herein designated GAM RNA, of GAM4432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4432 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4432 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4432 RNA correlate with, and may be deduced from, the identity of the GAM4432 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4446 7024 TCCCACAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGAGGAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAAGAAGAC Messenger 4446 (GAM4446) oligonucleotides modulates expression of respective target genes

TCTGTTGTTC whose function and utility is known in the art.

ATTGTTTTTA GAM4446 is a novel bioinformatically detectable regulatory, non protein coding,

TCTTTTTCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4446 was detected is

CAGATGCCTG described with additional reference to Figs. 9-15.

TGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4446 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4446

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4446

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4446 precursor RNA is designated SEQ ID:7024, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7024 is located from position 117986909 to position 117986983 relative to chromosome X on the `-` strand.

GAM4446 precursor RNA folds onto itself, forming GAM4446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4446 precursor RNA, designated SEQ ID NO: 7024, and a schematic representation of a predicted secondary folding of GAM4446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4446 folded precursor RNA yielding a GAM4446 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4446 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4446 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4446 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM4446 target RNA, herein designated GAM TARGET RNA. GAM4446 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4446 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4446 RNA, herein designated GAM RNA, to target binding sites on GAM4446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4446 target RNA into GAM4446 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4446 target genes. The mRNA of each one of this plurality of GAM4446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4446 RNA, herein designated GAM RNA, and which when bound by GAM4446 RNA causes inhibition of translation of the GAM4446 target mRNA into a corresponding GAM4446 target protein.

The mechanism of the translational inhibition exerted by GAM4446 RNA, herein designated GAM RNA, on one or more GAM4446 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4446 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4446 RNA, herein designated GAM RNA, of GAM4446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4446 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM4446 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4446 RNA correlate with, and may be deduced from, the identity of the GAM4446 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4448 6008 CACTTTCATG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGCCTTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCTGGAAG Messenger 4448 (GAM4448) oligonucleotides modulates expression of respective target genes
GTGCCTCCCT whose function and utility is known in the art.

ATTCCACAGA GAM4448 is a novel bioinformatically detectable regulatory, non protein coding,
CTTTGGATCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4448 was detected is

GTGGGTGTGG described with additional reference to Figs. 9-15.

GGGAATCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCAGACCAT encoded by the human genome.

GAAATG GAM4448 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4448
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4448
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4448 precursor RNA is designated SEQ ID:6008, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6008 is located from position 33327986 to position 33328081 relative to chromosome 10 on the `+` strand.

GAM4448 precursor RNA folds onto itself, forming GAM4448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4448 precursor RNA, designated SEQ ID NO: 6008, and a schematic representation of a predicted secondary folding of GAM4448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4448 folded precursor RNA yielding a GAM4448 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4448 RNA, hereby incorporated herein.

GAM4448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4448 target RNA, herein designated GAM TARGET RNA. GAM4448 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4448 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4448 RNA, herein designated GAM RNA, to target binding sites on GAM4448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4448 target RNA into GAM4448 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4448 target genes. The mRNA of each one of this plurality of GAM4448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4448 RNA, herein designated GAM RNA, and which when bound by GAM4448 RNA causes inhibition of translation of the GAM4448 target mRNA into a corresponding GAM4448 target protein.

The mechanism of the translational inhibition exerted by GAM4448 RNA, herein designated GAM RNA, on one or more GAM4448 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4448 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4448 RNA, herein designated GAM RNA, of GAM4448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4448 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4448 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4448 RNA correlate with, and may be deduced from, the identity of the GAM4448 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4459 6295 GAAGAGGCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTACTCCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTCTTCCAT Messenger 4459 (GAM4459) oligonucleotides modulates expression of respective target genes
TCTCACCCCT whose function and utility is known in the art.

CTGTTTCTGC GAM4459 is a novel bioinformatically detectable regulatory, non protein coding,
CAGAATTGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4459 was detected is

ACAGCAGGGC described with additional reference to Figs. 9-15.

AGAAAATGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTTTCGTGC encoded by the human genome.

AGAGTTGACA GAM4459 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4459
AGATACAGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4459
TAGTGAAGAC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
AAGAATCTTC to the nucleotide sequence of GAM4459 precursor RNA is designated SEQ ID:6295, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6295 is located from position 18267651 to position 18267780 relative to chromosome 7 on the `+` strand.

GAM4459 precursor RNA folds onto itself, forming GAM4459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4459 precursor RNA, designated SEQ ID NO: 6295, and a schematic representation of a predicted secondary folding of GAM4459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated

herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4459 folded precursor RNA yielding a GAM4459 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4459 RNA, hereby incorporated herein.

GAM4459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4459 target RNA, herein designated GAM TARGET RNA. GAM4459 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4459 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4459 RNA, herein designated GAM RNA, to target binding sites on GAM4459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4459 target RNA into GAM4459 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4459 target genes. The mRNA of each one of this plurality of GAM4459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4459 RNA, herein designated GAM RNA, and which when bound by GAM4459 RNA causes inhibition of translation of the GAM4459 target mRNA into a corresponding GAM4459 target protein.

The mechanism of the translational inhibition exerted by GAM4459 RNA, herein designated GAM RNA, on one or more GAM4459 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4459 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4459 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4459 RNA, herein designated GAM RNA, of GAM4459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4459 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4459 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4459 RNA correlate with, and may be deduced from, the identity of the GAM4459 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4516 6706 GGAGACGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACATACACAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGATTCAGA Messenger 4516 (GAM4516) oligonucleotides modulates expression of respective target genes

CACACTTGCA whose function and utility is known in the art.

ATGTATTGCT GAM4516 is a novel bioinformatically detectable regulatory, non protein coding,

GGGGATTCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4516 was detected is

CAGCATTGGC described with additional reference to Figs. 9-15.

ATGATGGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGTGGAGAA encoded by the human genome.

TCATTTGACC GAM4516 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4516

GCCTCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4516

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4516 precursor RNA is designated SEQ ID:6706, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6706 is located from position 50034558 to position 50034663 relative to chromosome 12 on the `+` strand.

GAM4516 precursor RNA folds onto itself, forming GAM4516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4516 precursor RNA, designated SEQ ID NO: 6706, and a schematic representation of a predicted secondary folding of GAM4516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4516 folded precursor RNA yielding a GAM4516 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4516 RNA, hereby incorporated herein.

GAM4516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4516 target RNA, herein designated GAM TARGET RNA. GAM4516 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4516 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4516 RNA, herein designated GAM RNA, to target binding sites on GAM4516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4516 target RNA into GAM4516 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4516 target genes. The mRNA of each one of this plurality of GAM4516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4516 RNA, herein designated GAM RNA, and which when bound by GAM4516 RNA causes inhibition of translation of the GAM4516 target mRNA into a corresponding GAM4516 target protein.

The mechanism of the translational inhibition exerted by GAM4516 RNA, herein designated GAM RNA, on one or more GAM4516 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4516 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4516 RNA, herein designated GAM RNA, of GAM4516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4516 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4516 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4516 RNA correlate with, and may be deduced from, the identity of the GAM4516 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4538 7030 TCCCTCCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCCCAAAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAAACACTC Messenger 4538 (GAM4538) oligonucleotides modulates expression of respective target genes

CTATATTTTG whose function and utility is known in the art.

TAGCGCCTTC GAM4538 is a novel bioinformatically detectable regulatory, non protein coding,

CAGAATGGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4538 was detected is

CAGCGGAAAC described with additional reference to Figs. 9-15.

TAGTGTTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAAGGAGG encoded by the human genome.

CGA GAM4538 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4538

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4538

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4538 precursor RNA is designated SEQ ID:7030, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7030 is located from position 53161338 to position 53161430 relative to chromosome 15 on the `-` strand.

GAM4538 precursor RNA folds onto itself, forming GAM4538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4538 precursor RNA, designated SEQ ID NO: 7030, and a schematic representation of a predicted secondary folding of GAM4538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4538 folded precursor RNA yielding a GAM4538 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4538 RNA, hereby incorporated herein.

GAM4538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4538 target RNA, herein designated GAM TARGET RNA. GAM4538 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4538 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4538 RNA, herein designated GAM RNA, to target binding sites on GAM4538 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4538 target RNA into GAM4538 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4538 target genes. The mRNA of each one of this plurality of GAM4538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4538 RNA, herein designated GAM RNA, and which when bound by GAM4538 RNA causes inhibition of translation

of the GAM4538 target mRNA into a corresponding GAM4538 target protein.

The mechanism of the translational inhibition exerted by GAM4538 RNA, herein designated GAM RNA, on one or more GAM4538 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4538 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4538 RNA, herein designated GAM RNA, of GAM4538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4538 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4538 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4538 RNA correlate with, and may be deduced from, the identity of the GAM4538 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4544 6981 TATGAACTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCACTTTTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGAAACCT Messenger 4544 (GAM4544) oligonucleotides modulates expression of respective target genes

GGTGGGCCAG whose function and utility is known in the art.

CTCTGTGGGG GAM4544 is a novel bioinformatically detectable regulatory, non protein coding,

TGATGCATTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4544 was detected is

AAAAGGGCAG described with additional reference to Figs. 9-15.

TTCATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4544 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4544

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4544

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM4544 precursor RNA is designated SEQ ID:6981, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6981 is located from position 100974291 to position 100974366 relative to chromosome 9 on the `+` strand.

GAM4544 precursor RNA folds onto itself, forming GAM4544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4544 precursor RNA, designated SEQ ID NO: 6981, and a schematic representation of a predicted secondary folding of GAM4544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4544 folded precursor RNA yielding a GAM4544 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4544 RNA, hereby incorporated herein.

GAM4544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4544 target RNA, herein designated GAM TARGET RNA. GAM4544 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4544 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4544 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4544 RNA, herein designated GAM RNA, to target binding sites on GAM4544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4544 target RNA into GAM4544 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4544 target genes. The mRNA of each one of this plurality of GAM4544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4544 RNA, herein designated GAM RNA, and which when bound by GAM4544 RNA causes inhibition of translation of the GAM4544 target mRNA into a corresponding GAM4544 target protein.

The mechanism of the translational inhibition exerted by GAM4544 RNA, herein designated GAM RNA, on one or more GAM4544 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4544 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4544 RNA, herein designated GAM RNA, of GAM4544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4544 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4544 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4544 RNA correlate with, and may be deduced from, the identity of the GAM4544 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4557 7285 TTAGCACCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTATATTAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTCATTTTG Messenger 4557 (GAM4557) oligonucleotides modulates expression of respective target genes
ATGGTTTGTA whose function and utility is known in the art.

TCTCAAAGGA GAM4557 is a novel bioinformatically detectable regulatory, non protein coding,
GTACAGTGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4557 was detected is

CGAAACTTGT described with additional reference to Figs. 9-15.

TTAAAGATAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACCGGAAAGA encoded by the human genome.

AAAAGAGAAG GAM4557 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4557

AGGCAGAGTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4557

GCTTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4557 precursor RNA is designated SEQ ID:7285, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7285 is located from position 88520248 to position 88520362 relative to chromosome 9 on the `+` strand.

GAM4557 precursor RNA folds onto itself, forming GAM4557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4557 precursor RNA, designated SEQ ID NO: 7285, and a schematic representation of a predicted secondary folding of GAM4557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4557 folded precursor RNA yielding a GAM4557 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4557 RNA, hereby incorporated herein.

GAM4557 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4557 target RNA, herein designated GAM TARGET RNA. GAM4557 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4557 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4557 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4557 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4557 RNA, herein designated GAM RNA, to target

binding sites on GAM4557 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4557 target RNA into GAM4557 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4557 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4557 target genes. The mRNA of each one of this plurality of GAM4557 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4557 RNA, herein designated GAM RNA, and which when bound by GAM4557 RNA causes inhibition of translation of the GAM4557 target mRNA into a corresponding GAM4557 target protein.

The mechanism of the translational inhibition exerted by GAM4557 RNA, herein designated GAM RNA, on one or more GAM4557 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4557 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4557 RNA, herein designated GAM RNA, of GAM4557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4557 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4557 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4557 RNA correlate with, and may be deduced from, the identity of the GAM4557 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4561 6047 CCACACCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTGTGACC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGGCTAGTA Messenger 4561 (GAM4561) oligonucleotides modulates expression of respective target genes
GACAGTGGCA whose function and utility is known in the art.

ACATAGTCAT GAM4561 is a novel bioinformatically detectable regulatory, non protein coding,
CCCCAAGATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4561 was detected is

CTAATCTTCT described with additional reference to Figs. 9-15.

GCTGGAACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCATACGTTA encoded by the human genome.

TCATGGTCAA GAM4561 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4561

TGTAAACCTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4561

GTTTGTGTGG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4561 precursor RNA is designated SEQ ID:6047, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6047 is located from position 158626687 to position 158626806 relative to chromosome 1 on the `+` strand.

GAM4561 precursor RNA folds onto itself, forming GAM4561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4561 precursor RNA, designated SEQ ID NO: 6047, and a schematic representation of a predicted secondary folding of GAM4561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4561 folded precursor RNA yielding a GAM4561 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4561 RNA, hereby incorporated herein. Expression of GAM4561 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM4561 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4561 target RNA, herein designated GAM TARGET RNA. GAM4561 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4561 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4561 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4561 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4561 RNA, herein designated GAM RNA, to target binding sites on GAM4561 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4561 target RNA into GAM4561 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4561 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4561 target genes. The mRNA of each one of this plurality of GAM4561 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4561 RNA, herein designated GAM RNA, and which when bound by GAM4561 RNA causes inhibition of translation of the GAM4561 target mRNA into a corresponding GAM4561 target protein.

The mechanism of the translational inhibition exerted by GAM4561 RNA, herein designated GAM RNA, on one or more GAM4561 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4561 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4561 RNA, herein designated GAM RNA, of GAM4561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4561 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4561 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4561 RNA correlate with, and may be deduced from, the identity of the GAM4561 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4571 5826 AGTTCTGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTGCTGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAACATTTT Messenger 4571 (GAM4571) oligonucleotides modulates expression of respective target genes

AGGTTCTGAT whose function and utility is known in the art.

AGCTGTATTC GAM4571 is a novel bioinformatically detectable regulatory, non protein coding,
TCAGTCCTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4571 was detected is

AGTGACAGGT described with additional reference to Figs. 9-15.

GTAGCCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTACT encoded by the human genome.

GAM4571 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4571

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4571

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4571 precursor RNA is designated SEQ ID:5826, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5826 is located from position 54394158 to position 54394243 relative to chromosome 19 on the `+` strand.

GAM4571 precursor RNA folds onto itself, forming GAM4571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4571 precursor RNA, designated SEQ ID NO: 5826, and a schematic representation of a predicted secondary folding of GAM4571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4571 folded precursor RNA yielding a GAM4571 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4571 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4571 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4571 target RNA, herein designated GAM TARGET RNA. GAM4571 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4571 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM4571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4571 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4571 RNA, herein designated GAM RNA, to target binding sites on GAM4571 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4571 target RNA into GAM4571 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4571 target genes. The mRNA of each one of this plurality of GAM4571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4571 RNA, herein designated GAM RNA, and which when bound by GAM4571 RNA causes inhibition of translation of the GAM4571 target mRNA into a corresponding GAM4571 target protein.

The mechanism of the translational inhibition exerted by GAM4571 RNA, herein designated GAM RNA, on one or more GAM4571 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4571 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4571 RNA, herein designated GAM RNA, of GAM4571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4571 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4571 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4571 RNA correlate with, and may be deduced from, the identity of the GAM4571 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4633 7197 TGCATTACCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCCCAACTT detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAATCTTTT Messenger 4633 (GAM4633) oligonucleotides modulates expression of respective target genes

GATAACCCAG whose function and utility is known in the art.

GCAGCTGGGT GAM4633 is a novel bioinformatically detectable regulatory, non protein coding,

TATCCCCAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4633 was detected is

TTAAAGTCTT described with additional reference to Figs. 9-15.

TTTGTTGTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGTATGGCA encoded by the human genome.

GAM4633 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4633

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4633

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4633 precursor RNA is designated SEQ ID:7197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7197 is located from position 71710862 to position 71710951 relative to chromosome X on the `-` strand.

GAM4633 precursor RNA folds onto itself, forming GAM4633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4633 precursor RNA, designated SEQ ID NO: 7197, and a schematic representation of a predicted secondary folding of GAM4633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4633 folded precursor RNA yielding a GAM4633 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4633 RNA, hereby incorporated herein.

GAM4633 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4633 target RNA, herein designated GAM TARGET RNA. GAM4633 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4633 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4633 RNA, herein designated GAM RNA, to target binding sites on GAM4633 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4633 target RNA into GAM4633 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4633 target genes. The mRNA of each one of this plurality of GAM4633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4633 RNA, herein designated GAM RNA, and which when bound by GAM4633 RNA causes inhibition of translation of the GAM4633 target mRNA into a corresponding GAM4633 target protein.

The mechanism of the translational inhibition exerted by GAM4633 RNA, herein designated GAM RNA, on one or more GAM4633 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4633 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4633 RNA, herein designated GAM RNA, of GAM4633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4633 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4633 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4633 RNA correlate with, and may be deduced from, the identity of the GAM4633 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4650 6608 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 4650 (GAM4650) oligonucleotides modulates expression of respective target genes
TTGCAGTGAG whose function and utility is known in the art.

CCAAGATCGT GAM4650 is a novel bioinformatically detectable regulatory, non protein coding,
GCCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4650 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GTGATAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM4650 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4650

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4650
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4650 precursor RNA is designated SEQ ID:6608, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6608 is located from position 66913128 to position 66913215 relative to chromosome 17 on the `+` strand.

GAM4650 precursor RNA folds onto itself, forming GAM4650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4650 precursor RNA, designated SEQ ID NO: 6608, and a schematic representation of a predicted secondary folding of GAM4650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4650 folded precursor RNA yielding a GAM4650 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM4650 RNA, hereby incorporated herein.

GAM4650 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4650 target RNA, herein designated GAM TARGET RNA. GAM4650 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4650 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4650 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4650 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4650 RNA, herein designated GAM RNA, to target binding sites on GAM4650 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4650 target RNA into GAM4650 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4650 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4650 target genes. The mRNA of each one of this plurality of GAM4650 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4650 RNA, herein designated GAM RNA, and which when bound by GAM4650 RNA causes inhibition of translation of the GAM4650 target mRNA into a corresponding GAM4650 target protein.

The mechanism of the translational inhibition exerted by GAM4650 RNA, herein designated GAM RNA, on one or more GAM4650 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4650 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4650 RNA, herein designated GAM RNA, of GAM4650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4650 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4650 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4650 RNA correlate with, and may be deduced from, the identity of the GAM4650 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4656 6976 TAGTGACAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCATCCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCACTTGCC Messenger 4656 (GAM4656) oligonucleotides modulates expression of respective target genes
CAGAGCTGCA whose function and utility is known in the art.

GAGTTGTGTG GAM4656 is a novel bioinformatically detectable regulatory, non protein coding,
TGCCATACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4656 was detected is

GCGGCTCAAA described with additional reference to Figs. 9-15.

GGGAAGGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTATCCCCT encoded by the human genome.

GAGTTTCTA GAM4656 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4656
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4656
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4656 precursor RNA is designated SEQ ID:6976, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6976 is located from position 142589577 to position 142589675 relative to chromosome 5 on the `+` strand.

GAM4656 precursor RNA folds onto itself, forming GAM4656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4656 precursor RNA, designated SEQ ID NO: 6976, and a schematic representation of a predicted secondary folding of GAM4656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4656 folded precursor RNA

yielding a GAM4656 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4656 RNA, hereby incorporated herein. Expression of GAM4656 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM4656 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4656 target RNA, herein designated GAM TARGET RNA. GAM4656 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4656 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4656 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4656 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4656 RNA, herein designated GAM RNA, to target binding sites on GAM4656 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4656 target RNA into GAM4656 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4656 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4656 target genes. The mRNA of each one of this plurality of GAM4656 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4656 RNA, herein designated GAM RNA, and which when bound by GAM4656 RNA causes inhibition of translation of the GAM4656 target mRNA into a corresponding GAM4656 target protein.

The mechanism of the translational inhibition exerted by GAM4656 RNA, herein designated GAM RNA, on one or more GAM4656 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4656 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4656 RNA, herein designated GAM RNA, of GAM4656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4656 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4656 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4656 RNA correlate with, and may be deduced from, the identity of the GAM4656 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4671 6087 CCCTGCCGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAGAGCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTCAGAGAT Messenger 4671 (GAM4671) oligonucleotides modulates expression of respective target genes
GCCCTGAGTG whose function and utility is known in the art.

ATCGTCACCA GAM4671 is a novel bioinformatically detectable regulatory, non protein coding,
GCTGCATCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4671 was detected is

GCAAACTTCA described with additional reference to Figs. 9-15.

TCTTGCTGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTGTGGCTT encoded by the human genome.

GG GAM4671 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4671
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4671
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4671 precursor RNA is designated SEQ ID:6087, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6087 is located from position 840148 to position 840239 relative to chromosome 10 on the `-` strand.

GAM4671 precursor RNA folds onto itself, forming GAM4671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4671 precursor RNA, designated SEQ ID NO: 6087, and a schematic representation of a predicted secondary folding of GAM4671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4671 folded precursor RNA yielding a GAM4671 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4671 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4671 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4671 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4671 target RNA, herein designated GAM TARGET RNA. GAM4671 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4671 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4671 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4671 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4671 RNA, herein designated GAM RNA, to target binding sites on GAM4671 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4671 target RNA into GAM4671 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4671 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4671 target genes. The mRNA of each one of this plurality of GAM4671 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4671 RNA, herein designated GAM RNA, and which when bound by GAM4671 RNA causes inhibition of translation of the GAM4671 target mRNA into a corresponding GAM4671 target protein.

The mechanism of the translational inhibition exerted by GAM4671 RNA, herein designated GAM RNA, on one or more GAM4671 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4671 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4671 RNA, herein designated GAM RNA, of GAM4671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4671 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4671 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4671 RNA correlate with, and may be deduced from, the identity of the GAM4671 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4685 7348 TTTTCAATTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAAAAATTA detected oligonucleotides of the present invention, referred to here as Genomic Address
GATTTATTGC Messenger 4685 (GAM4685) oligonucleotides modulates expression of respective target genes
AGACTGGCCT whose function and utility is known in the art.

CAAGCTCCCA GAM4685 is a novel bioinformatically detectable regulatory, non protein coding,
GACTATATTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4685 was detected is

TTTAGCTGCA described with additional reference to Figs. 9-15.

TTATTTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTGAAATGC encoded by the human genome.

CAGCTTTTGA GAM4685 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4685
GACTTTTGAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4685
AA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4685 precursor RNA is designated SEQ ID:7348, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7348 is located from position 26788414 to position 26788525 relative to chromosome 17 on the `+` strand.

GAM4685 precursor RNA folds onto itself, forming GAM4685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4685 precursor RNA, designated SEQ ID NO: 7348, and a schematic representation of a predicted secondary folding of GAM4685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4685 folded precursor RNA yielding a GAM4685 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4685 RNA, hereby incorporated herein.

GAM4685 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4685 target RNA, herein designated GAM TARGET RNA. GAM4685 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4685 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4685 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4685 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4685 RNA, herein designated GAM RNA, to target binding sites on GAM4685 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4685 target RNA into GAM4685 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4685 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4685 target genes. The mRNA of each one of this plurality of GAM4685 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4685 RNA, herein designated GAM RNA, and which when bound by GAM4685 RNA causes inhibition of translation

of the GAM4685 target mRNA into a corresponding GAM4685 target protein.

The mechanism of the translational inhibition exerted by GAM4685 RNA, herein designated GAM RNA, on one or more GAM4685 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4685 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4685 RNA, herein designated GAM RNA, of GAM4685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4685 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4685 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4685 RNA correlate with, and may be deduced from, the identity of the GAM4685 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4690 6943 GTTTCCCACT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTCTCCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTCATTTT Messenger 4690 (GAM4690) oligonucleotides modulates expression of respective target genes

TCTCTTTCCA whose function and utility is known in the art.

TAAAAAGCTA GAM4690 is a novel bioinformatically detectable regulatory, non protein coding,

ATGGTGACGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4690 was detected is

TATCAAAGAG described with additional reference to Figs. 9-15.

TGAAGGAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGGCTAAG encoded by the human genome.

GGTGGGGAAC GAM4690 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4690

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4690

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM4690 precursor RNA is designated SEQ ID:6943, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6943 is located from position 42013351 to position 42013450 relative to chromosome 20 on the `+` strand.

GAM4690 precursor RNA folds onto itself, forming GAM4690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4690 precursor RNA, designated SEQ ID NO: 6943, and a schematic representation of a predicted secondary folding of GAM4690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4690 folded precursor RNA yielding a GAM4690 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4690 RNA, hereby incorporated herein.

GAM4690 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4690 target RNA, herein designated GAM TARGET RNA. GAM4690 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4690 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4690 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4690 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4690 RNA, herein designated GAM RNA, to target binding sites on GAM4690 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4690 target RNA into GAM4690 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4690 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4690 target genes. The mRNA of each one of this plurality of GAM4690 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4690 RNA, herein designated GAM RNA, and which when bound by GAM4690 RNA causes inhibition of translation of the GAM4690 target mRNA into a corresponding GAM4690 target protein.

The mechanism of the translational inhibition exerted by GAM4690 RNA, herein designated GAM RNA, on one or more GAM4690 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4690 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4690 RNA, herein designated GAM RNA, of GAM4690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4690 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4690 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4690 RNA correlate with, and may be deduced from, the identity of the GAM4690 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4707 6407 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 4707 (GAM4707) oligonucleotides modulates expression of respective target genes

CGGAGGTTGT whose function and utility is known in the art.

GTTGAGCCGA GAM4707 is a novel bioinformatically detectable regulatory, non protein coding,

GATCTCGCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4707 was detected is

TTGCACTCCA described with additional reference to Figs. 9-15.

GCCTAGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCGAA encoded by the human genome.

ACTCCATCTC GAM4707 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4707 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4707 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4707 precursor RNA is designated SEQ ID:6407, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6407 is located from position 94524960 to position 94525059 relative to chromosome X on the `+` strand.

GAM4707 precursor RNA folds onto itself, forming GAM4707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4707 precursor RNA, designated SEQ ID NO: 6407, and a schematic representation of a predicted secondary folding of GAM4707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4707 folded precursor RNA yielding a GAM4707 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4707 RNA, hereby incorporated herein.

GAM4707 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4707 target RNA, herein designated GAM TARGET RNA. GAM4707 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4707 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4707 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4707 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4707 RNA, herein designated GAM RNA, to target

binding sites on GAM4707 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4707 target RNA into GAM4707 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4707 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4707 target genes. The mRNA of each one of this plurality of GAM4707 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4707 RNA, herein designated GAM RNA, and which when bound by GAM4707 RNA causes inhibition of translation of the GAM4707 target mRNA into a corresponding GAM4707 target protein.

The mechanism of the translational inhibition exerted by GAM4707 RNA, herein designated GAM RNA, on one or more GAM4707 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4707 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4707 RNA, herein designated GAM RNA, of GAM4707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4707 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4707 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4707 RNA correlate with, and may be deduced from, the identity of the GAM4707 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4709 6212 CTGCAGTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GATGTGTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACTTCAGGA Messenger 4709 (GAM4709) oligonucleotides modulates expression of respective target genes
CACCCCACTA whose function and utility is known in the art.

CCTGAATTGC GAM4709 is a novel bioinformatically detectable regulatory, non protein coding,
AGCAGTGTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4709 was detected is

CGAATCATCA described with additional reference to Figs. 9-15.

CTCTGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM4709 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4709 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4709 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4709 precursor RNA is designated SEQ ID:6212, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6212 is located from position 97691104 to position 97691181 relative to chromosome 9 on the `+` strand.

GAM4709 precursor RNA folds onto itself, forming GAM4709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4709 precursor RNA, designated SEQ ID NO: 6212, and a schematic representation of a predicted secondary folding of GAM4709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4709 folded precursor RNA yielding a GAM4709 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4709 RNA, hereby incorporated herein.

GAM4709 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4709 target RNA, herein designated GAM TARGET RNA. GAM4709 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4709 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4709 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4709 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4709 RNA, herein designated GAM RNA, to target binding sites on GAM4709 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4709 target RNA into GAM4709 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4709 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4709 target genes. The mRNA of each one of this plurality of GAM4709 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4709 RNA, herein designated GAM RNA, and which when bound by GAM4709 RNA causes inhibition of translation of the GAM4709 target mRNA into a corresponding GAM4709 target protein.

The mechanism of the translational inhibition exerted by GAM4709 RNA, herein designated GAM RNA, on one or more GAM4709 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4709 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4709 RNA, herein designated GAM RNA, of GAM4709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4709 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4709 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4709 RNA correlate with, and may be deduced from, the identity of the GAM4709 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4733 5648 AAACGTGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGATTGATGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTCATGGAC Messenger 4733 (GAM4733) oligonucleotides modulates expression of respective target genes

TCTGTTGCCC whose function and utility is known in the art.

CAAGTCCCCA GAM4733 is a novel bioinformatically detectable regulatory, non protein coding, AGCCTTGTAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4733 was detected is

CAGCGTTT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4733 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4733

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4733

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4733 precursor RNA is designated SEQ ID:5648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5648 is located from position 99149260 to position 99149327 relative to chromosome 13 on the `+` strand.

GAM4733 precursor RNA folds onto itself, forming GAM4733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4733 precursor RNA, designated SEQ ID NO: 5648, and a schematic representation of a predicted secondary folding of GAM4733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4733 folded precursor RNA yielding a GAM4733 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4733 RNA, hereby incorporated herein.

GAM4733 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4733 target RNA, herein designated GAM TARGET RNA. GAM4733 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4733 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4733 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM4733 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4733 RNA, herein designated GAM RNA, to target binding sites on GAM4733 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4733 target RNA into GAM4733 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4733 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4733 target genes. The mRNA of each one of this plurality of GAM4733 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4733 RNA, herein designated GAM RNA, and which when bound by GAM4733 RNA causes inhibition of translation of the GAM4733 target mRNA into a corresponding GAM4733 target protein.

The mechanism of the translational inhibition exerted by GAM4733 RNA, herein designated GAM RNA, on one or more GAM4733 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4733 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4733 RNA, herein designated GAM RNA, of GAM4733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4733 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4733 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4733 RNA correlate with, and may be deduced from, the identity of the GAM4733 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4738 5784 AGGCTGTATG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGTTAATGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TAATCGTGAT Messenger 4738 (GAM4738) oligonucleotides modulates expression of respective target
genes
AGGGGTTTTT whose function and utility is known in the art.

GCCTCCAACT GAM4738 is a novel bioinformatically detectable regulatory, non protein coding,
GACTCCTACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4738 was detected is

TATTAGCATT described with additional reference to Figs. 9-15.

AACAGTGTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
GATGCCT encoded by the human genome.

GAM4738 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4738

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM4738

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4738 precursor RNA is designated SEQ ID:5784, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5784 is located from position 25868152 to position 25868238 relative to chromosome 21 on the `+` strand.

GAM4738 precursor RNA folds onto itself, forming GAM4738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4738 precursor RNA, designated SEQ ID NO: 5784, and a schematic representation of a predicted secondary folding of GAM4738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4738 folded precursor RNA yielding a GAM4738 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4738 RNA, hereby incorporated herein.

GAM4738 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4738 target RNA, herein designated GAM TARGET RNA. GAM4738 target
RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4738 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4738 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4738 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4738 RNA, herein designated GAM RNA, to target binding sites on GAM4738 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4738 target RNA into GAM4738 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4738 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4738 target genes. The mRNA of each one of this plurality of GAM4738 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4738 RNA, herein designated GAM RNA, and which when bound by GAM4738 RNA causes inhibition of translation of the GAM4738 target mRNA into a corresponding GAM4738 target protein.

The mechanism of the translational inhibition exerted by GAM4738 RNA, herein designated GAM RNA, on one or more GAM4738 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4738 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4738 RNA, herein designated GAM RNA, of GAM4738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4738 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4738 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4738 RNA correlate with, and may be deduced from, the identity of the GAM4738 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4769 6231 CTGGGATTAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGCACCTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCCAAGTCT Messenger 4769 (GAM4769) oligonucleotides modulates expression of respective target genes
GGCTAATTTT whose function and utility is known in the art.

TGTATTTTTA GAM4769 is a novel bioinformatically detectable regulatory, non protein coding,
ATAGAGACGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4769 was detected is

GGTTTCGCTA described with additional reference to Figs. 9-15.

TGTTGGCCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTGGTCTCG encoded by the human genome.

AACTCCTGAT GAM4769 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4769
CTCAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4769

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4769 precursor RNA is designated SEQ ID:6231, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6231 is located from position 128497043 to position 128497147 relative to chromosome 8 on the `+` strand.

GAM4769 precursor RNA folds onto itself, forming GAM4769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4769 precursor RNA, designated SEQ ID NO: 6231, and a schematic representation of a predicted secondary folding of GAM4769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4769 folded precursor RNA yielding a GAM4769 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4769 RNA, hereby incorporated herein.

GAM4769 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM4769 target RNA, herein designated GAM TARGET RNA. GAM4769 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4769 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4769 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4769 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4769 RNA, herein designated GAM RNA, to target binding sites on GAM4769 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4769 target RNA into GAM4769 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4769 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4769 target genes. The mRNA of each one of this plurality of GAM4769 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4769 RNA, herein designated GAM RNA, and which when bound by GAM4769 RNA causes inhibition of translation of the GAM4769 target mRNA into a corresponding GAM4769 target protein.

The mechanism of the translational inhibition exerted by GAM4769 RNA, herein designated GAM RNA, on one or more GAM4769 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4769 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4769 RNA, herein designated GAM RNA, of GAM4769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4769 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM4769 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4769 RNA correlate with, and may be deduced from, the identity of the GAM4769 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4796 6951 TAAAACTCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CATCAAATAG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTAATCTT Messenger 4796 (GAM4796) oligonucleotides modulates expression of respective target genes

ATTAATTACA whose function and utility is known in the art.

CATTTTGTAT GAM4796 is a novel bioinformatically detectable regulatory, non protein coding,

TTTAATTATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4796 was detected is

TCAAGGAGTG described with additional reference to Figs. 9-15.

AAGAAAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTGTTTTTG encoded by the human genome.

TTTTTGTAGT GAM4796 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4796

TCTGATTACT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4796

CATTTATGCA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TTGTTTTG to the nucleotide sequence of GAM4796 precursor RNA is designated SEQ ID:6951, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6951 is located from position 37551256 to position 37551383 relative to chromosome 19 on the `+` strand.

GAM4796 precursor RNA folds onto itself, forming GAM4796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4796 precursor RNA, designated SEQ ID NO: 6951, and a schematic representation of a predicted secondary folding of GAM4796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4796 folded precursor RNA yielding a GAM4796 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor

product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4796 RNA, hereby incorporated herein.

GAM4796 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4796 target RNA, herein designated GAM TARGET RNA. GAM4796 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4796 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4796 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4796 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4796 RNA, herein designated GAM RNA, to target binding sites on GAM4796 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4796 target RNA into GAM4796 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4796 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4796 target genes. The mRNA of each one of this plurality of GAM4796 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4796 RNA, herein designated GAM RNA, and which when bound by GAM4796 RNA causes inhibition of translation of the GAM4796 target mRNA into a corresponding GAM4796 target protein.

The mechanism of the translational inhibition exerted by GAM4796 RNA, herein designated GAM RNA, on one or more GAM4796 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4796 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4796 RNA, herein designated GAM RNA, of GAM4796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4796 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4796 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4796 RNA correlate with, and may be deduced from, the identity of the GAM4796 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4800 6745 GGCCACTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
ACCTTCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCATAGGTGA Messenger 4800 (GAM4800) oligonucleotides modulates expression of respective target genes
CCCCTGTGGA whose function and utility is known in the art.

AAACAAGTAC GAM4800 is a novel bioinformatically detectable regulatory, non protein coding,
CCCTGGAACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4800 was detected is

TCCTAGAAGT described with additional reference to Figs. 9-15.

GGAGGTGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
C encoded by the human genome.

GAM4800 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4800

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4800
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4800 precursor RNA is designated SEQ ID:6745, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6745 is located from position 90601712 to position 90601792 relative to chromosome 15 on the `-` strand.

GAM4800 precursor RNA folds onto itself, forming GAM4800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4800 precursor RNA, designated SEQ ID NO: 6745, and a schematic representation of a predicted secondary folding of GAM4800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4800 folded precursor RNA yielding a GAM4800 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4800 RNA, hereby incorporated herein.

GAM4800 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4800 target RNA, herein designated GAM TARGET RNA. GAM4800 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4800 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4800 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4800 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4800 RNA, herein designated GAM RNA, to target binding sites on GAM4800 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4800 target RNA into GAM4800 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4800 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4800 target genes. The mRNA of each one of this plurality of GAM4800 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4800 RNA, herein designated GAM RNA, and which when bound by GAM4800 RNA causes inhibition of translation of the GAM4800 target mRNA into a corresponding GAM4800 target protein.

The mechanism of the translational inhibition exerted by GAM4800 RNA, herein designated GAM RNA, on one or more GAM4800 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4800 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4800 RNA, herein designated GAM RNA, of GAM4800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4800 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4800 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4800 RNA correlate with, and may be deduced from, the identity of the GAM4800 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4803 7220 TGGAGGAATG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGCTATGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAAATACTG Messenger 4803 (GAM4803) oligonucleotides modulates expression of respective target genes

GGAGCTGGCT whose function and utility is known in the art.

GGATGCCAGG GAM4803 is a novel bioinformatically detectable regulatory, non protein coding,

ATACAGCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4803 was detected is

CATCTGCCAT described with additional reference to Figs. 9-15.

CATTACCCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTTCAGGAT encoded by the human genome.

CCTCTA GAM4803 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4803

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4803

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4803 precursor RNA is designated SEQ ID:7220, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7220 is located from position 128048648 to position 128048743 relative to chromosome 7 on the `-` strand.

GAM4803 precursor RNA folds onto itself, forming GAM4803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4803 precursor RNA, designated SEQ ID NO: 7220, and a schematic representation of a predicted secondary folding of GAM4803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4803 folded precursor RNA yielding a GAM4803 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4803 RNA, hereby incorporated herein.

GAM4803 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4803 target RNA, herein designated GAM TARGET RNA. GAM4803 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4803 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4803 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4803 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4803 RNA, herein designated GAM RNA, to target binding sites on GAM4803 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4803 target RNA into GAM4803 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4803 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4803 target genes. The mRNA of each one of this plurality of GAM4803 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4803 RNA, herein designated GAM RNA, and which when bound by GAM4803 RNA causes inhibition of translation of the GAM4803 target mRNA into a corresponding GAM4803 target protein.

The mechanism of the translational inhibition exerted by GAM4803 RNA, herein designated GAM RNA, on one or more GAM4803 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4803 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4803 RNA, herein designated GAM RNA, of GAM4803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4803 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4803 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4803 RNA correlate with, and may be deduced from, the identity of the GAM4803 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4814 7047 TCGCTCTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCCCAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGAGTGCAG Messenger 4814 (GAM4814) oligonucleotides modulates expression of respective target genes

TGGCATGATC whose function and utility is known in the art.

TCGGCTCACT GAM4814 is a novel bioinformatically detectable regulatory, non protein coding,

GCAACCTCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4814 was detected is

CCTCCTGGGT described with additional reference to Figs. 9-15.

TCAAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM4814 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4814

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4814

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4814 precursor RNA is designated SEQ ID:7047, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7047 is located from position 51241197 to position 51241274 relative to chromosome 10 on the `+` strand.

GAM4814 precursor RNA folds onto itself, forming GAM4814 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4814 precursor RNA, designated SEQ ID NO: 7047, and a schematic representation of a predicted secondary folding of GAM4814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4814 folded precursor RNA yielding a GAM4814 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4814 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4814 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4814 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4814 target RNA, herein designated GAM TARGET RNA. GAM4814 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4814 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4814 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4814 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4814 RNA, herein designated GAM RNA, to target binding sites on GAM4814 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4814 target RNA into GAM4814 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4814 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4814 target genes. The mRNA of each one of this plurality of GAM4814 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4814 RNA, herein designated GAM RNA, and which when bound by GAM4814 RNA causes inhibition of translation

of the GAM4814 target mRNA into a corresponding GAM4814 target protein.

The mechanism of the translational inhibition exerted by GAM4814 RNA, herein designated GAM RNA, on one or more GAM4814 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4814 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4814 RNA, herein designated GAM RNA, of GAM4814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4814 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4814 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4814 RNA correlate with, and may be deduced from, the identity of the GAM4814 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4821 6985 TATTATTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACCTGTTAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGAGACACT Messenger 4821 (GAM4821) oligonucleotides modulates expression of respective target genes
GTCCTAGGCA whose function and utility is known in the art.

CTGTGGGATA GAM4821 is a novel bioinformatically detectable regulatory, non protein coding,
ACAACAGCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4821 was detected is

ACACTTCACA described with additional reference to Figs. 9-15.

CAACAGCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCTTCCTGT encoded by the human genome.

GTTTTACAAC GAM4821 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4821
AGCTCCTAAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4821
GATA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

to the nucleotide sequence of GAM4821 precursor RNA is designated SEQ ID:6985, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6985 is located from position 52745273 to position 52745386 relative to chromosome 20 on the `+` strand.

GAM4821 precursor RNA folds onto itself, forming GAM4821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4821 precursor RNA, designated SEQ ID NO: 6985, and a schematic representation of a predicted secondary folding of GAM4821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4821 folded precursor RNA yielding a GAM4821 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM4821 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4821 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM4821 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4821 target RNA, herein designated GAM TARGET RNA. GAM4821 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4821 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4821 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4821 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4821 RNA, herein designated GAM RNA, to target binding sites on GAM4821 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4821 target RNA into GAM4821 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4821 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4821 target genes. The mRNA of each one of this plurality of GAM4821 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4821 RNA, herein designated GAM RNA, and which when bound by GAM4821 RNA causes inhibition of translation of the GAM4821 target mRNA into a corresponding GAM4821 target protein.

The mechanism of the translational inhibition exerted by GAM4821 RNA, herein designated GAM RNA, on one or more GAM4821 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4821 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4821 RNA, herein designated GAM RNA, of GAM4821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4821 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4821 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4821 RNA correlate with, and may be deduced from, the identity of the GAM4821 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4844 7281 TGTTGATGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCATAACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AATATATTAA Messenger 4844 (GAM4844) oligonucleotides modulates expression of respective target genes

AAACTTAAAT whose function and utility is known in the art.

TGTATACTTT GAM4844 is a novel bioinformatically detectable regulatory, non protein coding,

AAGTTGGTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4844 was detected is

TTGTATGATA described with additional reference to Figs. 9-15.

TATGAGTTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATCAATA encoded by the human genome.

GAM4844 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4844 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4844 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4844 precursor RNA is designated SEQ ID:7281, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7281 is located from position 15101510 to position 15101596 relative to chromosome 16 on the `-` strand.

GAM4844 precursor RNA folds onto itself, forming GAM4844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4844 precursor RNA, designated SEQ ID NO: 7281, and a schematic representation of a predicted secondary folding of GAM4844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4844 folded precursor RNA yielding a GAM4844 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4844 RNA, hereby incorporated herein.

GAM4844 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4844 target RNA, herein designated GAM TARGET RNA. GAM4844 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4844 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4844 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4844 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4844 RNA, herein designated GAM RNA, to target binding sites on GAM4844 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4844 target RNA into GAM4844 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4844 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4844 target genes. The mRNA of each one of this plurality of GAM4844 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4844 RNA, herein designated GAM RNA, and which when bound by GAM4844 RNA causes inhibition of translation of the GAM4844 target mRNA into a corresponding GAM4844 target protein.

The mechanism of the translational inhibition exerted by GAM4844 RNA, herein designated GAM RNA, on one or more GAM4844 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4844 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4844 RNA, herein designated GAM RNA, of GAM4844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4844 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4844 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4844 RNA correlate with, and may be deduced from, the identity of the GAM4844 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4895 6171 CTCGTGGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGCTGCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCTCTCCCT Messenger 4895 (GAM4895) oligonucleotides modulates expression of respective target genes
CTCCCTCCTC whose function and utility is known in the art.

CAGGCCACGG GAM4895 is a novel bioinformatically detectable regulatory, non protein coding,
ATTTCATGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4895 was detected is

CCTGTGACTG described with additional reference to Figs. 9-15.

GTGGGGCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGAGGAGAC encoded by the human genome.

AGGAAGCCTC GAM4895 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4895

AAGTTCCAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4895

GCAGAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4895 precursor RNA is designated SEQ ID:6171, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6171 is located from position 119323982 to position 119324097 relative to chromosome 11 on the `-` strand.

GAM4895 precursor RNA folds onto itself, forming GAM4895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4895 precursor RNA, designated SEQ ID NO: 6171, and a schematic representation of a predicted secondary folding of GAM4895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4895 folded precursor RNA yielding a GAM4895 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4895 RNA, hereby incorporated herein.

GAM4895 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4895 target RNA, herein designated GAM TARGET RNA. GAM4895 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4895 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4895 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4895 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4895 RNA, herein designated GAM RNA, to target binding sites on GAM4895 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4895 target RNA into GAM4895 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4895 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4895 target genes. The mRNA of each one of this plurality of GAM4895 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4895 RNA, herein designated GAM RNA, and which when bound by GAM4895 RNA causes inhibition of translation of the GAM4895 target mRNA into a corresponding GAM4895 target protein.

The mechanism of the translational inhibition exerted by GAM4895 RNA, herein designated GAM RNA, on one or more GAM4895 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4895 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4895 RNA, herein designated GAM RNA, of GAM4895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4895 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4895 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4895 RNA correlate with, and may be deduced from, the identity of the GAM4895 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4904 6847 GGTGGCACTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCAGGATGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTCCTGAGG Messenger 4904 (GAM4904) oligonucleotides modulates expression of respective target genes

TGTGTCGAGT whose function and utility is known in the art.

GTTCTCTACA TGGGGCACTG TGGAGGTGTC ATCGGCTCAG TTCCCC GAM4904 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM4904 was detected is described with additional reference to Figs. 9-15. GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM4904 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4904 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4904 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4904 precursor RNA is designated SEQ ID:6847, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6847 is located from position 118036640 to position 118036725 relative to chromosome 9 on the `-` strand.

GAM4904 precursor RNA folds onto itself, forming GAM4904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4904 precursor RNA, designated SEQ ID NO: 6847, and a schematic representation of a predicted secondary folding of GAM4904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4904 folded precursor RNA yielding a GAM4904 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4904 RNA, hereby incorporated herein.

GAM4904 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4904 target RNA, herein designated GAM TARGET RNA. GAM4904 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4904 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4904 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4904 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4904 RNA, herein designated GAM RNA, to target binding sites on GAM4904 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4904 target RNA into GAM4904 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4904 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4904 target genes. The mRNA of each one of this plurality of GAM4904 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4904 RNA, herein designated GAM RNA, and which when bound by GAM4904 RNA causes inhibition of translation of the GAM4904 target mRNA into a corresponding GAM4904 target protein.

The mechanism of the translational inhibition exerted by GAM4904 RNA, herein designated GAM RNA, on one or more GAM4904 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4904 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4904 RNA, herein designated GAM RNA, of GAM4904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4904 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4904 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4904 RNA correlate with, and may be deduced from, the identity of the GAM4904 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4913 5654 AAATCTCTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCACTGCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTTTTAAAA Messenger 4913 (GAM4913) oligonucleotides modulates expression of respective target genes

GTCTGGCGCA whose function and utility is known in the art.

TCTTGACTTT GAM4913 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTTCACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4913 was detected is

ATAACAGCCA described with additional reference to Figs. 9-15.

GCTTGGATTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTTGAGAGA encoded by the human genome.

TTT GAM4913 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4913 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4913 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4913 precursor RNA is designated SEQ ID:5654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5654 is located from position 52918008 to position 52918100 relative to chromosome 18 on the `+` strand.

GAM4913 precursor RNA folds onto itself, forming GAM4913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4913 precursor RNA, designated SEQ ID NO: 5654, and a schematic representation of a predicted secondary folding of GAM4913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4913 folded precursor RNA yielding a GAM4913 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4913 RNA, hereby incorporated herein.

GAM4913 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4913 target RNA, herein designated GAM TARGET RNA. GAM4913 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4913 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4913 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4913 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4913 RNA, herein designated GAM RNA, to target binding sites on GAM4913 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4913 target RNA into GAM4913 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4913 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4913 target genes. The mRNA of each one of this plurality of GAM4913 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4913 RNA, herein designated GAM RNA, and which when bound by GAM4913 RNA causes inhibition of translation of the GAM4913 target mRNA into a corresponding GAM4913 target protein.

The mechanism of the translational inhibition exerted by GAM4913 RNA, herein designated GAM RNA, on one or more GAM4913 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4913 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4913 RNA, herein designated GAM RNA, of GAM4913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4913 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4913 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4913 RNA correlate with, and may be deduced from, the identity of the GAM4913 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4932 7273 TGTGGAGAAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TAAAAAGGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTGAGGCTG Messenger 4932 (GAM4932) oligonucleotides modulates expression of respective target genes
GCATTTATAG whose function and utility is known in the art.

AATCTGGCTT GAM4932 is a novel bioinformatically detectable regulatory, non protein coding,
TCTTGTATTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM4932 was detected is

GGTGGAAAGC described with additional reference to Figs. 9-15.

TAGATGAAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGTTTCTCT encoded by the human genome.

CAGCCTTTTC GAM4932 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4932
TCTCCTCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4932

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4932 precursor RNA is designated SEQ ID:7273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7273 is located from position 116757833 to position 116757940 relative to chromosome 9 on the `-` strand.

GAM4932 precursor RNA folds onto itself, forming GAM4932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4932 precursor RNA, designated SEQ ID NO: 7273, and a schematic representation of a predicted secondary folding of GAM4932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4932 folded precursor RNA yielding a GAM4932 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4932 RNA, hereby incorporated herein.

GAM4932 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4932 target RNA, herein designated GAM TARGET RNA. GAM4932 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4932 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4932 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4932 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4932 RNA, herein designated GAM RNA, to target binding sites on GAM4932 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4932 target RNA into GAM4932 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4932 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4932 target genes. The mRNA of each one of this plurality of GAM4932 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4932 RNA, herein designated GAM RNA, and which when bound by GAM4932 RNA causes inhibition of translation of the GAM4932 target mRNA into a corresponding GAM4932 target protein.

The mechanism of the translational inhibition exerted by GAM4932 RNA, herein designated GAM RNA, on one or more GAM4932 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4932 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4932 RNA, herein designated GAM RNA, of GAM4932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM4932 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4932 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4932 RNA correlate with, and may be deduced from, the identity of the GAM4932 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4946 6977 TAGTGAGATG Fig. 8 further provides a conceptual description of another novel bioinformatically
AACCCGGTAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCAGATGGA Messenger 4946 (GAM4946) oligonucleotides modulates expression of respective target genes
AATGGAGAAA whose function and utility is known in the art.

TCGCCTGTCT GAM4946 is a novel bioinformatically detectable regulatory, non protein coding,
TCTGCGTCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM4946 was detected is

TCACGCTGGG described with additional reference to Figs. 9-15.

AGCTGTAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGGAGCTGTT encoded by the human genome.

CCTATTTGGC GAM4946 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4946
CATCTTGGCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4946
CCTCTCTCCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CTG to the nucleotide sequence of GAM4946 precursor RNA is designated SEQ ID:6977, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6977 is located from position 129644 to position 129766 relative to chromosome 9 on the `-` strand.

GAM4946 precursor RNA folds onto itself, forming GAM4946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4946 precursor RNA, designated SEQ ID NO: 6977, and a schematic representation of a predicted secondary folding of GAM4946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4946 folded precursor RNA yielding a GAM4946 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4946 RNA, hereby incorporated herein.

GAM4946 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4946 target RNA, herein designated GAM TARGET RNA. GAM4946 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4946 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4946 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4946 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4946 RNA, herein designated GAM RNA, to target binding sites on GAM4946 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4946 target RNA into GAM4946 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4946 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4946 target genes. The mRNA of each one of this plurality of GAM4946 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4946 RNA, herein designated GAM RNA, and which when bound by GAM4946 RNA causes inhibition of translation of the GAM4946 target mRNA into a corresponding GAM4946 target protein.

The mechanism of the translational inhibition exerted by GAM4946 RNA, herein designated GAM RNA, on one or more GAM4946 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4946 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4946 RNA, herein designated GAM RNA, of

GAM4946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4946 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4946 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4946 RNA correlate with, and may be deduced from, the identity of the GAM4946 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4969 6546 GCTGGATGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCCTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTTCAGGTG Messenger 4969 (GAM4969) oligonucleotides modulates expression of respective target genes

GCTCCAAAAA whose function and utility is known in the art.

GAATGTTGCA GAM4969 is a novel bioinformatically detectable regulatory, non protein coding,

TGTGTTCAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4969 was detected is

CCATCCTGAG described with additional reference to Figs. 9-15.

CAGAGCCACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAATTTAGTG encoded by the human genome.

ACAGTGTCTA GAM4969 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4969

GC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4969

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4969 precursor RNA is designated SEQ ID:6546, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6546 is located from position 43463077 to position 43463178 relative to chromosome 20 on the `-` strand.

GAM4969 precursor RNA folds onto itself, forming GAM4969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4969 precursor RNA, designated SEQ ID NO: 6546, and a schematic representation of a predicted secondary folding of GAM4969 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4969 folded precursor RNA yielding a GAM4969 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4969 RNA, hereby incorporated herein.

GAM4969 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4969 target RNA, herein designated GAM TARGET RNA. GAM4969 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4969 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4969 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4969 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4969 RNA, herein designated GAM RNA, to target binding sites on GAM4969 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4969 target RNA into GAM4969 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4969 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4969 target genes. The mRNA of each one of this plurality of GAM4969 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4969 RNA, herein designated GAM RNA, and which when bound by GAM4969 RNA causes inhibition of translation of the GAM4969 target mRNA into a corresponding GAM4969 target protein.

The mechanism of the translational inhibition exerted by GAM4969 RNA, herein designated GAM RNA, on one or more GAM4969 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4969 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM4969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4969 RNA, herein designated GAM RNA, of GAM4969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4969 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4969 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4969 RNA correlate with, and may be deduced from, the identity of the GAM4969 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4971 7020 TCCAGACACT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCTTCCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTTCAGGGA Messenger 4971 (GAM4971) oligonucleotides modulates expression of respective target genes

ACCCTCAATA whose function and utility is known in the art.

CACAGTAAGA GAM4971 is a novel bioinformatically detectable regulatory, non protein coding,

ATGAAGAGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4971 was detected is

TGCAGGTCTG described with additional reference to Figs. 9-15.

AGCTTGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGACTGGA encoded by the human genome.

GAM4971 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4971

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4971

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4971 precursor RNA is designated SEQ ID:7020, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7020 is located from position 37937921 to position 37938008 relative to chromosome 15 on the `+` strand.

GAM4971 precursor RNA folds onto itself, forming GAM4971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4971 precursor RNA, designated SEQ ID NO: 7020, and a schematic representation of a predicted secondary folding of GAM4971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4971 folded precursor RNA yielding a GAM4971 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4971 RNA, hereby incorporated herein.

GAM4971 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4971 target RNA, herein designated GAM TARGET RNA. GAM4971 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4971 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4971 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4971 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4971 RNA, herein designated GAM RNA, to target binding sites on GAM4971 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4971 target RNA into GAM4971 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4971 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4971 target genes. The mRNA of each one of this plurality of GAM4971 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4971 RNA, herein designated GAM RNA, and which when bound by GAM4971 RNA causes inhibition of translation of the GAM4971 target mRNA into a corresponding GAM4971 target protein.

The mechanism of the translational inhibition exerted by GAM4971 RNA, herein designated GAM RNA, on one or more GAM4971 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4971 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4971 RNA, herein designated GAM RNA, of GAM4971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4971 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4971 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4971 RNA correlate with, and may be deduced from, the identity of the GAM4971 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4975 6048 CCACAGTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGCCCGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGGTCCCA Messenger 4975 (GAM4975) oligonucleotides modulates expression of respective target genes

CTGGGGAAGC whose function and utility is known in the art.

TCAAGGCAGC GAM4975 is a novel bioinformatically detectable regulatory, non protein coding,

CCTGGCCTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM4975 was detected is

CCCTCATTCT described with additional reference to Figs. 9-15.

CCACCCAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGGCCCCTGC encoded by the human genome.

GTGG GAM4975 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4975

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4975

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM4975 precursor RNA is designated SEQ ID:6048, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6048 is located from position 142992769 to position 142992862 relative to chromosome 8 on the `+` strand.

GAM4975 precursor RNA folds onto itself, forming GAM4975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4975 precursor RNA, designated SEQ ID NO: 6048, and a schematic representation of a predicted secondary folding of GAM4975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4975 folded precursor RNA yielding a GAM4975 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4975 RNA, hereby incorporated herein.

GAM4975 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4975 target RNA, herein designated GAM TARGET RNA. GAM4975 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4975 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4975 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4975 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4975 RNA, herein designated GAM RNA, to target binding sites on GAM4975 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4975 target RNA into GAM4975 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM4975 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4975 target genes. The mRNA of each one of this plurality of GAM4975 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4975 RNA, herein

designated GAM RNA, and which when bound by GAM4975 RNA causes inhibition of translation of the GAM4975 target mRNA into a corresponding GAM4975 target protein.

The mechanism of the translational inhibition exerted by GAM4975 RNA, herein designated GAM RNA, on one or more GAM4975 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4975 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4975 RNA, herein designated GAM RNA, of GAM4975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4975 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4975 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4975 RNA correlate with, and may be deduced from, the identity of the GAM4975 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM4986 6036 CATCAAAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TAAATAAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTCTAATTG Messenger 4986 (GAM4986) oligonucleotides modulates expression of respective target genes
CCAAGAATTC whose function and utility is known in the art.

ACATGTGGTT GAM4986 is a novel bioinformatically detectable regulatory, non protein coding,
GTATGCAGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM4986 was detected is

TTACTGGGAA described with additional reference to Figs. 9-15.

ATTGAAGTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATCTGCATGT encoded by the human genome.

GATTCTGCTG GAM4986 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM4986
TGATGGACAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM4986

TTGTAAGTTT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar GTTCCTGGAG to the nucleotide sequence of GAM4986 precursor RNA is designated SEQ ID:6036, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6036 is located from position 43025631 to position 43025760 relative to chromosome 9 on the `-` strand.

GAM4986 precursor RNA folds onto itself, forming GAM4986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM4986 precursor RNA, designated SEQ ID NO: 6036, and a schematic representation of a predicted secondary folding of GAM4986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM4986 folded precursor RNA yielding a GAM4986 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM4986 RNA, hereby incorporated herein.

GAM4986 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM4986 target RNA, herein designated GAM TARGET RNA. GAM4986 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM4986 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM4986 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM4986 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM4986 RNA, herein designated GAM RNA, to target binding sites on GAM4986 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM4986 target RNA into GAM4986 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM4986 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM4986 target genes. The mRNA of each one of this plurality of GAM4986 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM4986 RNA, herein designated GAM RNA, and which when bound by GAM4986 RNA causes inhibition of translation of the GAM4986 target mRNA into a corresponding GAM4986 target protein.

The mechanism of the translational inhibition exerted by GAM4986 RNA, herein designated GAM RNA, on one or more GAM4986 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM4986 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM4986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM4986 RNA, herein designated GAM RNA, of GAM4986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM4986 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM4986 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM4986 RNA correlate with, and may be deduced from, the identity of the GAM4986 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5000 6573 GGAAACTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCTTCTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTACTAGTG Messenger 5000 (GAM5000) oligonucleotides modulates expression of respective target genes

AGTAAGACAT whose function and utility is known in the art.

TTTGCAACAG GAM5000 is a novel bioinformatically detectable regulatory, non protein coding,

TGCTGAGTAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5000 was detected is

GAAAGGCCCT described with additional reference to Figs. 9-15.

GGTCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5000 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5000 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5000 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5000 precursor RNA is designated SEQ ID:6573, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6573 is located from position 116259939 to position 116260015 relative to chromosome 12 on the `-` strand.

GAM5000 precursor RNA folds onto itself, forming GAM5000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5000 precursor RNA, designated SEQ ID NO: 6573, and a schematic representation of a predicted secondary folding of GAM5000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5000 folded precursor RNA yielding a GAM5000 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5000 RNA, hereby incorporated herein.

GAM5000 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5000 target RNA, herein designated GAM TARGET RNA. GAM5000 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5000 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5000 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5000 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5000 RNA, herein designated GAM RNA, to target binding sites on GAM5000 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5000 target RNA into GAM5000 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5000 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5000 target genes. The mRNA of each one of this plurality of GAM5000 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5000 RNA, herein designated GAM RNA, and which when bound by GAM5000 RNA causes inhibition of translation of the GAM5000 target mRNA into a corresponding GAM5000 target protein.

The mechanism of the translational inhibition exerted by GAM5000 RNA, herein designated GAM RNA, on one or more GAM5000 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5000 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5000 RNA, herein designated GAM RNA, of GAM5000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5000 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5000 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5000 RNA correlate with, and may be deduced from, the identity of the GAM5000 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5008 6211 CTGCAGGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGCCTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTTTAGGT Messenger 5008 (GAM5008) oligonucleotides modulates expression of respective target genes

TCTGATAGCT whose function and utility is known in the art.

GTATTCTCAG GAM5008 is a novel bioinformatically detectable regulatory, non protein coding,

TCCTGGAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5008 was detected is

ACAGGTGTAG described with additional reference to Figs. 9-15.

CCTGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM5008 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5008 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5008 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5008 precursor RNA is designated SEQ ID:6211, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6211 is located from position 54394162 to position 54394238 relative to chromosome 19 on the `+` strand.

GAM5008 precursor RNA folds onto itself, forming GAM5008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5008 precursor RNA, designated SEQ ID NO: 6211, and a schematic representation of a predicted secondary folding of GAM5008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5008 folded precursor RNA yielding a GAM5008 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5008 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5008 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5008 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5008 target RNA, herein designated GAM TARGET RNA. GAM5008 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5008 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5008 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5008 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5008 RNA, herein designated GAM RNA, to target binding sites on GAM5008 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5008 target RNA into GAM5008 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5008 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5008 target genes. The mRNA of each one of this plurality of GAM5008 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5008 RNA, herein designated GAM RNA, and which when bound by GAM5008 RNA causes inhibition of translation of the GAM5008 target mRNA into a corresponding GAM5008 target protein.

The mechanism of the translational inhibition exerted by GAM5008 RNA, herein designated GAM RNA, on one or more GAM5008 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5008 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5008 RNA, herein designated GAM RNA, of GAM5008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5008 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5008 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5008 RNA correlate with, and may be deduced from, the identity of the GAM5008 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5011 6892 GTCTTCATAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCCAGGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTGGAGCA Messenger 5011 (GAM5011) oligonucleotides modulates expression of respective target genes

ATTACCTCCC whose function and utility is known in the art.

CCATCTGGCT CCTTAGGACC TAGAGGTAGT AAAGGC GAM5011 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM5011 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM5011 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5011 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5011 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5011 precursor RNA is designated SEQ ID:6892, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6892 is located from position 45580563 to position 45580638 relative to chromosome 15 on the `+` strand.

GAM5011 precursor RNA folds onto itself, forming GAM5011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5011 precursor RNA, designated SEQ ID NO: 6892, and a schematic representation of a predicted secondary folding of GAM5011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5011 folded precursor RNA yielding a GAM5011 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5011 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5011 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5011 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5011 target RNA, herein designated GAM TARGET RNA. GAM5011 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5011 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM5011 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5011 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5011 RNA, herein designated GAM RNA, to target binding sites on GAM5011 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5011 target RNA into GAM5011 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5011 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5011 target genes. The mRNA of each one of this plurality of GAM5011 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5011 RNA, herein designated GAM RNA, and which when bound by GAM5011 RNA causes inhibition of translation of the GAM5011 target mRNA into a corresponding GAM5011 target protein.

The mechanism of the translational inhibition exerted by GAM5011 RNA, herein designated GAM RNA, on one or more GAM5011 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5011 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5011 RNA, herein designated GAM RNA, of GAM5011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5011 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5011 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5011 RNA correlate with, and may be deduced from, the identity of the GAM5011 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5035 6875 GTCCACTGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTTCTTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTAGGTCCTC Messenger 5035 (GAM5035) oligonucleotides modulates expression of respective target genes

ACACACAGCT whose function and utility is known in the art.

CTGCTCAGTT GAM5035 is a novel bioinformatically detectable regulatory, non protein coding,

CAATCACCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5035 was detected is

GAATGCAGGC described with additional reference to Figs. 9-15.

TGGTTGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCAAATTTG encoded by the human genome.

GACAGAAGAA GAM5035 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5035

GTCAGTGTCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5035

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5035 precursor RNA is designated SEQ ID:6875, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6875 is located from position 71813551 to position 71813660 relative to chromosome 9 on the `+` strand.

GAM5035 precursor RNA folds onto itself, forming GAM5035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5035 precursor RNA, designated SEQ ID NO: 6875, and a schematic representation of a predicted secondary folding of GAM5035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5035 folded precursor RNA yielding a GAM5035 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5035 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5035 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5035 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5035 target RNA, herein designated GAM TARGET RNA. GAM5035 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5035 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5035 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5035 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5035 RNA, herein designated GAM RNA, to target binding sites on GAM5035 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5035 target RNA into GAM5035 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5035 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5035 target genes. The mRNA of each one of this plurality of GAM5035 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5035 RNA, herein designated GAM RNA, and which when bound by GAM5035 RNA causes inhibition of translation of the GAM5035 target mRNA into a corresponding GAM5035 target protein.

The mechanism of the translational inhibition exerted by GAM5035 RNA, herein designated GAM RNA, on one or more GAM5035 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5035 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5035 RNA, herein designated GAM RNA, of GAM5035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5035 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5035 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5035 RNA correlate with, and may be deduced from, the identity of the GAM5035 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5048 6565 GCTTGCTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTACAGATG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAAAGATCT Messenger 5048 (GAM5048) oligonucleotides modulates expression of respective target genes

GGCAAATTAA whose function and utility is known in the art.

AAATAGCCTT GAM5048 is a novel bioinformatically detectable regulatory, non protein coding,

AGGCCAAAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5048 was detected is

TCAAACCCAA described with additional reference to Figs. 9-15.

GGTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5048 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5048

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5048

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5048 precursor RNA is designated SEQ ID:6565, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6565 is located from position 118768043 to position 118768119 relative to chromosome 12 on the `+` strand.

GAM5048 precursor RNA folds onto itself, forming GAM5048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5048 precursor RNA, designated SEQ ID NO: 6565, and a schematic representation of a predicted secondary folding of GAM5048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5048 folded precursor RNA yielding a GAM5048 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM5048 RNA, hereby incorporated herein.

GAM5048 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5048 target RNA, herein designated GAM TARGET RNA. GAM5048 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5048 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5048 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5048 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5048 RNA, herein designated GAM RNA, to target binding sites on GAM5048 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5048 target RNA into GAM5048 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5048 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5048 target genes. The mRNA of each one of this plurality of GAM5048 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5048 RNA, herein designated GAM RNA, and which when bound by GAM5048 RNA causes inhibition of translation of the GAM5048 target mRNA into a corresponding GAM5048 target protein.

The mechanism of the translational inhibition exerted by GAM5048 RNA, herein designated GAM RNA, on one or more GAM5048 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5048 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5048 RNA, herein designated GAM RNA, of GAM5048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5048 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5048 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5048 RNA correlate with, and may be deduced from, the identity of the GAM5048 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5058 6700 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAATCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 5058 (GAM5058) oligonucleotides modulates expression of respective target genes
TTGCAGTGAG whose function and utility is known in the art.

CTGAGATCAT GAM5058 is a novel bioinformatically detectable regulatory, non protein coding,
GCCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5058 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GACACTCC encoded by the human genome.

GAM5058 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5058

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5058
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5058 precursor RNA is designated SEQ ID:6700, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6700 is located from position 122025582 to position 122025669 relative to chromosome 12 on the `+` strand.

GAM5058 precursor RNA folds onto itself, forming GAM5058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5058 precursor RNA, designated SEQ ID NO: 6700, and a schematic representation of a predicted secondary folding of GAM5058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5058 folded precursor RNA

yielding a GAM5058 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5058 RNA, hereby incorporated herein.

GAM5058 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5058 target RNA, herein designated GAM TARGET RNA. GAM5058 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5058 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5058 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5058 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5058 RNA, herein designated GAM RNA, to target binding sites on GAM5058 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5058 target RNA into GAM5058 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5058 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5058 target genes. The mRNA of each one of this plurality of GAM5058 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5058 RNA, herein designated GAM RNA, and which when bound by GAM5058 RNA causes inhibition of translation of the GAM5058 target mRNA into a corresponding GAM5058 target protein.

The mechanism of the translational inhibition exerted by GAM5058 RNA, herein designated GAM RNA, on one or more GAM5058 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5058 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5058 RNA, herein designated GAM RNA, of GAM5058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5058 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5058 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5058 RNA correlate with, and may be deduced from, the identity of the GAM5058 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5082 6833 GGTATACTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTAGCATATT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATATAGCTCT Messenger 5082 (GAM5082) oligonucleotides modulates expression of respective target genes

AAGAGTGTAG whose function and utility is known in the art.

AGTTATATGA GAM5082 is a novel bioinformatically detectable regulatory, non protein coding,

TGTGCTAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5082 was detected is

AAGTGTATT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5082 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5082

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5082

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5082 precursor RNA is designated SEQ ID:6833, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6833 is located from position 101882283 to position 101882351 relative to chromosome 8 on the `+` strand.

GAM5082 precursor RNA folds onto itself, forming GAM5082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5082 precursor RNA, designated SEQ ID NO: 6833, and a

schematic representation of a predicted secondary folding of GAM5082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5082 folded precursor RNA yielding a GAM5082 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5082 RNA, hereby incorporated herein.

GAM5082 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5082 target RNA, herein designated GAM TARGET RNA. GAM5082 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5082 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5082 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5082 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5082 RNA, herein designated GAM RNA, to target binding sites on GAM5082 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5082 target RNA into GAM5082 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5082 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5082 target genes. The mRNA of each one of this plurality of GAM5082 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5082 RNA, herein designated GAM RNA, and which when bound by GAM5082 RNA causes inhibition of translation of the GAM5082 target mRNA into a corresponding GAM5082 target protein.

The mechanism of the translational inhibition exerted by GAM5082 RNA, herein designated GAM RNA, on one or more GAM5082 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5082 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5082 RNA, herein designated GAM RNA, of GAM5082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5082 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5082 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5082 RNA correlate with, and may be deduced from, the identity of the GAM5082 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5085 6779 GGGACATCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAATAAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCTGCTCTA Messenger 5085 (GAM5085) oligonucleotides modulates expression of respective target genes
ATTGCCAAGA whose function and utility is known in the art.

ATTCACATGT GAM5085 is a novel bioinformatically detectable regulatory, non protein coding,
GGTTGTATGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5085 was detected is

AGCATTACTG described with additional reference to Figs. 9-15.

GGAAATTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGTATCTGC encoded by the human genome.

ATGTGATTCT GAM5085 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5085
GCTGTGATGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5085
ACACTTGTAA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
GTTTGTTCC to the nucleotide sequence of GAM5085 precursor RNA is designated SEQ ID:6779, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6779 is located from position 43025636 to position 43025764 relative to chromosome 9 on the `-` strand.

GAM5085 precursor RNA folds onto itself, forming GAM5085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5085 precursor RNA, designated SEQ ID NO: 6779, and a schematic representation of a predicted secondary folding of GAM5085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5085 folded precursor RNA yielding a GAM5085 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5085 RNA, hereby incorporated herein.

GAM5085 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5085 target RNA, herein designated GAM TARGET RNA. GAM5085 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5085 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5085 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5085 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5085 RNA, herein designated GAM RNA, to target binding sites on GAM5085 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5085 target RNA into GAM5085 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5085 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5085 target genes. The mRNA of each one of this plurality of GAM5085 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5085 RNA, herein designated GAM RNA, and which when bound by GAM5085 RNA causes inhibition of translation of the GAM5085 target mRNA into a corresponding GAM5085 target protein.

The mechanism of the translational inhibition exerted by GAM5085 RNA, herein designated GAM RNA, on one or more GAM5085 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5085 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5085 RNA, herein designated GAM RNA, of GAM5085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5085 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5085 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5085 RNA correlate with, and may be deduced from, the identity of the GAM5085 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5090 6215 CTGCCCCCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCTGGACC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGAGTGACTC Messenger 5090 (GAM5090) oligonucleotides modulates expression of respective target genes

AGGCCTTTGT whose function and utility is known in the art.

TTGTCCTTCC GAM5090 is a novel bioinformatically detectable regulatory, non protein coding,

TGGTAGAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5090 was detected is

GGGTTCCCTC described with additional reference to Figs. 9-15.

CCTCGGCAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGCCGGAGT encoded by the human genome.

GCTGGGATGG GAM5090 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5090

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5090

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5090 precursor RNA is designated SEQ ID:6215, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6215 is located from position 58268693 to position 58268792 relative to chromosome 16 on the `+` strand.

GAM5090 precursor RNA folds onto itself, forming GAM5090 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5090 precursor RNA, designated SEQ ID NO: 6215, and a schematic representation of a predicted secondary folding of GAM5090 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5090 folded precursor RNA yielding a GAM5090 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5090 RNA, hereby incorporated herein.

GAM5090 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5090 target RNA, herein designated GAM TARGET RNA. GAM5090 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5090 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5090 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5090 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5090 RNA, herein designated GAM RNA, to target binding sites on GAM5090 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5090 target RNA into GAM5090 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5090 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5090 target genes. The mRNA of each one of this

plurality of GAM5090 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5090 RNA, herein designated GAM RNA, and which when bound by GAM5090 RNA causes inhibition of translation of the GAM5090 target mRNA into a corresponding GAM5090 target protein.

The mechanism of the translational inhibition exerted by GAM5090 RNA, herein designated GAM RNA, on one or more GAM5090 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5090 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5090 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5090 RNA, herein designated GAM RNA, of GAM5090 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5090 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5090 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5090 RNA correlate with, and may be deduced from, the identity of the GAM5090 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5127 6789 GGGAGGAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGAACCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATTCTGAG Messenger 5127 (GAM5127) oligonucleotides modulates expression of respective target genes
AAACACACCA whose function and utility is known in the art.

GGATGACTAG GAM5127 is a novel bioinformatically detectable regulatory, non protein coding,
GCCTGGAGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5127 was detected is

GTCCAGGGTG described with additional reference to Figs. 9-15.

GGCCTCAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTCACTTCT encoded by the human genome.

TGTCTGGCAC GAM5127 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5127

CTCCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5127 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5127 precursor RNA is designated SEQ ID:6789, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6789 is located from position 43743986 to position 43744090 relative to chromosome 13 on the `+` strand.

GAM5127 precursor RNA folds onto itself, forming GAM5127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5127 precursor RNA, designated SEQ ID NO: 6789, and a schematic representation of a predicted secondary folding of GAM5127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5127 folded precursor RNA yielding a GAM5127 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5127 RNA, hereby incorporated herein.

GAM5127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5127 target RNA, herein designated GAM TARGET RNA. GAM5127 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5127 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5127 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5127 RNA, herein designated GAM RNA, to target binding sites on GAM5127 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5127 target RNA

into GAM5127 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5127 target genes. The mRNA of each one of this plurality of GAM5127 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5127 RNA, herein designated GAM RNA, and which when bound by GAM5127 RNA causes inhibition of translation of the GAM5127 target mRNA into a corresponding GAM5127 target protein.

The mechanism of the translational inhibition exerted by GAM5127 RNA, herein designated GAM RNA, on one or more GAM5127 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5127 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5127 RNA, herein designated GAM RNA, of GAM5127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5127 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5127 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5127 RNA correlate with, and may be deduced from, the identity of the GAM5127 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5142 5806 AGTCTCACTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTCACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGGAGTGC Messenger 5142 (GAM5142) oligonucleotides modulates expression of respective target genes
AGTGGCATGA whose function and utility is known in the art.

TCTTGGTTCA GAM5142 is a novel bioinformatically detectable regulatory, non protein coding,
CTGCAACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5142 was detected is

TGCTTCTGGG described with additional reference to Figs. 9-15.

ATTCAAGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TT encoded by the human genome.

GAM5142 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5142 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5142 precursor RNA is designated SEQ ID:5806, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5806 is located from position 4104693 to position 4104774 relative to chromosome 20 on the `+` strand.

GAM5142 precursor RNA folds onto itself, forming GAM5142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5142 precursor RNA, designated SEQ ID NO: 5806, and a schematic representation of a predicted secondary folding of GAM5142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5142 folded precursor RNA yielding a GAM5142 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5142 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5142 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5142 target RNA, herein designated GAM TARGET RNA. GAM5142 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5142 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5142 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5142 RNA, herein designated GAM RNA, to target binding sites on GAM5142 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5142 target RNA into GAM5142 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5142 target genes. The mRNA of each one of this plurality of GAM5142 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5142 RNA, herein designated GAM RNA, and which when bound by GAM5142 RNA causes inhibition of translation of the GAM5142 target mRNA into a corresponding GAM5142 target protein.

The mechanism of the translational inhibition exerted by GAM5142 RNA, herein designated GAM RNA, on one or more GAM5142 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5142 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5142 RNA, herein designated GAM RNA, of GAM5142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5142 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5142 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5142 RNA correlate with, and may be deduced from, the identity of the GAM5142 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5209 6580 GGAAGCCTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTTACCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCTGGTTGA Messenger 5209 (GAM5209) oligonucleotides modulates expression of respective target genes

GGGCCCCCTG whose function and utility is known in the art.

GGCTGTTTTC GAM5209 is a novel bioinformatically detectable regulatory, non protein coding,

ACTGGTTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5209 was detected is

GGTATCTGAT described with additional reference to Figs. 9-15.

CCCTTCCAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGAGGTTCC encoded by the human genome.

TGGAGGGCCA GAM5209 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5209

GTCCAGGTCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5209

GAGGTCTGGT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TCATGCTTCC to the nucleotide sequence of GAM5209 precursor RNA is designated SEQ ID:6580, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6580 is located from position 72669608 to position 72669737 relative to chromosome 11 on the `-` strand.

GAM5209 precursor RNA folds onto itself, forming GAM5209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5209 precursor RNA, designated SEQ ID NO: 6580, and a schematic representation of a predicted secondary folding of GAM5209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5209 folded precursor RNA yielding a GAM5209 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5209 RNA, hereby incorporated herein.

GAM5209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5209 target RNA, herein designated GAM TARGET RNA. GAM5209 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM5209 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5209 RNA, herein designated GAM RNA, to target binding sites on GAM5209 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5209 target RNA into GAM5209 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5209 target genes. The mRNA of each one of this plurality of GAM5209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5209 RNA, herein designated GAM RNA, and which when bound by GAM5209 RNA causes inhibition of translation of the GAM5209 target mRNA into a corresponding GAM5209 target protein.

The mechanism of the translational inhibition exerted by GAM5209 RNA, herein designated GAM RNA, on one or more GAM5209 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5209 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5209 RNA, herein designated GAM RNA, of GAM5209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5209 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5209 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5209 RNA correlate with, and may be deduced from, the identity of the GAM5209 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5217 5686 ACACTGGACA Fig. 8 further provides a conceptual description of another novel bioinformatically

GATGGATGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GATGAGCTTG Messenger 5217 (GAM5217) oligonucleotides modulates expression of respective target genes
TGTGCAGCAG whose function and utility is known in the art.

TTCTACTGGA GAM5217 is a novel bioinformatically detectable regulatory, non protein coding,
AGTATGTACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5217 was detected is

AGGGGCTCAG described with additional reference to Figs. 9-15.

CCAGCCAATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGACGGTGT encoded by the human genome.

GAM5217 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5217

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5217

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5217 precursor RNA is designated SEQ ID:5686, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5686 is located from position 22848134 to position 22848223 relative to chromosome 7 on the `-` strand.

GAM5217 precursor RNA folds onto itself, forming GAM5217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5217 precursor RNA, designated SEQ ID NO: 5686, and a schematic representation of a predicted secondary folding of GAM5217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5217 folded precursor RNA yielding a GAM5217 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5217 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5217 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5217 target RNA, herein designated GAM TARGET RNA. GAM5217 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN

CODING and 3`UTR respectively.

GAM5217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5217 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5217 RNA, herein designated GAM RNA, to target binding sites on GAM5217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5217 target RNA into GAM5217 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5217 target genes. The mRNA of each one of this plurality of GAM5217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5217 RNA, herein designated GAM RNA, and which when bound by GAM5217 RNA causes inhibition of translation of the GAM5217 target mRNA into a corresponding GAM5217 target protein.

The mechanism of the translational inhibition exerted by GAM5217 RNA, herein designated GAM RNA, on one or more GAM5217 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5217 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5217 RNA, herein designated GAM RNA, of GAM5217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5217 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5217 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5217 RNA

correlate with, and may be deduced from, the identity of the GAM5217 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5222 5953 ATATGCTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGGACAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCTAAGGAT Messenger 5222 (GAM5222) oligonucleotides modulates expression of respective target genes
AGAGGTGAGG whose function and utility is known in the art.

AAACCCGCAG GAM5222 is a novel bioinformatically detectable regulatory, non protein coding,
ACAACAGCGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5222 was detected is

CATGCTCCTC described with additional reference to Figs. 9-15.

ATCTTTGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCCAGCGAAC encoded by the human genome.

CTTTCCACTG GAM5222 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5222
TGTGTGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5222

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5222 precursor RNA is designated SEQ ID:5953, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5953 is located from position 34060088 to position 34060194 relative to chromosome 17 on the `+` strand.

GAM5222 precursor RNA folds onto itself, forming GAM5222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5222 precursor RNA, designated SEQ ID NO: 5953, and a schematic representation of a predicted secondary folding of GAM5222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5222 folded precursor RNA yielding a GAM5222 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5222 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5222 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5222 target RNA, herein designated GAM TARGET RNA. GAM5222 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5222 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5222 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5222 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5222 RNA, herein designated GAM RNA, to target binding sites on GAM5222 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5222 target RNA into GAM5222 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5222 target genes. The mRNA of each one of this plurality of GAM5222 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5222 RNA, herein designated GAM RNA, and which when bound by GAM5222 RNA causes inhibition of translation of the GAM5222 target mRNA into a corresponding GAM5222 target protein.

The mechanism of the translational inhibition exerted by GAM5222 RNA, herein designated GAM RNA, on one or more GAM5222 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5222 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5222 RNA, herein designated GAM RNA, of GAM5222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM5222 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5222 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5222 RNA correlate with, and may be deduced from, the identity of the GAM5222 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5254 7187 TGAGTGTATG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGAGAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AATGTTATGT Messenger 5254 (GAM5254) oligonucleotides modulates expression of respective target genes
TTATCACTGA whose function and utility is known in the art.

GTTCCCATTG GAM5254 is a novel bioinformatically detectable regulatory, non protein coding,
TTTCATTCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5254 was detected is

ATAGCACTTA described with additional reference to Figs. 9-15.

TTTCTTCATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTTCTATAC encoded by the human genome.

ACATTTACTC GAM5254 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5254
G precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5254
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5254 precursor RNA is designated SEQ ID:7187, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7187 is located from position 107483900 to position 107484000 relative to chromosome X on the `+` strand.

GAM5254 precursor RNA folds onto itself, forming GAM5254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5254 precursor RNA, designated SEQ ID NO: 7187, and a schematic representation of a predicted secondary folding of GAM5254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5254 folded precursor RNA yielding a GAM5254 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5254 RNA, hereby incorporated herein.

GAM5254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5254 target RNA, herein designated GAM TARGET RNA. GAM5254 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5254 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5254 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5254 RNA, herein designated GAM RNA, to target binding sites on GAM5254 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5254 target RNA into GAM5254 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5254 target genes. The mRNA of each one of this plurality of GAM5254 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5254 RNA, herein designated GAM RNA, and which when bound by GAM5254 RNA causes inhibition of translation of the GAM5254 target mRNA into a corresponding GAM5254 target protein.

The mechanism of the translational inhibition exerted by GAM5254 RNA, herein designated GAM RNA, on one or more GAM5254 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5254 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5254 RNA, herein designated GAM RNA, of

GAM5254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5254 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5254 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5254 RNA correlate with, and may be deduced from, the identity of the GAM5254 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5266 6996 TCACTCTGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCCAGGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTGCAGTG Messenger 5266 (GAM5266) oligonucleotides modulates expression of respective target genes

GTGCAATCTT whose function and utility is known in the art.

GGCTCACTGC GAM5266 is a novel bioinformatically detectable regulatory, non protein coding,

AACCTCCACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5266 was detected is

TCCCGGGTTC described with additional reference to Figs. 9-15.

AAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5266 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5266

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5266

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5266 precursor RNA is designated SEQ ID:6996, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6996 is located from position 28924785 to position 28924860 relative to chromosome 6 on the `+` strand.

GAM5266 precursor RNA folds onto itself, forming GAM5266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5266 precursor RNA, designated SEQ ID NO: 6996, and a schematic representation of a predicted secondary folding of GAM5266 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5266 folded precursor RNA yielding a GAM5266 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5266 RNA, hereby incorporated herein.

GAM5266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5266 target RNA, herein designated GAM TARGET RNA. GAM5266 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5266 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5266 RNA, herein designated GAM RNA, to target binding sites on GAM5266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5266 target RNA into GAM5266 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5266 target genes. The mRNA of each one of this plurality of GAM5266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5266 RNA, herein designated GAM RNA, and which when bound by GAM5266 RNA causes inhibition of translation of the GAM5266 target mRNA into a corresponding GAM5266 target protein.

The mechanism of the translational inhibition exerted by GAM5266 RNA, herein designated GAM RNA, on one or more GAM5266 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5266 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM5266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5266 RNA, herein designated GAM RNA, of GAM5266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5266 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5266 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5266 RNA correlate with, and may be deduced from, the identity of the GAM5266 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5270 6071 CCCAGACAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCCGTTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGATGTGACC Messenger 5270 (GAM5270) oligonucleotides modulates expression of respective target genes

TGGTGGCCAC whose function and utility is known in the art.

CAAATGCCTT GAM5270 is a novel bioinformatically detectable regulatory, non protein coding,

GGCCTCAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5270 was detected is

CAAACTAAGC described with additional reference to Figs. 9-15.

AGGGCACACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCTGGG encoded by the human genome.

GAM5270 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5270

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5270

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5270 precursor RNA is designated SEQ ID:6071, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6071 is located from position 99045264 to position 99045350 relative to chromosome 10 on the `+` strand.

GAM5270 precursor RNA folds onto itself, forming GAM5270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5270 precursor RNA, designated SEQ ID NO: 6071, and a schematic representation of a predicted secondary folding of GAM5270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5270 folded precursor RNA yielding a GAM5270 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5270 RNA, hereby incorporated herein.

GAM5270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5270 target RNA, herein designated GAM TARGET RNA. GAM5270 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5270 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5270 RNA, herein designated GAM RNA, to target binding sites on GAM5270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5270 target RNA into GAM5270 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5270 target genes. The mRNA of each one of this plurality of GAM5270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5270 RNA, herein designated GAM RNA, and which when bound by GAM5270 RNA causes inhibition of translation of the GAM5270 target mRNA into a corresponding GAM5270 target protein.

The mechanism of the translational inhibition exerted by GAM5270 RNA, herein designated GAM RNA, on one or more GAM5270 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5270 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5270 RNA, herein designated GAM RNA, of GAM5270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5270 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5270 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5270 RNA correlate with, and may be deduced from, the identity of the GAM5270 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5272 6782 GGGACTTAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGAGGATC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGTAGCAG Messenger 5272 (GAM5272) oligonucleotides modulates expression of respective target genes

ACACCCTAAG whose function and utility is known in the art.

AGCATGTCAT GAM5272 is a novel bioinformatically detectable regulatory, non protein coding,

TGTCTTCTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5272 was detected is

CCAGTTACTC described with additional reference to Figs. 9-15.

TCCAGTTGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGAGTCCC encoded by the human genome.

GAM5272 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5272

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5272

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5272 precursor RNA is designated SEQ ID:6782, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6782 is located from position 93734228 to position 93734316 relative to chromosome 12 on the `-` strand.

GAM5272 precursor RNA folds onto itself, forming GAM5272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5272 precursor RNA, designated SEQ ID NO: 6782, and a schematic representation of a predicted secondary folding of GAM5272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5272 folded precursor RNA yielding a GAM5272 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5272 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5272 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5272 target RNA, herein designated GAM TARGET RNA. GAM5272 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5272 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5272 RNA, herein designated GAM RNA, to target binding sites on GAM5272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5272 target RNA into GAM5272 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5272 target genes. The mRNA of each one of this plurality of GAM5272 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM5272 RNA, herein designated GAM RNA, and which when bound by GAM5272 RNA causes inhibition of translation of the GAM5272 target mRNA into a corresponding GAM5272 target protein.

The mechanism of the translational inhibition exerted by GAM5272 RNA, herein designated GAM RNA, on one or more GAM5272 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5272 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5272 RNA, herein designated GAM RNA, of GAM5272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5272 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5272 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5272 RNA correlate with, and may be deduced from, the identity of the GAM5272 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5278 7035 TCCCTTTTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAACCATCTT detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCTTTCTCG Messenger 5278 (GAM5278) oligonucleotides modulates expression of respective target genes
AGTATACACA whose function and utility is known in the art.

AGTAGAAAAG GAM5278 is a novel bioinformatically detectable regulatory, non protein coding,
AAACAGTGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5278 was detected is

GTACCCCGAT described with additional reference to Figs. 9-15.

AGGGAGGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGAGAGGAT encoded by the human genome.

GGGA GAM5278 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5278
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5278

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5278 precursor RNA is designated SEQ ID:7035, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7035 is located from position 58433646 to position 58433739 relative to chromosome 16 on the `+` strand.

GAM5278 precursor RNA folds onto itself, forming GAM5278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5278 precursor RNA, designated SEQ ID NO: 7035, and a schematic representation of a predicted secondary folding of GAM5278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5278 folded precursor RNA yielding a GAM5278 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5278 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5278 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5278 target RNA, herein designated GAM TARGET RNA. GAM5278 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5278 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5278 RNA, herein designated GAM RNA, to target binding sites on GAM5278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5278 target RNA into GAM5278 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM5278 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5278 target genes. The mRNA of each one of this plurality of GAM5278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5278 RNA, herein designated GAM RNA, and which when bound by GAM5278 RNA causes inhibition of translation of the GAM5278 target mRNA into a corresponding GAM5278 target protein.

The mechanism of the translational inhibition exerted by GAM5278 RNA, herein designated GAM RNA, on one or more GAM5278 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5278 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5278 RNA, herein designated GAM RNA, of GAM5278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5278 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5278 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5278 RNA correlate with, and may be deduced from, the identity of the GAM5278 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5292 7198 TGCCCTGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCAGAATTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTAGATTGC Messenger 5292 (GAM5292) oligonucleotides modulates expression of respective target genes

TATTACAATG whose function and utility is known in the art.

CTGATTATAT GAM5292 is a novel bioinformatically detectable regulatory, non protein coding,

TTTATAGCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5292 was detected is

TTACTGACAT described with additional reference to Figs. 9-15.

AAGGTTATAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGGGCA encoded by the human genome.

GAM5292 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5292 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5292 precursor RNA is designated SEQ ID:7198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7198 is located from position 96304363 to position 96304450 relative to chromosome 11 on the `-` strand.

GAM5292 precursor RNA folds onto itself, forming GAM5292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5292 precursor RNA, designated SEQ ID NO: 7198, and a schematic representation of a predicted secondary folding of GAM5292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5292 folded precursor RNA yielding a GAM5292 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5292 RNA, hereby incorporated herein.

GAM5292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5292 target RNA, herein designated GAM TARGET RNA. GAM5292 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5292 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5292 RNA, herein designated GAM RNA, to target binding sites on GAM5292 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5292 target RNA into GAM5292 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5292 target genes. The mRNA of each one of this plurality of GAM5292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5292 RNA, herein designated GAM RNA, and which when bound by GAM5292 RNA causes inhibition of translation of the GAM5292 target mRNA into a corresponding GAM5292 target protein.

The mechanism of the translational inhibition exerted by GAM5292 RNA, herein designated GAM RNA, on one or more GAM5292 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5292 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5292 RNA, herein designated GAM RNA, of GAM5292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5292 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5292 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5292 RNA correlate with, and may be deduced from, the identity of the GAM5292 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5324 7006 TCACTTTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GATATCATGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGGTGTAC Messenger 5324 (GAM5324) oligonucleotides modulates expression of respective target genes

TTCCGGTGAT whose function and utility is known in the art.

GCCTAGAGGT GAM5324 is a novel bioinformatically detectable regulatory, non protein coding,

CACGTCCTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5324 was detected is

GATGTCATTA described with additional reference to Figs. 9-15.

GGCTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM5324 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5324 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5324 precursor RNA is designated SEQ ID:7006, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7006 is located from position 51118141 to position 51118216 relative to chromosome 19 on the `-` strand.

GAM5324 precursor RNA folds onto itself, forming GAM5324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5324 precursor RNA, designated SEQ ID NO: 7006, and a schematic representation of a predicted secondary folding of GAM5324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5324 folded precursor RNA yielding a GAM5324 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5324 RNA, hereby incorporated herein.

GAM5324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5324 target RNA, herein designated GAM TARGET RNA. GAM5324 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5324 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5324 RNA, herein designated GAM RNA, to target binding sites on GAM5324 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5324 target RNA into GAM5324 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5324 target genes. The mRNA of each one of this plurality of GAM5324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5324 RNA, herein designated GAM RNA, and which when bound by GAM5324 RNA causes inhibition of translation of the GAM5324 target mRNA into a corresponding GAM5324 target protein.

The mechanism of the translational inhibition exerted by GAM5324 RNA, herein designated GAM RNA, on one or more GAM5324 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5324 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5324 RNA, herein designated GAM RNA, of GAM5324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5324 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5324 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5324 RNA correlate with, and may be deduced from, the identity of the GAM5324 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5329 7194 TGATTCAAAG CAAGATGGTA GCATTGGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 5329 (GAM5329) oligonucleotides modulates expression of respective target genes

GGATGAGATA whose function and utility is known in the art.

TGGTCAGATG GAM5329 is a novel bioinformatically detectable regulatory, non protein coding, AGGATATATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5329 was detected is

TTAAAAGTTG described with additional reference to Figs. 9-15.

AGCTAACAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTTGCTGAG encoded by the human genome.

GAATCA GAM5329 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5329 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5329 precursor RNA is designated SEQ ID:7194, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7194 is located from position 133099409 to position 133099504 relative to chromosome 7 on the `+` strand.

GAM5329 precursor RNA folds onto itself, forming GAM5329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5329 precursor RNA, designated SEQ ID NO: 7194, and a schematic representation of a predicted secondary folding of GAM5329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5329 folded precursor RNA yielding a GAM5329 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5329 RNA, hereby incorporated herein.

GAM5329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5329 target RNA, herein designated GAM TARGET RNA. GAM5329 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5329 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5329 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5329 RNA, herein designated GAM RNA, to target binding sites on GAM5329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5329 target RNA into GAM5329 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5329 target genes. The mRNA of each one of this plurality of GAM5329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5329 RNA, herein designated GAM RNA, and which when bound by GAM5329 RNA causes inhibition of translation of the GAM5329 target mRNA into a corresponding GAM5329 target protein.

The mechanism of the translational inhibition exerted by GAM5329 RNA, herein designated GAM RNA, on one or more GAM5329 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5329 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5329 RNA, herein designated GAM RNA, of GAM5329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5329 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5329 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5329 RNA correlate with, and may be deduced from, the identity of the GAM5329 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5340 5764 AGGCACACAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GCATGGTTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTTTTATA Messenger 5340 (GAM5340) oligonucleotides modulates expression of respective target genes

TGCTAGATTT whose function and utility is known in the art.

CATCCCTGAC GAM5340 is a novel bioinformatically detectable regulatory, non protein coding,

AGCAGAAAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5340 was detected is

GATTGGCAAT described with additional reference to Figs. 9-15.

GGTTATGACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGAACATGC encoded by the human genome.

AATAGCGTGG GAM5340 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5340

TCCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5340

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5340 precursor RNA is designated SEQ ID:5764, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5764 is located from position 65014377 to position 65014480 relative to chromosome 8 on the `+` strand.

GAM5340 precursor RNA folds onto itself, forming GAM5340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5340 precursor RNA, designated SEQ ID NO: 5764, and a schematic representation of a predicted secondary folding of GAM5340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5340 folded precursor RNA yielding a GAM5340 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5340 RNA, hereby incorporated herein.

GAM5340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5340 target RNA, herein designated GAM TARGET RNA. GAM5340 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5340 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5340 RNA, herein designated GAM RNA, to target binding sites on GAM5340 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5340 target RNA into GAM5340 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5340 target genes. The mRNA of each one of this plurality of GAM5340 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5340 RNA, herein designated GAM RNA, and which when bound by GAM5340 RNA causes inhibition of translation of the GAM5340 target mRNA into a corresponding GAM5340 target protein.

The mechanism of the translational inhibition exerted by GAM5340 RNA, herein designated GAM RNA, on one or more GAM5340 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5340 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5340 RNA, herein designated GAM RNA, of GAM5340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5340 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5340 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5340 RNA correlate with, and may be deduced from, the identity of the GAM5340 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5342 5656 AACCTCCAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACACCACCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAATAGCAG Messenger 5342 (GAM5342) oligonucleotides modulates expression of respective target genes

TAATACCAGC whose function and utility is known in the art.

ATAATTGTCT GAM5342 is a novel bioinformatically detectable regulatory, non protein coding,

GCAGTTCTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5342 was detected is

TGAGATACGT described with additional reference to Figs. 9-15.

GCTCTATTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTGGCTTGG encoded by the human genome.

CTGTAGGTT GAM5342 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5342

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5342

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5342 precursor RNA is designated SEQ ID:5656, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5656 is located from position 9563450 to position 9563548 relative to chromosome 19 on the `-` strand.

GAM5342 precursor RNA folds onto itself, forming GAM5342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5342 precursor RNA, designated SEQ ID NO: 5656, and a schematic representation of a predicted secondary folding of GAM5342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5342 folded precursor RNA yielding a GAM5342 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5342 RNA, hereby incorporated herein.

GAM5342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5342 target RNA, herein designated GAM TARGET RNA. GAM5342 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5342 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5342 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5342 RNA, herein designated GAM RNA, to target binding sites on GAM5342 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5342 target RNA into GAM5342 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5342 target genes. The mRNA of each one of this plurality of GAM5342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5342 RNA, herein designated GAM RNA, and which when bound by GAM5342 RNA causes inhibition of translation of the GAM5342 target mRNA into a corresponding GAM5342 target protein.

The mechanism of the translational inhibition exerted by GAM5342 RNA, herein designated GAM RNA, on one or more GAM5342 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5342 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5342 RNA, herein designated GAM RNA, of GAM5342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM5342 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5342 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5342 RNA correlate with, and may be deduced from, the identity of the GAM5342 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5354 7278 TGTGTCAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGATAGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTGCTGTA Messenger 5354 (GAM5354) oligonucleotides modulates expression of respective target genes
ACAAACAGCC whose function and utility is known in the art.

CTCAAATCTC GAM5354 is a novel bioinformatically detectable regulatory, non protein coding,
AGTGGCTGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5354 was detected is

CACCATACAG described with additional reference to Figs. 9-15.

CTCTGCTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCTCACACA encoded by the human genome.

GAM5354 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5354

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5354

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5354 precursor RNA is designated SEQ ID:7278, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7278 is located from position 68147756 to position 68147845 relative to chromosome 11 on the `-` strand.

GAM5354 precursor RNA folds onto itself, forming GAM5354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5354 precursor RNA, designated SEQ ID NO: 7278, and a schematic representation of a predicted secondary folding of GAM5354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5354 folded precursor RNA yielding a GAM5354 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5354 RNA, hereby incorporated herein.

GAM5354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5354 target RNA, herein designated GAM TARGET RNA. GAM5354 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5354 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5354 RNA, herein designated GAM RNA, to target binding sites on GAM5354 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5354 target RNA into GAM5354 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5354 target genes. The mRNA of each one of this plurality of GAM5354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5354 RNA, herein designated GAM RNA, and which when bound by GAM5354 RNA causes inhibition of translation of the GAM5354 target mRNA into a corresponding GAM5354 target protein.

The mechanism of the translational inhibition exerted by GAM5354 RNA, herein designated GAM RNA, on one or more GAM5354 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5354 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5354 RNA, herein designated GAM RNA, of

GAM5354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5354 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5354 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5354 RNA correlate with, and may be deduced from, the identity of the GAM5354 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5370 5957 ATCCTGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGACCCTACC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTCATTTT Messenger 5370 (GAM5370) oligonucleotides modulates expression of respective target genes

ATCTACCCCA whose function and utility is known in the art.

ACCATGGTTA GAM5370 is a novel bioinformatically detectable regulatory, non protein coding,

AAGTGGCTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5370 was detected is

AGTGGAGTCT described with additional reference to Figs. 9-15.

TGGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5370 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5370

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5370

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5370 precursor RNA is designated SEQ ID:5957, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5957 is located from position 26652582 to position 26652656 relative to chromosome 11 on the `-` strand.

GAM5370 precursor RNA folds onto itself, forming GAM5370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5370 precursor RNA, designated SEQ ID NO: 5957, and a schematic representation of a predicted secondary folding of GAM5370 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5370 folded precursor RNA yielding a GAM5370 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5370 RNA, hereby incorporated herein.

GAM5370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5370 target RNA, herein designated GAM TARGET RNA. GAM5370 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5370 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5370 RNA, herein designated GAM RNA, to target binding sites on GAM5370 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5370 target RNA into GAM5370 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5370 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5370 target genes. The mRNA of each one of this plurality of GAM5370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5370 RNA, herein designated GAM RNA, and which when bound by GAM5370 RNA causes inhibition of translation of the GAM5370 target mRNA into a corresponding GAM5370 target protein.

The mechanism of the translational inhibition exerted by GAM5370 RNA, herein designated GAM RNA, on one or more GAM5370 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5370 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM5370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5370 RNA, herein designated GAM RNA, of GAM5370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5370 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5370 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5370 RNA correlate with, and may be deduced from, the identity of the GAM5370 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5371 5812 AGTCTTGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTCACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGGAGTGC Messenger 5371 (GAM5371) oligonucleotides modulates expression of respective target genes

AGTGGTGCCA whose function and utility is known in the art.

TCTTGGCTCA GAM5371 is a novel bioinformatically detectable regulatory, non protein coding,

CTGCAACCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5371 was detected is

CGCCTCCCCA described with additional reference to Figs. 9-15.

GTTCAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TT encoded by the human genome.

GAM5371 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5371

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5371

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5371 precursor RNA is designated SEQ ID:5812, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5812 is located from position 17214638 to position 17214719 relative to chromosome 19 on the `-` strand.

GAM5371 precursor RNA folds onto itself, forming GAM5371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5371 precursor RNA, designated SEQ ID NO: 5812, and a schematic representation of a predicted secondary folding of GAM5371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5371 folded precursor RNA yielding a GAM5371 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5371 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5371 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5371 target RNA, herein designated GAM TARGET RNA. GAM5371 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5371 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5371 RNA, herein designated GAM RNA, to target binding sites on GAM5371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5371 target RNA into GAM5371 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5371 target genes. The mRNA of each one of this plurality of GAM5371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5371 RNA, herein designated GAM RNA, and which when bound by GAM5371 RNA causes inhibition of translation of the GAM5371 target mRNA into a corresponding GAM5371 target protein.

The mechanism of the translational inhibition exerted by GAM5371 RNA, herein

designated GAM RNA, on one or more GAM5371 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5371 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5371 RNA, herein designated GAM RNA, of GAM5371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5371 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5371 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5371 RNA correlate with, and may be deduced from, the identity of the GAM5371 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5374 6042 CATTAAAACT Fig. 8 further provides a conceptual description of another novel bioinformatically
CACCATCAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGATGTAAT Messenger 5374 (GAM5374) oligonucleotides modulates expression of respective target genes
CTTATTAATT whose function and utility is known in the art.

ACACATTTTG GAM5374 is a novel bioinformatically detectable regulatory, non protein coding,
TATTTTAATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5374 was detected is

ATTTCAAGGA described with additional reference to Figs. 9-15.

GTGAAGAAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGGGTGTTT encoded by the human genome.

TTGTTTTTGT GAM5374 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5374
AGTTCTGATT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5374
ACTCATTTAT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
GCATTGTTTT to the nucleotide sequence of GAM5374 precursor RNA is designated SEQ ID:6042, and is

G provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6042 is located from position 37551253 to position 37551383 relative to chromosome 19 on the `+` strand.

GAM5374 precursor RNA folds onto itself, forming GAM5374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5374 precursor RNA, designated SEQ ID NO: 6042, and a schematic representation of a predicted secondary folding of GAM5374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5374 folded precursor RNA yielding a GAM5374 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5374 RNA, hereby incorporated herein.

GAM5374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5374 target RNA, herein designated GAM TARGET RNA. GAM5374 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5374 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5374 RNA, herein designated GAM RNA, to target binding sites on GAM5374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5374 target RNA into GAM5374 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5374 target genes. The mRNA of each one of this

plurality of GAM5374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5374 RNA, herein designated GAM RNA, and which when bound by GAM5374 RNA causes inhibition of translation of the GAM5374 target mRNA into a corresponding GAM5374 target protein.

The mechanism of the translational inhibition exerted by GAM5374 RNA, herein designated GAM RNA, on one or more GAM5374 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5374 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5374 RNA, herein designated GAM RNA, of GAM5374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5374 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5374 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5374 RNA correlate with, and may be deduced from, the identity of the GAM5374 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5385 6032 CAGTGGGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGGGCCGAT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACACTGTACG Messenger 5385 (GAM5385) oligonucleotides modulates expression of respective target genes

AGAGTGAGTA whose function and utility is known in the art.

GCAGGTCTCA GAM5385 is a novel bioinformatically detectable regulatory, non protein coding,

CAGTGAACCG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5385 was detected is

GTCTCTTTCC described with additional reference to Figs. 9-15.

CTACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5385 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5385

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5385 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5385 precursor RNA is designated SEQ ID:6032, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6032 is located from position 35621432 to position 35621507 relative to chromosome 3 on the `+` strand.

GAM5385 precursor RNA folds onto itself, forming GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5385 precursor RNA, designated SEQ ID NO: 6032, and a schematic representation of a predicted secondary folding of GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5385 folded precursor RNA yielding a GAM5385 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5385 RNA, hereby incorporated herein. Expression of GAM5385 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM5385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5385 target RNA, herein designated GAM TARGET RNA. GAM5385 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5385 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5385 RNA, herein designated GAM RNA, to target

binding sites on GAM5385 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5385 target RNA into GAM5385 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5385 target genes. The mRNA of each one of this plurality of GAM5385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5385 RNA, herein designated GAM RNA, and which when bound by GAM5385 RNA causes inhibition of translation of the GAM5385 target mRNA into a corresponding GAM5385 target protein.

The mechanism of the translational inhibition exerted by GAM5385 RNA, herein designated GAM RNA, on one or more GAM5385 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5385 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5385 RNA, herein designated GAM RNA, of GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5385 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5385 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5385 RNA correlate with, and may be deduced from, the identity of the GAM5385 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5415 6188 CTCTTGCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTGGAGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTGGTATG Messenger 5415 (GAM5415) oligonucleotides modulates expression of respective target genes

ATCACAACTC whose function and utility is known in the art.

TCCTAAGCCT GAM5415 is a novel bioinformatically detectable regulatory, non protein coding,

CAAACACCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5415 was detected is

GGATCAAGTG described with additional reference to Figs. 9-15.

ATCCTCTGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCAGCCTCC encoded by the human genome.

CAAGTAG GAM5415 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5415 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5415 precursor RNA is designated SEQ ID:6188, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6188 is located from position 41537048 to position 41537144 relative to chromosome 18 on the `+` strand.

GAM5415 precursor RNA folds onto itself, forming GAM5415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5415 precursor RNA, designated SEQ ID NO: 6188, and a schematic representation of a predicted secondary folding of GAM5415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5415 folded precursor RNA yielding a GAM5415 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5415 RNA, hereby incorporated herein.

GAM5415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5415 target RNA, herein designated GAM TARGET RNA. GAM5415 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5415 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5415 RNA, herein designated GAM RNA, to target binding sites on GAM5415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5415 target RNA into GAM5415 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5415 target genes. The mRNA of each one of this plurality of GAM5415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5415 RNA, herein designated GAM RNA, and which when bound by GAM5415 RNA causes inhibition of translation of the GAM5415 target mRNA into a corresponding GAM5415 target protein.

The mechanism of the translational inhibition exerted by GAM5415 RNA, herein designated GAM RNA, on one or more GAM5415 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5415 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5415 RNA, herein designated GAM RNA, of GAM5415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5415 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5415 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5415 RNA correlate with, and may be deduced from, the identity of the GAM5415 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5422 6915 GTGGGAGGAG GACTGGCAAA AATATGAGAG TAGGAGTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 5422 (GAM5422) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GGCTCTTGAG GAM5422 is a novel bioinformatically detectable regulatory, non protein coding, CTTGGGCCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5422 was detected is

GCCTTCAAAT described with additional reference to Figs. 9-15.

TTCCACTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCACTCAC encoded by the human genome.

GAM5422 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5422 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5422 precursor RNA is designated SEQ ID:6915, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6915 is located from position 47243046 to position 47243133 relative to chromosome X on the `+` strand.

GAM5422 precursor RNA folds onto itself, forming GAM5422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5422 precursor RNA, designated SEQ ID NO: 6915, and a schematic representation of a predicted secondary folding of GAM5422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5422 folded precursor RNA yielding a GAM5422 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5422 RNA, hereby incorporated herein.

GAM5422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5422 target RNA, herein designated GAM TARGET RNA. GAM5422 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM5422 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5422 RNA, herein designated GAM RNA, to target binding sites on GAM5422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5422 target RNA into GAM5422 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5422 target genes. The mRNA of each one of this plurality of GAM5422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5422 RNA, herein designated GAM RNA, and which when bound by GAM5422 RNA causes inhibition of translation of the GAM5422 target mRNA into a corresponding GAM5422 target protein.

The mechanism of the translational inhibition exerted by GAM5422 RNA, herein designated GAM RNA, on one or more GAM5422 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5422 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5422 RNA, herein designated GAM RNA, of GAM5422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5422 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5422 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5422 RNA correlate with, and may be deduced from, the identity of the GAM5422 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5444 6297 GAAGGGTACC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCTGGAGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGTGTGGTT Messenger 5444 (GAM5444) oligonucleotides modulates expression of respective target
genes
TGTGGGGTGG whose function and utility is known in the art.

GTTTCTTATA GAM5444 is a novel bioinformatically detectable regulatory, non protein coding,
TCACTGAATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5444 was detected is

TAAAGTGGGT described with additional reference to Figs. 9-15.

GCCTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
encoded by the human genome.

GAM5444 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5444

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM5444
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5444 precursor RNA is designated SEQ ID:6297, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6297 is located from position 127094099 to position 127094175 relative to chromosome 9 on the `+` strand.

GAM5444 precursor RNA folds onto itself, forming GAM5444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5444 precursor RNA, designated SEQ ID NO: 6297, and a schematic representation of a predicted secondary folding of GAM5444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5444 folded precursor RNA yielding a GAM5444 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5444 RNA, hereby incorporated herein.

GAM5444 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5444 target RNA, herein designated GAM TARGET RNA. GAM5444 target
RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5444 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5444 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5444 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5444 RNA, herein designated GAM RNA, to target binding sites on GAM5444 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5444 target RNA into GAM5444 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5444 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5444 target genes. The mRNA of each one of this plurality of GAM5444 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5444 RNA, herein designated GAM RNA, and which when bound by GAM5444 RNA causes inhibition of translation of the GAM5444 target mRNA into a corresponding GAM5444 target protein.

The mechanism of the translational inhibition exerted by GAM5444 RNA, herein designated GAM RNA, on one or more GAM5444 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5444 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5444 RNA, herein designated GAM RNA, of GAM5444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5444 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5444 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5444 RNA correlate with, and may be deduced from, the identity of the GAM5444 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5454 6600 GGAGAAGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTTGCATAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGCACAGTG Messenger 5454 (GAM5454) oligonucleotides modulates expression of respective target genes
GATGGGGAAT whose function and utility is known in the art.

GGTGTGACCT GAM5454 is a novel bioinformatically detectable regulatory, non protein coding,
CTGTCCCTGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5454 was detected is

TCTCTTCTCT described with additional reference to Figs. 9-15.

GCTGGCTTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGTCTATTC encoded by the human genome.

TCC GAM5454 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5454
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5454
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5454 precursor RNA is designated SEQ ID:6600, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6600 is located from position 101393105 to position 101393197 relative to chromosome X on the `+` strand.

GAM5454 precursor RNA folds onto itself, forming GAM5454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5454 precursor RNA, designated SEQ ID NO: 6600, and a schematic representation of a predicted secondary folding of GAM5454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5454 folded precursor RNA yielding a GAM5454 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5454 RNA, hereby incorporated herein.

GAM5454 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM5454 target RNA, herein designated GAM TARGET RNA. GAM5454 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5454 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5454 RNA, herein designated GAM RNA, to target binding sites on GAM5454 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5454 target RNA into GAM5454 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5454 target genes. The mRNA of each one of this plurality of GAM5454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5454 RNA, herein designated GAM RNA, and which when bound by GAM5454 RNA causes inhibition of translation of the GAM5454 target mRNA into a corresponding GAM5454 target protein.

The mechanism of the translational inhibition exerted by GAM5454 RNA, herein designated GAM RNA, on one or more GAM5454 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5454 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5454 RNA, herein designated GAM RNA, of GAM5454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5454 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM5454 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5454 RNA correlate with, and may be deduced from, the identity of the GAM5454 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5486 6265 CTTGAGAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GACAACTAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTGAGGAA Messenger 5486 (GAM5486) oligonucleotides modulates expression of respective target genes
GGTGTGAGAA whose function and utility is known in the art.

ATGAGCCTAA GAM5486 is a novel bioinformatically detectable regulatory, non protein coding,
AGAGGTAGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5486 was detected is

GAGACTCAAA described with additional reference to Figs. 9-15.

GGAGGCTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAAGATACCA encoded by the human genome.

CAGCTACAAG GAM5486 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5486
TTTTTGTTAT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5486
ATTCTGAAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5486 precursor RNA is designated SEQ ID:6265, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6265 is located from position 71909012 to position 71909130 relative to chromosome 11 on the `-` strand.

GAM5486 precursor RNA folds onto itself, forming GAM5486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5486 precursor RNA, designated SEQ ID NO: 6265, and a schematic representation of a predicted secondary folding of GAM5486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5486 folded precursor RNA yielding a GAM5486 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5486 RNA, hereby incorporated herein.

GAM5486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5486 target RNA, herein designated GAM TARGET RNA. GAM5486 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5486 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5486 RNA, herein designated GAM RNA, to target binding sites on GAM5486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5486 target RNA into GAM5486 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5486 target genes. The mRNA of each one of this plurality of GAM5486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5486 RNA, herein designated GAM RNA, and which when bound by GAM5486 RNA causes inhibition of translation of the GAM5486 target mRNA into a corresponding GAM5486 target protein.

The mechanism of the translational inhibition exerted by GAM5486 RNA, herein designated GAM RNA, on one or more GAM5486 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5486 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5486 RNA, herein designated GAM RNA, of GAM5486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5486 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5486 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5486 RNA correlate with, and may be deduced from, the identity of the GAM5486 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5498 5821 AGTTCACAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTGAAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTCCCATAA Messenger 5498 (GAM5498) oligonucleotides modulates expression of respective target genes
GACCCTGAAT whose function and utility is known in the art.

CTAGCAGCCA GAM5498 is a novel bioinformatically detectable regulatory, non protein coding,
CTGTGTACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5498 was detected is

described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5498 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5498

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5498

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5498 precursor RNA is designated SEQ ID:5821, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5821 is located from position 3674783 to position 3674841 relative to chromosome 16 on the `+` strand.

GAM5498 precursor RNA folds onto itself, forming GAM5498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5498 precursor RNA, designated SEQ ID NO: 5821, and a schematic representation of a predicted secondary folding of GAM5498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5498 folded precursor RNA yielding a GAM5498 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5498 RNA, hereby incorporated herein.

GAM5498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5498 target RNA, herein designated GAM TARGET RNA. GAM5498 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5498 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5498 RNA, herein designated GAM RNA, to target binding sites on GAM5498 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5498 target RNA into GAM5498 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5498 target genes. The mRNA of each one of this plurality of GAM5498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5498 RNA, herein designated GAM RNA, and which when bound by GAM5498 RNA causes inhibition of translation of the GAM5498 target mRNA into a corresponding GAM5498 target protein.

The mechanism of the translational inhibition exerted by GAM5498 RNA, herein designated GAM RNA, on one or more GAM5498 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5498 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5498 RNA, herein designated GAM RNA, of GAM5498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5498 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5498 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5498 RNA correlate with, and may be deduced from, the identity of the GAM5498 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5512 5758 AGGAGGGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGAGAAAG Messenger 5512 (GAM5512) oligonucleotides modulates expression of respective target genes

GCAGACTCAG whose function and utility is known in the art.

CCAGGGATGG GAM5512 is a novel bioinformatically detectable regulatory, non protein coding,

GTGAGGGTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5512 was detected is

CCCTGTCCCA described with additional reference to Figs. 9-15.

AAGCAAGACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGCT encoded by the human genome.

GAM5512 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5512

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5512

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5512 precursor RNA is designated SEQ ID:5758, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5758 is located from position 54100819 to position 54100904 relative to chromosome 19 on the `+` strand.

GAM5512 precursor RNA folds onto itself, forming GAM5512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5512 precursor RNA, designated SEQ ID NO: 5758, and a schematic representation of a predicted secondary folding of GAM5512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5512 folded precursor RNA yielding a GAM5512 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5512 RNA, hereby incorporated herein.

GAM5512 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5512 target RNA, herein designated GAM TARGET RNA. GAM5512 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5512 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5512 RNA, herein designated GAM RNA, to target binding sites on GAM5512 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5512 target RNA into GAM5512 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5512 target genes. The mRNA of each one of this plurality of GAM5512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5512 RNA, herein designated GAM RNA, and which when bound by GAM5512 RNA causes inhibition of translation of the GAM5512 target mRNA into a corresponding GAM5512 target protein.

The mechanism of the translational inhibition exerted by GAM5512 RNA, herein designated GAM RNA, on one or more GAM5512 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5512 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5512 RNA, herein designated GAM RNA, of GAM5512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5512 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5512 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5512 RNA correlate with, and may be deduced from, the identity of the GAM5512 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5514 6856 GGTTGCCGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGAGGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTACCAGC Messenger 5514 (GAM5514) oligonucleotides modulates expression of respective target genes

GTCTGCTGGG whose function and utility is known in the art.

CAGAGACCAG GAM5514 is a novel bioinformatically detectable regulatory, non protein coding,

GGATGCTGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5514 was detected is

CCACATCCCA described with additional reference to Figs. 9-15.

CAATGCACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACAATC encoded by the human genome.

GAM5514 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5514

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5514

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5514 precursor RNA is designated SEQ ID:6856, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6856 is located from position 25442199 to position 25442285 relative to chromosome 22 on the `+` strand.

GAM5514 precursor RNA folds onto itself, forming GAM5514 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5514 precursor RNA, designated SEQ ID NO: 6856, and a schematic representation of a predicted secondary folding of GAM5514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5514 folded precursor RNA yielding a GAM5514 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5514 RNA, hereby incorporated herein.

GAM5514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5514 target RNA, herein designated GAM TARGET RNA. GAM5514 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5514 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5514 RNA, herein designated GAM RNA, to target binding sites on GAM5514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5514 target RNA into GAM5514 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5514 target genes. The mRNA of each one of this plurality of GAM5514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5514 RNA, herein designated GAM RNA, and which when bound by GAM5514 RNA causes inhibition of translation of the GAM5514 target mRNA into a corresponding GAM5514 target protein.

The mechanism of the translational inhibition exerted by GAM5514 RNA, herein designated GAM RNA, on one or more GAM5514 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5514 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5514 RNA, herein designated GAM RNA, of GAM5514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5514 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5514 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5514 RNA correlate with, and may be deduced from, the identity of the GAM5514 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5526 6448 GAGGGCTTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAATGCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCAGAGCTG Messenger 5526 (GAM5526) oligonucleotides modulates expression of respective target genes

CACCCCAGAC whose function and utility is known in the art.

CAACAAAATC GAM5526 is a novel bioinformatically detectable regulatory, non protein coding,

AGACTCTCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5526 was detected is

GGATGCGGCC described with additional reference to Figs. 9-15.

AAGGCATCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TATGTGGAAA encoded by the human genome.

GCTTTC GAM5526 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5526

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5526

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5526 precursor RNA is designated SEQ ID:6448, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6448 is located from position 79906276 to position 79906371 relative to chromosome 14 on the `-` strand.

GAM5526 precursor RNA folds onto itself, forming GAM5526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5526 precursor RNA, designated SEQ ID NO: 6448, and a schematic representation of a predicted secondary folding of GAM5526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5526 folded precursor RNA yielding a GAM5526 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5526 RNA, hereby incorporated herein.

GAM5526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5526 target RNA, herein designated GAM TARGET RNA. GAM5526 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5526 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5526 RNA, herein designated GAM RNA, to target binding sites on GAM5526 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5526 target RNA into GAM5526 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5526 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM5526 target genes. The mRNA of each one of this plurality of GAM5526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5526 RNA, herein designated GAM RNA, and which when bound by GAM5526 RNA causes inhibition of translation of the GAM5526 target mRNA into a corresponding GAM5526 target protein.

The mechanism of the translational inhibition exerted by GAM5526 RNA, herein designated GAM RNA, on one or more GAM5526 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5526 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5526 RNA, herein designated GAM RNA, of GAM5526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5526 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5526 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5526 RNA correlate with, and may be deduced from, the identity of the GAM5526 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5560 7062 TCTATATGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTAACTAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTATTTGCCC Messenger 5560 (GAM5560) oligonucleotides modulates expression of respective target genes

CTTGGAGCTT whose function and utility is known in the art.

TTATAGTCTT GAM5560 is a novel bioinformatically detectable regulatory, non protein coding,

TAAAATGAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5560 was detected is

TAATGTCTGT described with additional reference to Figs. 9-15.

GAAATGCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGGACACTG encoded by the human genome.

CCTGGCATAA GAM5560 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5560

ACACTCATGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5560 AGA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5560 precursor RNA is designated SEQ ID:7062, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7062 is located from position 86570029 to position 86570141 relative to chromosome 11 on the `+` strand.

GAM5560 precursor RNA folds onto itself, forming GAM5560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5560 precursor RNA, designated SEQ ID NO: 7062, and a schematic representation of a predicted secondary folding of GAM5560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5560 folded precursor RNA yielding a GAM5560 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5560 RNA, hereby incorporated herein.

GAM5560 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5560 target RNA, herein designated GAM TARGET RNA. GAM5560 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5560 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5560 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5560 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5560 RNA, herein designated GAM RNA, to target binding sites on GAM5560 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5560 target RNA

into GAM5560 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5560 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5560 target genes. The mRNA of each one of this plurality of GAM5560 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5560 RNA, herein designated GAM RNA, and which when bound by GAM5560 RNA causes inhibition of translation of the GAM5560 target mRNA into a corresponding GAM5560 target protein.

The mechanism of the translational inhibition exerted by GAM5560 RNA, herein designated GAM RNA, on one or more GAM5560 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5560 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5560 RNA, herein designated GAM RNA, of GAM5560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5560 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5560 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5560 RNA correlate with, and may be deduced from, the identity of the GAM5560 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5597 5819 AGTGTTGGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGACTTGAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGTGATT Messenger 5597 (GAM5597) oligonucleotides modulates expression of respective target genes
GTTTTAGAAG whose function and utility is known in the art.

AAGGTCAGAA GAM5597 is a novel bioinformatically detectable regulatory, non protein coding,
GACTAGATTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5597 was detected is

GCTTTTCTCT described with additional reference to Figs. 9-15.

CCAATTTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATACCTCTTC encoded by the human genome.

TATTCGAGGA GAM5597 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5597

CACCCAGGAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5597

CATT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5597 precursor RNA is designated SEQ ID:5819, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5819 is located from position 42550378 to position 42550491 relative to chromosome 17 on the `-` strand.

GAM5597 precursor RNA folds onto itself, forming GAM5597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5597 precursor RNA, designated SEQ ID NO: 5819, and a schematic representation of a predicted secondary folding of GAM5597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5597 folded precursor RNA yielding a GAM5597 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5597 RNA, hereby incorporated herein.

GAM5597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5597 target RNA, herein designated GAM TARGET RNA. GAM5597 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5597 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5597 RNA, herein designated GAM RNA, to target binding sites on GAM5597 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5597 target RNA into GAM5597 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5597 target genes. The mRNA of each one of this plurality of GAM5597 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5597 RNA, herein designated GAM RNA, and which when bound by GAM5597 RNA causes inhibition of translation of the GAM5597 target mRNA into a corresponding GAM5597 target protein.

The mechanism of the translational inhibition exerted by GAM5597 RNA, herein designated GAM RNA, on one or more GAM5597 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5597 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5597 RNA, herein designated GAM RNA, of GAM5597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5597 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5597 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5597 RNA correlate with, and may be deduced from, the identity of the GAM5597 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5615 6172 CTCTCACCCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTAGCCTTA detected oligonucleotides of the present invention, referred to here as Genomic Address
AATCCAGAAT Messenger 5615 (GAM5615) oligonucleotides modulates expression of respective target genes
CTAGACTGAA whose function and utility is known in the art.

TATGGACTGA GAM5615 is a novel bioinformatically detectable regulatory, non protein coding,
ATGGGTCAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5615 was detected is

TTTGGGGAAA described with additional reference to Figs. 9-15.

TGTGTTTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGACAGCTG encoded by the human genome.

AGGGACCAGA GAM5615 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5615

GAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5615

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5615 precursor RNA is designated SEQ ID:6172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6172 is located from position 51339544 to position 51339646 relative to chromosome 12 on the `-` strand.

GAM5615 precursor RNA folds onto itself, forming GAM5615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5615 precursor RNA, designated SEQ ID NO: 6172, and a schematic representation of a predicted secondary folding of GAM5615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5615 folded precursor RNA yielding a GAM5615 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5615 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5615 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5615 target RNA, herein designated GAM TARGET RNA. GAM5615 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5615 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5615 RNA, herein designated GAM RNA, to target binding sites on GAM5615 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5615 target RNA into GAM5615 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5615 target genes. The mRNA of each one of this plurality of GAM5615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5615 RNA, herein designated GAM RNA, and which when bound by GAM5615 RNA causes inhibition of translation of the GAM5615 target mRNA into a corresponding GAM5615 target protein.

The mechanism of the translational inhibition exerted by GAM5615 RNA, herein designated GAM RNA, on one or more GAM5615 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5615 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5615 RNA, herein designated GAM RNA, of GAM5615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5615 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5615 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5615 RNA correlate with, and may be deduced from, the identity of the GAM5615 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5617 6758 GGCTAAGAGT AACAGGTGCT GGAGCCAGAC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 5617 (GAM5617) oligonucleotides modulates expression of respective target genes

TTCCTGGGTT whose function and utility is known in the art.

CATATCCTGG GAM5617 is a novel bioinformatically detectable regulatory, non protein coding,
TTCTACCAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5617 was detected is

TTACCAGCTG described with additional reference to Figs. 9-15.

TGTGAACTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAAAATTCC encoded by the human genome.

TCTCCGCCTC GAM5617 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5617
TTAGTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5617

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5617 precursor RNA is designated SEQ ID:6758, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6758 is located from position 47865219 to position 47865324 relative to chromosome X on the `-` strand.

GAM5617 precursor RNA folds onto itself, forming GAM5617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5617 precursor RNA, designated SEQ ID NO: 6758, and a schematic representation of a predicted secondary folding of GAM5617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5617 folded precursor RNA yielding a GAM5617 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5617 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5617 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5617 target RNA, herein designated GAM TARGET RNA. GAM5617 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5617 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM5617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5617 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5617 RNA, herein designated GAM RNA, to target binding sites on GAM5617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5617 target RNA into GAM5617 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5617 target genes. The mRNA of each one of this plurality of GAM5617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5617 RNA, herein designated GAM RNA, and which when bound by GAM5617 RNA causes inhibition of translation of the GAM5617 target mRNA into a corresponding GAM5617 target protein.

The mechanism of the translational inhibition exerted by GAM5617 RNA, herein designated GAM RNA, on one or more GAM5617 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5617 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5617 RNA, herein designated GAM RNA, of GAM5617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5617 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5617 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5617 RNA correlate with, and may be deduced from, the identity of the GAM5617 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5623 5747 AGCATATGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCAAGACAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGCCCTGGA Messenger 5623 (GAM5623) oligonucleotides modulates expression of respective target genes
ATCCTCCGTG whose function and utility is known in the art.

TCACATGTGG GAM5623 is a novel bioinformatically detectable regulatory, non protein coding,
GCTGCTGACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5623 was detected is

GGAAGAATGT described with additional reference to Figs. 9-15.

GCTTTTGTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGTTGTT encoded by the human genome.

GAM5623 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5623

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5623

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5623 precursor RNA is designated SEQ ID:5747, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5747 is located from position 113971966 to position 113972053 relative to chromosome 11 on the `+` strand.

GAM5623 precursor RNA folds onto itself, forming GAM5623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5623 precursor RNA, designated SEQ ID NO: 5747, and a schematic representation of a predicted secondary folding of GAM5623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5623 folded precursor RNA yielding a GAM5623 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5623 RNA, hereby incorporated herein.

GAM5623 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5623 target RNA, herein designated GAM TARGET RNA. GAM5623 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5623 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5623 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5623 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5623 RNA, herein designated GAM RNA, to target binding sites on GAM5623 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5623 target RNA into GAM5623 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5623 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5623 target genes. The mRNA of each one of this plurality of GAM5623 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5623 RNA, herein designated GAM RNA, and which when bound by GAM5623 RNA causes inhibition of translation of the GAM5623 target mRNA into a corresponding GAM5623 target protein.

The mechanism of the translational inhibition exerted by GAM5623 RNA, herein designated GAM RNA, on one or more GAM5623 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5623 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5623 RNA, herein designated GAM RNA, of GAM5623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5623 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5623 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5623 RNA correlate with, and may be deduced from, the identity of the GAM5623 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5640 5802 AGTATTATTA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGACTTTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGGTCTGGG Messenger 5640 (GAM5640) oligonucleotides modulates expression of respective target
genes
CTGTGCCTGT whose function and utility is known in the art.

TGCTGCCTCT GAM5640 is a novel bioinformatically detectable regulatory, non protein coding,
GAGACAAGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5640 was detected is

AGCCTAATAC described with additional reference to Figs. 9-15.

AGGAAAAGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
TAATTCTCT encoded by the human genome.

GAM5640 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5640

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM5640
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5640 precursor RNA is designated SEQ ID:5802, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5802 is located from position 16837776 to position 16837864 relative to chromosome 19 on the `-` strand.

GAM5640 precursor RNA folds onto itself, forming GAM5640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5640 precursor RNA, designated SEQ ID NO: 5802, and a schematic representation of a predicted secondary folding of GAM5640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5640 folded precursor RNA yielding a GAM5640 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM5640 RNA, hereby incorporated herein.

GAM5640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5640 target RNA, herein designated GAM TARGET RNA. GAM5640 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5640 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5640 RNA, herein designated GAM RNA, to target binding sites on GAM5640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5640 target RNA into GAM5640 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5640 target genes. The mRNA of each one of this plurality of GAM5640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5640 RNA, herein designated GAM RNA, and which when bound by GAM5640 RNA causes inhibition of translation of the GAM5640 target mRNA into a corresponding GAM5640 target protein.

The mechanism of the translational inhibition exerted by GAM5640 RNA, herein designated GAM RNA, on one or more GAM5640 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5640 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5640 RNA, herein designated GAM RNA, of GAM5640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5640 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5640 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5640 RNA correlate with, and may be deduced from, the identity of the GAM5640 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5653 6703 GGAGAATTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 5653 (GAM5653) oligonucleotides modulates expression of respective target genes
TTGCAGTGAG whose function and utility is known in the art.

CCGAGATTGC GAM5653 is a novel bioinformatically detectable regulatory, non protein coding,
GCCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5653 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GCAACAGAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM5653 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5653

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5653
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5653 precursor RNA is designated SEQ ID:6703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6703 is located from position 77350810 to position 77350897 relative to chromosome 8 on the `+` strand.

GAM5653 precursor RNA folds onto itself, forming GAM5653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5653 precursor RNA, designated SEQ ID NO: 6703, and a schematic representation of a predicted secondary folding of GAM5653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5653 folded precursor RNA

yielding a GAM5653 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5653 RNA, hereby incorporated herein. Expression of GAM5653 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM5653 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5653 target RNA, herein designated GAM TARGET RNA. GAM5653 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5653 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5653 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5653 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5653 RNA, herein designated GAM RNA, to target binding sites on GAM5653 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5653 target RNA into GAM5653 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5653 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5653 target genes. The mRNA of each one of this plurality of GAM5653 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5653 RNA, herein designated GAM RNA, and which when bound by GAM5653 RNA causes inhibition of translation of the GAM5653 target mRNA into a corresponding GAM5653 target protein.

The mechanism of the translational inhibition exerted by GAM5653 RNA, herein designated GAM RNA, on one or more GAM5653 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5653 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5653 RNA, herein designated GAM RNA, of GAM5653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5653 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5653 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5653 RNA correlate with, and may be deduced from, the identity of the GAM5653 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5654 5652 AAATACAAAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCTGGGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTGGCAGAC Messenger 5654 (GAM5654) oligonucleotides modulates expression of respective target genes

TTGCTAAATC whose function and utility is known in the art.

AGAATCTCCA GAM5654 is a novel bioinformatically detectable regulatory, non protein coding,

GGGGATCCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5654 was detected is

GAATTGGTGT described with additional reference to Figs. 9-15.

TT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5654 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5654

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5654

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5654 precursor RNA is designated SEQ ID:5652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5652 is located from position 21698933 to position 21699004 relative to chromosome 16 on the `+` strand.

GAM5654 precursor RNA folds onto itself, forming GAM5654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5654 precursor RNA, designated SEQ ID NO: 5652, and a schematic representation of a predicted secondary folding of GAM5654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5654 folded precursor RNA yielding a GAM5654 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5654 RNA, hereby incorporated herein.

GAM5654 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5654 target RNA, herein designated GAM TARGET RNA. GAM5654 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5654 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5654 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5654 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5654 RNA, herein designated GAM RNA, to target binding sites on GAM5654 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5654 target RNA into GAM5654 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5654 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5654 target genes. The mRNA of each one of this plurality of GAM5654 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5654 RNA, herein designated GAM RNA, and which when bound by GAM5654 RNA causes inhibition of translation of the GAM5654 target mRNA into a corresponding GAM5654 target protein.

The mechanism of the translational inhibition exerted by GAM5654 RNA, herein designated GAM RNA, on one or more GAM5654 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5654 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5654 RNA, herein designated GAM RNA, of GAM5654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5654 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5654 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5654 RNA correlate with, and may be deduced from, the identity of the GAM5654 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5657 6791 GGGAGGATCG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGAGCCTA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGGTCAAG Messenger 5657 (GAM5657) oligonucleotides modulates expression of respective target genes

GCTGCAGTGA whose function and utility is known in the art.

GCTGAGATCA GAM5657 is a novel bioinformatically detectable regulatory, non protein coding,

CACCACTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5657 was detected is

CTCCTGCCTA described with additional reference to Figs. 9-15.

GGTGACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACTGTC encoded by the human genome.

GAM5657 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5657

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5657

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5657 precursor RNA is designated SEQ ID:6791, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6791 is located from position 1344537 to position 1344626 relative to chromosome 12 on the `+` strand.

GAM5657 precursor RNA folds onto itself, forming GAM5657 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5657 precursor RNA, designated SEQ ID NO: 6791, and a schematic representation of a predicted secondary folding of GAM5657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5657 folded precursor RNA yielding a GAM5657 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5657 RNA, hereby incorporated herein.

GAM5657 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5657 target RNA, herein designated GAM TARGET RNA. GAM5657 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5657 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5657 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5657 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5657 RNA, herein designated GAM RNA, to target binding sites on GAM5657 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5657 target RNA into GAM5657 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5657 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5657 target genes. The mRNA of each one of this plurality of GAM5657 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5657 RNA, herein designated GAM RNA, and which when bound by GAM5657 RNA causes inhibition of translation of the GAM5657 target mRNA into a corresponding GAM5657 target protein.

The mechanism of the translational inhibition exerted by GAM5657 RNA, herein designated GAM RNA, on one or more GAM5657 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5657 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5657 RNA, herein designated GAM RNA, of GAM5657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5657 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5657 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5657 RNA correlate with, and may be deduced from, the identity of the GAM5657 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5673 5816 AGTGGTAATG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCGTGTGTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATAGAAATAT Messenger 5673 (GAM5673) oligonucleotides modulates expression of respective target genes
GTAATCGATC whose function and utility is known in the art.

TTTTCTTTGG GAM5673 is a novel bioinformatically detectable regulatory, non protein coding,
TGGGCAATTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5673 was detected is

GCAATATTGA described with additional reference to Figs. 9-15.

GGAAAGTTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGATGTATGT encoded by the human genome.

ATCCCTACCA GAM5673 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5673
CTTGAAACAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5673
CTGGAAATGC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CATT to the nucleotide sequence of GAM5673 precursor RNA is designated SEQ ID:5816, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5816 is located from position 7772009 to position 7772132 relative to chromosome X on the `-` strand.

GAM5673 precursor RNA folds onto itself, forming GAM5673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5673 precursor RNA, designated SEQ ID NO: 5816, and a schematic representation of a predicted secondary folding of GAM5673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5673 folded precursor RNA yielding a GAM5673 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5673 RNA, hereby incorporated herein.

GAM5673 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5673 target RNA, herein designated GAM TARGET RNA. GAM5673 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5673 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5673 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5673 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5673 RNA, herein designated GAM RNA, to target binding sites on GAM5673 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5673 target RNA into GAM5673 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5673 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM5673 target genes. The mRNA of each one of this plurality of GAM5673 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5673 RNA, herein designated GAM RNA, and which when bound by GAM5673 RNA causes inhibition of translation of the GAM5673 target mRNA into a corresponding GAM5673 target protein.

The mechanism of the translational inhibition exerted by GAM5673 RNA, herein designated GAM RNA, on one or more GAM5673 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5673 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5673 RNA, herein designated GAM RNA, of GAM5673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5673 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5673 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5673 RNA correlate with, and may be deduced from, the identity of the GAM5673 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5691 6774 GGGAAAGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGAGGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAAAGGCAG Messenger 5691 (GAM5691) oligonucleotides modulates expression of respective target genes

ACTCAGCCAG whose function and utility is known in the art.

GGATGGGTGA GAM5691 is a novel bioinformatically detectable regulatory, non protein coding,

GGGTTTCCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5691 was detected is

GTCCCAAAGC described with additional reference to Figs. 9-15.

AAGACCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5691 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5691 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5691 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5691 precursor RNA is designated SEQ ID:6774, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6774 is located from position 54100823 to position 54100899 relative to chromosome 19 on the `+` strand.

GAM5691 precursor RNA folds onto itself, forming GAM5691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5691 precursor RNA, designated SEQ ID NO: 6774, and a schematic representation of a predicted secondary folding of GAM5691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5691 folded precursor RNA yielding a GAM5691 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5691 RNA, hereby incorporated herein.

GAM5691 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5691 target RNA, herein designated GAM TARGET RNA. GAM5691 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5691 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5691 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5691 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5691 RNA, herein designated GAM RNA, to target

binding sites on GAM5691 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5691 target RNA into GAM5691 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5691 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5691 target genes. The mRNA of each one of this plurality of GAM5691 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5691 RNA, herein designated GAM RNA, and which when bound by GAM5691 RNA causes inhibition of translation of the GAM5691 target mRNA into a corresponding GAM5691 target protein.

The mechanism of the translational inhibition exerted by GAM5691 RNA, herein designated GAM RNA, on one or more GAM5691 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5691 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5691 RNA, herein designated GAM RNA, of GAM5691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5691 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5691 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5691 RNA correlate with, and may be deduced from, the identity of the GAM5691 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5697 5966 ATGAGTATTG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATCTGTCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCTGTGCAT Messenger 5697 (GAM5697) oligonucleotides modulates expression of respective target genes
TGCTCCGAGG whose function and utility is known in the art.

CAGTTCTGAG GAM5697 is a novel bioinformatically detectable regulatory, non protein coding,
TGGATGATGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5697 was detected is

ACAGATGGGA described with additional reference to Figs. 9-15.

TTCCTCAGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAT encoded by the human genome.

GAM5697 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5697 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5697 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5697 precursor RNA is designated SEQ ID:5966, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5966 is located from position 31719324 to position 31719406 relative to chromosome 16 on the `+` strand.

GAM5697 precursor RNA folds onto itself, forming GAM5697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5697 precursor RNA, designated SEQ ID NO: 5966, and a schematic representation of a predicted secondary folding of GAM5697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5697 folded precursor RNA yielding a GAM5697 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5697 RNA, hereby incorporated herein.

GAM5697 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5697 target RNA, herein designated GAM TARGET RNA. GAM5697 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5697 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5697 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5697 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5697 RNA, herein designated GAM RNA, to target binding sites on GAM5697 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5697 target RNA into GAM5697 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5697 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5697 target genes. The mRNA of each one of this plurality of GAM5697 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5697 RNA, herein designated GAM RNA, and which when bound by GAM5697 RNA causes inhibition of translation of the GAM5697 target mRNA into a corresponding GAM5697 target protein.

The mechanism of the translational inhibition exerted by GAM5697 RNA, herein designated GAM RNA, on one or more GAM5697 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5697 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5697 RNA, herein designated GAM RNA, of GAM5697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5697 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5697 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5697 RNA correlate with, and may be deduced from, the identity of the GAM5697 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5703 6311 GACATGTCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCAGGAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCTGATCGA Messenger 5703 (GAM5703) oligonucleotides modulates expression of respective target genes
CCTTAGACTT whose function and utility is known in the art.

GGCAAGCTGG GAM5703 is a novel bioinformatically detectable regulatory, non protein coding, TGGCTAAGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5703 was detected is

CAGTGCTCAC described with additional reference to Figs. 9-15.

TGCCGACATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTC encoded by the human genome.

GAM5703 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5703 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5703 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5703 precursor RNA is designated SEQ ID:6311, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6311 is located from position 32944217 to position 32944300 relative to chromosome 19 on the `-` strand.

GAM5703 precursor RNA folds onto itself, forming GAM5703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5703 precursor RNA, designated SEQ ID NO: 6311, and a schematic representation of a predicted secondary folding of GAM5703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5703 folded precursor RNA yielding a GAM5703 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5703 RNA, hereby incorporated herein.

GAM5703 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5703 target RNA, herein designated GAM TARGET RNA. GAM5703 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5703 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5703 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM5703 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5703 RNA, herein designated GAM RNA, to target binding sites on GAM5703 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5703 target RNA into GAM5703 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5703 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5703 target genes. The mRNA of each one of this plurality of GAM5703 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5703 RNA, herein designated GAM RNA, and which when bound by GAM5703 RNA causes inhibition of translation of the GAM5703 target mRNA into a corresponding GAM5703 target protein.

The mechanism of the translational inhibition exerted by GAM5703 RNA, herein designated GAM RNA, on one or more GAM5703 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5703 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5703 RNA, herein designated GAM RNA, of GAM5703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5703 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5703 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5703 RNA correlate with, and may be deduced from, the identity of the GAM5703 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5728 6174 CTCTCATGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCATGTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address AGCAGCTGCA Messenger 5728 (GAM5728) oligonucleotides modulates expression of respective target genes GGTGTGTGAG whose function and utility is known in the art.

CAAATGTGCA GAM5728 is a novel bioinformatically detectable regulatory, non protein coding, TCACTGGGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5728 was detected is

ACAGGTGTCT described with additional reference to Figs. 9-15.

GTGGATGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene G encoded by the human genome.

GAM5728 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5728 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5728 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5728 precursor RNA is designated SEQ ID:6174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6174 is located from position 79169049 to position 79169129 relative to chromosome 10 on the `+` strand.

GAM5728 precursor RNA folds onto itself, forming GAM5728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5728 precursor RNA, designated SEQ ID NO: 6174, and a schematic representation of a predicted secondary folding of GAM5728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5728 folded precursor RNA yielding a GAM5728 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5728 RNA, hereby incorporated herein.

GAM5728 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5728 target RNA, herein designated GAM TARGET RNA. GAM5728 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5728 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5728 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5728 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5728 RNA, herein designated GAM RNA, to target binding sites on GAM5728 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5728 target RNA into GAM5728 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5728 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5728 target genes. The mRNA of each one of this plurality of GAM5728 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5728 RNA, herein designated GAM RNA, and which when bound by GAM5728 RNA causes inhibition of translation of the GAM5728 target mRNA into a corresponding GAM5728 target protein.

The mechanism of the translational inhibition exerted by GAM5728 RNA, herein designated GAM RNA, on one or more GAM5728 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5728 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5728 RNA, herein designated GAM RNA, of GAM5728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5728 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5728 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5728 RNA correlate with, and may be deduced from, the identity of the GAM5728 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5744 6979 TAGTGTTCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGTTGCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTTTGCTAA Messenger 5744 (GAM5744) oligonucleotides modulates expression of respective target genes
CTGATAAATC whose function and utility is known in the art.

ATTTAATCCT GAM5744 is a novel bioinformatically detectable regulatory, non protein coding,
CTTCTTCATA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5744 was detected is

TGTATGAGTA described with additional reference to Figs. 9-15.

CTATCTTATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTGTGGTCA encoded by the human genome.

AGAGTGAGGT GAM5744 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5744
AAGCAAGCTC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5744
CAACAGACCC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
TGAGAACCTA to the nucleotide sequence of GAM5744 precursor RNA is designated SEQ ID:6979, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6979 is located from position 901080 to position 901209 relative to chromosome 18 on the `+` strand.

GAM5744 precursor RNA folds onto itself, forming GAM5744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5744 precursor RNA, designated SEQ ID NO: 6979, and a schematic representation of a predicted secondary folding of GAM5744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5744 folded precursor RNA yielding a GAM5744 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5744 RNA, hereby incorporated herein.

GAM5744 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5744 target RNA, herein designated GAM TARGET RNA. GAM5744 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5744 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5744 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5744 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5744 RNA, herein designated GAM RNA, to target binding sites on GAM5744 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5744 target RNA into GAM5744 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5744 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5744 target genes. The mRNA of each one of this plurality of GAM5744 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5744 RNA, herein designated GAM RNA, and which when bound by GAM5744 RNA causes inhibition of translation of the GAM5744 target mRNA into a corresponding GAM5744 target protein.

The mechanism of the translational inhibition exerted by GAM5744 RNA, herein designated GAM RNA, on one or more GAM5744 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5744 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5744 RNA, herein designated GAM RNA, of GAM5744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM5744 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5744 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5744 RNA correlate with, and may be deduced from, the identity of the GAM5744 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5749 5824 AGTTCCTATG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCCCCACAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAAGCGCCC Messenger 5749 (GAM5749) oligonucleotides modulates expression of respective target genes
TTAACCACTG whose function and utility is known in the art.

ATGAGTGTTG GAM5749 is a novel bioinformatically detectable regulatory, non protein coding,
ATGTTTTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5749 was detected is

GCACTAGAAG described with additional reference to Figs. 9-15.

GCACTATGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAACT encoded by the human genome.

GAM5749 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5749

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5749
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5749 precursor RNA is designated SEQ ID:5824, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5824 is located from position 18721900 to position 18721984 relative to chromosome 16 on the `-` strand.

GAM5749 precursor RNA folds onto itself, forming GAM5749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5749 precursor RNA, designated SEQ ID NO: 5824, and a schematic representation of a predicted secondary folding of GAM5749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5749 folded precursor RNA yielding a GAM5749 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5749 RNA, hereby incorporated herein.

GAM5749 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5749 target RNA, herein designated GAM TARGET RNA. GAM5749 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5749 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5749 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5749 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5749 RNA, herein designated GAM RNA, to target binding sites on GAM5749 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5749 target RNA into GAM5749 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5749 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5749 target genes. The mRNA of each one of this plurality of GAM5749 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5749 RNA, herein designated GAM RNA, and which when bound by GAM5749 RNA causes inhibition of translation of the GAM5749 target mRNA into a corresponding GAM5749 target protein.

The mechanism of the translational inhibition exerted by GAM5749 RNA, herein designated GAM RNA, on one or more GAM5749 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5749 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5749 RNA, herein designated GAM RNA, of

GAM5749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5749 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5749 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5749 RNA correlate with, and may be deduced from, the identity of the GAM5749 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5764 6586 GGACATCAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATAAATAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGCTCTAA Messenger 5764 (GAM5764) oligonucleotides modulates expression of respective target genes

TTGCCAAGAA whose function and utility is known in the art.

TTCACATGTG GAM5764 is a novel bioinformatically detectable regulatory, non protein coding,

GTTGTATGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5764 was detected is

GCTTTACTGG described with additional reference to Figs. 9-15.

GAGACTGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTATCTGCA encoded by the human genome.

TGTGATTCTG GAM5764 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5764

CTGTGATGGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5764

CACTTGTAAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TTTGTGCC to the nucleotide sequence of GAM5764 precursor RNA is designated SEQ ID:6586, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6586 is located from position 62131098 to position 62131225 relative to chromosome 9 on the `-` strand.

GAM5764 precursor RNA folds onto itself, forming GAM5764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5764 precursor RNA, designated SEQ ID NO: 6586, and a

schematic representation of a predicted secondary folding of GAM5764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5764 folded precursor RNA yielding a GAM5764 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5764 RNA, hereby incorporated herein.

GAM5764 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5764 target RNA, herein designated GAM TARGET RNA. GAM5764 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5764 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5764 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5764 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5764 RNA, herein designated GAM RNA, to target binding sites on GAM5764 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5764 target RNA into GAM5764 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5764 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5764 target genes. The mRNA of each one of this plurality of GAM5764 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5764 RNA, herein designated GAM RNA, and which when bound by GAM5764 RNA causes inhibition of translation of the GAM5764 target mRNA into a corresponding GAM5764 target protein.

The mechanism of the translational inhibition exerted by GAM5764 RNA, herein designated GAM RNA, on one or more GAM5764 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5764 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5764 RNA, herein designated GAM RNA, of GAM5764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5764 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5764 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5764 RNA correlate with, and may be deduced from, the identity of the GAM5764 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5798 6055 CCAGGGAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGTAAGTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TATAGTTATC Messenger 5798 (GAM5798) oligonucleotides modulates expression of respective target genes

TTCTAATTGG whose function and utility is known in the art.

GGCCTAATAT GAM5798 is a novel bioinformatically detectable regulatory, non protein coding,

CCCTACCCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5798 was detected is

CAACAATACA described with additional reference to Figs. 9-15.

ACTTACTACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCACCCTGG encoded by the human genome.

GAM5798 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5798

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5798

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5798 precursor RNA is designated SEQ ID:6055, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6055 is located from position 52222704 to position 52222792 relative to chromosome X on the `+` strand.

GAM5798 precursor RNA folds onto itself, forming GAM5798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5798 precursor RNA, designated SEQ ID NO: 6055, and a schematic representation of a predicted secondary folding of GAM5798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5798 folded precursor RNA yielding a GAM5798 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5798 RNA, hereby incorporated herein.

GAM5798 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5798 target RNA, herein designated GAM TARGET RNA. GAM5798 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5798 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5798 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5798 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5798 RNA, herein designated GAM RNA, to target binding sites on GAM5798 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5798 target RNA into GAM5798 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5798 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5798 target genes. The mRNA of each one of this plurality of GAM5798 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5798 RNA, herein designated GAM RNA, and which when bound by GAM5798 RNA causes inhibition of translation of the GAM5798 target mRNA into a corresponding GAM5798 target protein.

The mechanism of the translational inhibition exerted by GAM5798 RNA, herein

designated GAM RNA, on one or more GAM5798 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5798 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5798 RNA, herein designated GAM RNA, of GAM5798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5798 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5798 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5798 RNA correlate with, and may be deduced from, the identity of the GAM5798 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5800 7280 TGTTCCTCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGTTGTCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
AATAAGTGCA Messenger 5800 (GAM5800) oligonucleotides modulates expression of respective target genes
TCATTACCAA whose function and utility is known in the art.

GTATTACAGC GAM5800 is a novel bioinformatically detectable regulatory, non protein coding,
AGGTACTGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5800 was detected is

TTGCATCAGG described with additional reference to Figs. 9-15.

GCTGCTGACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGTCTGTGG encoded by the human genome.

GCATTGTTAA GAM5800 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5800
GAAACCAATC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5800
TGGGAAACA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5800 precursor RNA is designated SEQ ID:7280, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7280 is located from position 35297121 to position 35297239 relative to chromosome 22

on the `+` strand.

GAM5800 precursor RNA folds onto itself, forming GAM5800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5800 precursor RNA, designated SEQ ID NO: 7280, and a schematic representation of a predicted secondary folding of GAM5800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5800 folded precursor RNA yielding a GAM5800 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5800 RNA, hereby incorporated herein.

GAM5800 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5800 target RNA, herein designated GAM TARGET RNA. GAM5800 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5800 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5800 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5800 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5800 RNA, herein designated GAM RNA, to target binding sites on GAM5800 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5800 target RNA into GAM5800 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5800 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5800 target genes. The mRNA of each one of this plurality of GAM5800 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM5800 RNA, herein designated GAM RNA, and which when bound by GAM5800 RNA causes inhibition of translation of the GAM5800 target mRNA into a corresponding GAM5800 target protein.

The mechanism of the translational inhibition exerted by GAM5800 RNA, herein designated GAM RNA, on one or more GAM5800 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5800 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5800 RNA, herein designated GAM RNA, of GAM5800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5800 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5800 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5800 RNA correlate with, and may be deduced from, the identity of the GAM5800 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5806 7270 TGTGAGCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGGAGTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCCTGAGTC Messenger 5806 (GAM5806) oligonucleotides modulates expression of respective target genes

TGTGGGTCAT whose function and utility is known in the art.

CTAGCACATC GAM5806 is a novel bioinformatically detectable regulatory, non protein coding,

CTTAATAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5806 was detected is

TGATTGCCTG described with additional reference to Figs. 9-15.

GATGTGACCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCTCACCCC encoded by the human genome.

CAACCCTCAC GAM5806 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5806

ACA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5806

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5806 precursor RNA is designated SEQ ID:7270, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7270 is located from position 23608784 to position 23608886 relative to chromosome 16 on the `+` strand.

GAM5806 precursor RNA folds onto itself, forming GAM5806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5806 precursor RNA, designated SEQ ID NO: 7270, and a schematic representation of a predicted secondary folding of GAM5806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5806 folded precursor RNA yielding a GAM5806 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5806 RNA, hereby incorporated herein.

GAM5806 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5806 target RNA, herein designated GAM TARGET RNA. GAM5806 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5806 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5806 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5806 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5806 RNA, herein designated GAM RNA, to target binding sites on GAM5806 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5806 target RNA into GAM5806 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5806 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5806 target genes. The mRNA of each one of this plurality of GAM5806 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5806 RNA, herein designated GAM RNA, and which when bound by GAM5806 RNA causes inhibition of translation of the GAM5806 target mRNA into a corresponding GAM5806 target protein.

The mechanism of the translational inhibition exerted by GAM5806 RNA, herein designated GAM RNA, on one or more GAM5806 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5806 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5806 RNA, herein designated GAM RNA, of GAM5806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5806 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5806 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5806 RNA correlate with, and may be deduced from, the identity of the GAM5806 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5809 7307 TTCTGTCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAATTCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CGTGACTGGG Messenger 5809 (GAM5809) oligonucleotides modulates expression of respective target genes
GCTAAACAAC whose function and utility is known in the art.

TGTCACTGGC GAM5809 is a novel bioinformatically detectable regulatory, non protein coding,
AAGTGACAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5809 was detected is

AGGCACAGAC described with additional reference to Figs. 9-15.

AGCAGGGGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAAAAAGAG encoded by the human genome.

AGAA GAM5809 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5809 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5809 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5809 precursor RNA is designated SEQ ID:7307, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7307 is located from position 114373899 to position 114373992 relative to chromosome 10 on the `+` strand.

GAM5809 precursor RNA folds onto itself, forming GAM5809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5809 precursor RNA, designated SEQ ID NO: 7307, and a schematic representation of a predicted secondary folding of GAM5809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5809 folded precursor RNA yielding a GAM5809 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5809 RNA, hereby incorporated herein.

GAM5809 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5809 target RNA, herein designated GAM TARGET RNA. GAM5809 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5809 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5809 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5809 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5809 RNA, herein designated GAM RNA, to target binding sites on GAM5809 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5809 target RNA into GAM5809 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5809 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5809 target genes. The mRNA of each one of this plurality of GAM5809 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5809 RNA, herein designated GAM RNA, and which when bound by GAM5809 RNA causes inhibition of translation of the GAM5809 target mRNA into a corresponding GAM5809 target protein.

The mechanism of the translational inhibition exerted by GAM5809 RNA, herein designated GAM RNA, on one or more GAM5809 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5809 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5809 RNA, herein designated GAM RNA, of GAM5809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5809 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5809 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5809 RNA correlate with, and may be deduced from, the identity of the GAM5809 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5814 5719 AGACACTGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGACATTG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTCCTTTT Messenger 5814 (GAM5814) oligonucleotides modulates expression of respective target genes
CTCTGCGTCG whose function and utility is known in the art.

AAATGTCAAG GAM5814 is a novel bioinformatically detectable regulatory, non protein coding,
GAAAGTTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5814 was detected is

AGTCTGTGAT described with additional reference to Figs. 9-15.

TTTGTGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM5814 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5814 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5814 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5814 precursor RNA is designated SEQ ID:5719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5719 is located from position 58108888 to position 58108966 relative to chromosome 20 on the `+` strand.

GAM5814 precursor RNA folds onto itself, forming GAM5814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5814 precursor RNA, designated SEQ ID NO: 5719, and a schematic representation of a predicted secondary folding of GAM5814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5814 folded precursor RNA yielding a GAM5814 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5814 RNA, hereby incorporated herein.

GAM5814 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5814 target RNA, herein designated GAM TARGET RNA. GAM5814 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5814 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5814 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5814 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5814 RNA, herein designated GAM RNA, to target binding sites on GAM5814 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5814 target RNA into GAM5814 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5814 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5814 target genes. The mRNA of each one of this plurality of GAM5814 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5814 RNA, herein designated GAM RNA, and which when bound by GAM5814 RNA causes inhibition of translation of the GAM5814 target mRNA into a corresponding GAM5814 target protein.

The mechanism of the translational inhibition exerted by GAM5814 RNA, herein designated GAM RNA, on one or more GAM5814 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5814 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5814 RNA, herein designated GAM RNA, of GAM5814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5814 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5814 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5814 RNA correlate with, and may be deduced from, the identity of the GAM5814 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5823 6964 TAGAAATATG TAATCGATCT TTTCTTTGGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 5823 (GAM5823) oligonucleotides modulates expression of respective target genes

GGGCAATTAG whose function and utility is known in the art.

CAATATTGAG GAM5823 is a novel bioinformatically detectable regulatory, non protein coding, GAAAGTTAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5823 was detected is

GATGTATGTA described with additional reference to Figs. 9-15.

TCCCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5823 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5823

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5823

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5823 precursor RNA is designated SEQ ID:6964, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6964 is located from position 7772036 to position 7772111 relative to chromosome X on the `-` strand.

GAM5823 precursor RNA folds onto itself, forming GAM5823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5823 precursor RNA, designated SEQ ID NO: 6964, and a schematic representation of a predicted secondary folding of GAM5823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5823 folded precursor RNA yielding a GAM5823 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5823 RNA, hereby incorporated herein.

GAM5823 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5823 target RNA, herein designated GAM TARGET RNA. GAM5823 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5823 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5823 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5823 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5823 RNA, herein designated GAM RNA, to target binding sites on GAM5823 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5823 target RNA into GAM5823 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5823 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5823 target genes. The mRNA of each one of this plurality of GAM5823 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5823 RNA, herein designated GAM RNA, and which when bound by GAM5823 RNA causes inhibition of translation of the GAM5823 target mRNA into a corresponding GAM5823 target protein.

The mechanism of the translational inhibition exerted by GAM5823 RNA, herein designated GAM RNA, on one or more GAM5823 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5823 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5823 RNA, herein designated GAM RNA, of GAM5823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5823 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5823 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5823 RNA correlate with, and may be deduced from, the identity of the GAM5823 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5826 6765 GGCTGGGACT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGTCATGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGTCAGGT Messenger 5826 (GAM5826) oligonucleotides modulates expression of respective target genes
TCCAAAGAGC whose function and utility is known in the art.

GCCAGGAAGA GAM5826 is a novel bioinformatically detectable regulatory, non protein coding,
CTCTGAGACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5826 was detected is

ACAGAGCACG described with additional reference to Figs. 9-15.

GCCTGCTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCCAGCC encoded by the human genome.

GAM5826 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5826

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5826
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5826 precursor RNA is designated SEQ ID:6765, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6765 is located from position 492716 to position 492803 relative to chromosome 16 on the `+` strand.

GAM5826 precursor RNA folds onto itself, forming GAM5826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5826 precursor RNA, designated SEQ ID NO: 6765, and a schematic representation of a predicted secondary folding of GAM5826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5826 folded precursor RNA yielding a GAM5826 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5826 RNA, hereby incorporated herein.

GAM5826 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5826 target RNA, herein designated GAM TARGET RNA. GAM5826 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5826 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5826 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5826 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5826 RNA, herein designated GAM RNA, to target binding sites on GAM5826 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5826 target RNA into GAM5826 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5826 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5826 target genes. The mRNA of each one of this plurality of GAM5826 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5826 RNA, herein designated GAM RNA, and which when bound by GAM5826 RNA causes inhibition of translation of the GAM5826 target mRNA into a corresponding GAM5826 target protein.

The mechanism of the translational inhibition exerted by GAM5826 RNA, herein designated GAM RNA, on one or more GAM5826 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5826 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5826 RNA, herein designated GAM RNA, of GAM5826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5826 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5826 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5826 RNA correlate with, and may be deduced from, the identity of the GAM5826 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5836 5829 AGTTTCACTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTCACCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTGGAGTG Messenger 5836 (GAM5836) oligonucleotides modulates expression of respective target genes

CAGTGGTGCC whose function and utility is known in the art.

ATCTTGGCTC GAM5836 is a novel bioinformatically detectable regulatory, non protein coding,

ACTGCAACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5836 was detected is

CCGCCTGCCG described with additional reference to Figs. 9-15.

AGTTCAAGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTCT encoded by the human genome.

GAM5836 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5836

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5836

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5836 precursor RNA is designated SEQ ID:5829, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5829 is located from position 232531653 to position 232531737 relative to chromosome 2 on the `+` strand.

GAM5836 precursor RNA folds onto itself, forming GAM5836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5836 precursor RNA, designated SEQ ID NO: 5829, and a schematic representation of a predicted secondary folding of GAM5836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5836 folded precursor RNA yielding a GAM5836 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5836 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5836 RNA and an

alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5836 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5836 target RNA, herein designated GAM TARGET RNA. GAM5836 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5836 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5836 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5836 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5836 RNA, herein designated GAM RNA, to target binding sites on GAM5836 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5836 target RNA into GAM5836 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5836 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5836 target genes. The mRNA of each one of this plurality of GAM5836 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5836 RNA, herein designated GAM RNA, and which when bound by GAM5836 RNA causes inhibition of translation of the GAM5836 target mRNA into a corresponding GAM5836 target protein.

The mechanism of the translational inhibition exerted by GAM5836 RNA, herein designated GAM RNA, on one or more GAM5836 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5836 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5836 RNA, herein designated GAM RNA, of GAM5836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5836 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5836 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5836 RNA correlate with, and may be deduced from, the identity of the GAM5836 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5859 6447 GAGGGCTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCATTAGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTCGGAGC Messenger 5859 (GAM5859) oligonucleotides modulates expression of respective target genes

TGGGAGAAGT whose function and utility is known in the art.

CCCTGAGCCC GAM5859 is a novel bioinformatically detectable regulatory, non protein coding,

TGAAGGGTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5859 was detected is

TTTGGGCAGT described with additional reference to Figs. 9-15.

ATGTGACAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTC encoded by the human genome.

GAM5859 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5859

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5859

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5859 precursor RNA is designated SEQ ID:6447, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6447 is located from position 120684537 to position 120684620 relative to chromosome 8 on the `+` strand.

GAM5859 precursor RNA folds onto itself, forming GAM5859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5859 precursor RNA, designated SEQ ID NO: 6447, and a schematic representation of a predicted secondary folding of GAM5859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5859 folded precursor RNA

yielding a GAM5859 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5859 RNA, hereby incorporated herein.

GAM5859 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5859 target RNA, herein designated GAM TARGET RNA. GAM5859 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5859 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5859 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5859 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5859 RNA, herein designated GAM RNA, to target binding sites on GAM5859 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5859 target RNA into GAM5859 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5859 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5859 target genes. The mRNA of each one of this plurality of GAM5859 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5859 RNA, herein designated GAM RNA, and which when bound by GAM5859 RNA causes inhibition of translation of the GAM5859 target mRNA into a corresponding GAM5859 target protein.

The mechanism of the translational inhibition exerted by GAM5859 RNA, herein designated GAM RNA, on one or more GAM5859 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5859 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5859 RNA, herein designated GAM RNA, of GAM5859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5859 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5859 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5859 RNA correlate with, and may be deduced from, the identity of the GAM5859 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5868 6037 CATCACCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGTTCTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCAACAGAC Messenger 5868 (GAM5868) oligonucleotides modulates expression of respective target genes

ATGTCCAGTG whose function and utility is known in the art.

GACCGTAGTG GAM5868 is a novel bioinformatically detectable regulatory, non protein coding,

TTGTGACGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5868 was detected is

CGCCCATCTG described with additional reference to Figs. 9-15.

CGCCCAGTAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTCGGATCAT encoded by the human genome.

GCGGAACATG GAM5868 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5868

TTGTCAAAGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5868

TGCAGATTGC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

CTGTGACAAC to the nucleotide sequence of GAM5868 precursor RNA is designated SEQ ID:6037, and is

G provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6037 is located from position 56320934 to position 56321064 relative to chromosome 12 on the `-` strand.

GAM5868 precursor RNA folds onto itself, forming GAM5868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5868 precursor RNA, designated SEQ ID NO: 6037, and a schematic representation of a predicted secondary folding of GAM5868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5868 folded precursor RNA yielding a GAM5868 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5868 RNA, hereby incorporated herein.

GAM5868 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5868 target RNA, herein designated GAM TARGET RNA. GAM5868 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5868 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5868 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5868 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5868 RNA, herein designated GAM RNA, to target binding sites on GAM5868 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5868 target RNA into GAM5868 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5868 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5868 target genes. The mRNA of each one of this plurality of GAM5868 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5868 RNA, herein designated GAM RNA, and which when bound by GAM5868 RNA causes inhibition of translation of the GAM5868 target mRNA into a corresponding GAM5868 target protein.

The mechanism of the translational inhibition exerted by GAM5868 RNA, herein designated GAM RNA, on one or more GAM5868 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5868 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5868 RNA, herein designated GAM RNA, of GAM5868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5868 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5868 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5868 RNA correlate with, and may be deduced from, the identity of the GAM5868 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5872 6941 GTTTAAATGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTATCCGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAATTCCTGT Messenger 5872 (GAM5872) oligonucleotides modulates expression of respective target genes

TGTGTGGAAG whose function and utility is known in the art.

ATGCTTTGCC GAM5872 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTCTTCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5872 was detected is

CTGGAAATCA described with additional reference to Figs. 9-15.

TTTTTCCATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTTAGGTCA encoded by the human genome.

CAGCTTAAAC GAM5872 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5872

ATGATTTTCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5872

CAGGAATTTT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TCTCTGACCA to the nucleotide sequence of GAM5872 precursor RNA is designated SEQ ID:6941, and is

C provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6941 is located from position 78069309 to position 78069439 relative to chromosome 7 on the `+` strand.

GAM5872 precursor RNA folds onto itself, forming GAM5872 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5872 precursor RNA, designated SEQ ID NO: 6941, and a schematic representation of a predicted secondary folding of GAM5872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5872 folded precursor RNA yielding a GAM5872 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5872 RNA, hereby incorporated herein.

GAM5872 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5872 target RNA, herein designated GAM TARGET RNA. GAM5872 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5872 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5872 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5872 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5872 RNA, herein designated GAM RNA, to target binding sites on GAM5872 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5872 target RNA into GAM5872 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5872 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5872 target genes. The mRNA of each one of this plurality of GAM5872 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5872 RNA, herein designated GAM RNA, and which when bound by GAM5872 RNA causes inhibition of translation of the GAM5872 target mRNA into a corresponding GAM5872 target protein.

The mechanism of the translational inhibition exerted by GAM5872 RNA, herein designated GAM RNA, on one or more GAM5872 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5872 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5872 RNA, herein designated GAM RNA, of GAM5872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5872 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5872 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5872 RNA correlate with, and may be deduced from, the identity of the GAM5872 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5874 6244 CTGTGCTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GATAACAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTTTGAGGG Messenger 5874 (GAM5874) oligonucleotides modulates expression of respective target genes

ACAACTTTCA whose function and utility is known in the art.

CATTTGAGTT GAM5874 is a novel bioinformatically detectable regulatory, non protein coding,

TTTCCAAAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5874 was detected is

TAAAGGTTGT described with additional reference to Figs. 9-15.

AGAAGAGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAG encoded by the human genome.

GAM5874 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5874

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5874

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5874 precursor RNA is designated SEQ ID:6244, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6244 is located from position 31954910 to position 31954992 relative to chromosome 21 on the `+` strand.

GAM5874 precursor RNA folds onto itself, forming GAM5874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5874 precursor RNA, designated SEQ ID NO: 6244, and a schematic representation of a predicted secondary folding of GAM5874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5874 folded precursor RNA yielding a GAM5874 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5874 RNA, hereby incorporated herein.

GAM5874 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5874 target RNA, herein designated GAM TARGET RNA. GAM5874 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5874 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5874 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5874 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5874 RNA, herein designated GAM RNA, to target binding sites on GAM5874 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5874 target RNA into GAM5874 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5874 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM5874 target genes. The mRNA of each one of this plurality of GAM5874 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5874 RNA, herein designated GAM RNA, and which when bound by GAM5874 RNA causes inhibition of translation of the GAM5874 target mRNA into a corresponding GAM5874 target protein.

The mechanism of the translational inhibition exerted by GAM5874 RNA, herein designated GAM RNA, on one or more GAM5874 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5874 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5874 RNA, herein designated GAM RNA, of GAM5874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5874 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5874 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5874 RNA correlate with, and may be deduced from, the identity of the GAM5874 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5884 6796 GGGATAGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTTTTGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAGTTTAGA Messenger 5884 (GAM5884) oligonucleotides modulates expression of respective target genes
ACATTTAAAA whose function and utility is known in the art.

TGTGGGAAAT GAM5884 is a novel bioinformatically detectable regulatory, non protein coding,
TCAAATAAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5884 was detected is

ATGCAAATTT described with additional reference to Figs. 9-15.

TCACTGTTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAAAAAGTC encoded by the human genome.

AGATCAACAT GAM5884 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5884

TGCTGGCCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5884 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5884 precursor RNA is designated SEQ ID:6796, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6796 is located from position 65430589 to position 65430697 relative to chromosome 14 on the `+` strand.

GAM5884 precursor RNA folds onto itself, forming GAM5884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5884 precursor RNA, designated SEQ ID NO: 6796, and a schematic representation of a predicted secondary folding of GAM5884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5884 folded precursor RNA yielding a GAM5884 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5884 RNA, hereby incorporated herein.

GAM5884 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5884 target RNA, herein designated GAM TARGET RNA. GAM5884 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5884 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5884 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5884 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5884 RNA, herein designated GAM RNA, to target binding sites on GAM5884 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5884 target RNA

into GAM5884 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5884 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5884 target genes. The mRNA of each one of this plurality of GAM5884 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5884 RNA, herein designated GAM RNA, and which when bound by GAM5884 RNA causes inhibition of translation of the GAM5884 target mRNA into a corresponding GAM5884 target protein.

The mechanism of the translational inhibition exerted by GAM5884 RNA, herein designated GAM RNA, on one or more GAM5884 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5884 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5884 RNA, herein designated GAM RNA, of GAM5884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5884 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5884 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5884 RNA correlate with, and may be deduced from, the identity of the GAM5884 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5886 6772 GGCTTTATCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGCCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTCCTACAT Messenger 5886 (GAM5886) oligonucleotides modulates expression of respective target genes

TATCAACAAA whose function and utility is known in the art.

GTGAGAGTTT GAM5886 is a novel bioinformatically detectable regulatory, non protein coding,

AAGATCTCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5886 was detected is

GGGCAGGAGA described with additional reference to Figs. 9-15.

TTTCAGAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

C encoded by the human genome.

GAM5886 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5886 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5886 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5886 precursor RNA is designated SEQ ID:6772, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6772 is located from position 101743923 to position 101744003 relative to chromosome 10 on the `+` strand.

GAM5886 precursor RNA folds onto itself, forming GAM5886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5886 precursor RNA, designated SEQ ID NO: 6772, and a schematic representation of a predicted secondary folding of GAM5886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5886 folded precursor RNA yielding a GAM5886 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5886 RNA, hereby incorporated herein.

GAM5886 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5886 target RNA, herein designated GAM TARGET RNA. GAM5886 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5886 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5886 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5886 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5886 RNA, herein designated GAM RNA, to target binding sites on GAM5886 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5886 target RNA into GAM5886 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5886 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5886 target genes. The mRNA of each one of this plurality of GAM5886 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5886 RNA, herein designated GAM RNA, and which when bound by GAM5886 RNA causes inhibition of translation of the GAM5886 target mRNA into a corresponding GAM5886 target protein.

The mechanism of the translational inhibition exerted by GAM5886 RNA, herein designated GAM RNA, on one or more GAM5886 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5886 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5886 RNA, herein designated GAM RNA, of GAM5886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5886 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5886 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5886 RNA correlate with, and may be deduced from, the identity of the GAM5886 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5910 7087 TGAATCACTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGAAAACAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGTAATTCA Messenger 5910 (GAM5910) oligonucleotides modulates expression of respective target genes
ACAACCTTGC whose function and utility is known in the art.

TGCTGACCTC GAM5910 is a novel bioinformatically detectable regulatory, non protein coding,
TTATTCAGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM5910 was detected is

AAATGAGAGC described with additional reference to Figs. 9-15.

AAGTGTTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGCTGGTG encoded by the human genome.

GTGGTTCACA GAM5910 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5910

TCAAAATCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5910

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5910 precursor RNA is designated SEQ ID:7087, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7087 is located from position 24156183 to position 24156291 relative to chromosome 22 on the `-` strand.

GAM5910 precursor RNA folds onto itself, forming GAM5910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5910 precursor RNA, designated SEQ ID NO: 7087, and a schematic representation of a predicted secondary folding of GAM5910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5910 folded precursor RNA yielding a GAM5910 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5910 RNA, hereby incorporated herein.

GAM5910 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5910 target RNA, herein designated GAM TARGET RNA. GAM5910 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5910 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5910 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5910 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5910 RNA, herein designated GAM RNA, to target binding sites on GAM5910 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5910 target RNA into GAM5910 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5910 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5910 target genes. The mRNA of each one of this plurality of GAM5910 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5910 RNA, herein designated GAM RNA, and which when bound by GAM5910 RNA causes inhibition of translation of the GAM5910 target mRNA into a corresponding GAM5910 target protein.

The mechanism of the translational inhibition exerted by GAM5910 RNA, herein designated GAM RNA, on one or more GAM5910 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5910 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5910 RNA, herein designated GAM RNA, of GAM5910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5910 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5910 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5910 RNA correlate with, and may be deduced from, the identity of the GAM5910 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5916 6237 CTGTACAAAG CAGCCTTGGA CCAGGAGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 5916 (GAM5916) oligonucleotides modulates expression of respective target genes

AAACCCCAAG whose function and utility is known in the art.

GCTCTGCAGC GAM5916 is a novel bioinformatically detectable regulatory, non protein coding,
CTCCCTGCTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5916 was detected is

CCCTCCGTTT described with additional reference to Figs. 9-15.

AAGGCTGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAG encoded by the human genome.

GAM5916 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5916

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5916

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5916 precursor RNA is designated SEQ ID:6237, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6237 is located from position 3852983 to position 3853066 relative to chromosome 20 on the `+` strand.

GAM5916 precursor RNA folds onto itself, forming GAM5916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5916 precursor RNA, designated SEQ ID NO: 6237, and a schematic representation of a predicted secondary folding of GAM5916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5916 folded precursor RNA yielding a GAM5916 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5916 RNA, hereby incorporated herein.

GAM5916 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5916 target RNA, herein designated GAM TARGET RNA. GAM5916 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5916 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5916 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5916 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5916 RNA, herein designated GAM RNA, to target binding sites on GAM5916 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5916 target RNA into GAM5916 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5916 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5916 target genes. The mRNA of each one of this plurality of GAM5916 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5916 RNA, herein designated GAM RNA, and which when bound by GAM5916 RNA causes inhibition of translation of the GAM5916 target mRNA into a corresponding GAM5916 target protein.

The mechanism of the translational inhibition exerted by GAM5916 RNA, herein designated GAM RNA, on one or more GAM5916 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5916 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5916 RNA, herein designated GAM RNA, of GAM5916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5916 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5916 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5916 RNA correlate with, and may be deduced from, the identity of the GAM5916 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5958 5675 AATGCTGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTATCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCTGCAGGG Messenger 5958 (GAM5958) oligonucleotides modulates expression of respective target genes

GGTAAAGTGT whose function and utility is known in the art.

CATCCTTGGG GAM5958 is a novel bioinformatically detectable regulatory, non protein coding,

AAATTCAAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5958 was detected is

CTGGCCTGTA described with additional reference to Figs. 9-15.

CCTGCTGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCACCAGGGA encoded by the human genome.

TATGGTCACA GAM5958 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5958

TT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5958

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5958 precursor RNA is designated SEQ ID:5675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5675 is located from position 90601847 to position 90601948 relative to chromosome 15 on the `-` strand.

GAM5958 precursor RNA folds onto itself, forming GAM5958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5958 precursor RNA, designated SEQ ID NO: 5675, and a schematic representation of a predicted secondary folding of GAM5958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5958 folded precursor RNA yielding a GAM5958 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5958 RNA, hereby incorporated herein.

GAM5958 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5958 target RNA, herein designated GAM TARGET RNA. GAM5958 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5958 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5958 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5958 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5958 RNA, herein designated GAM RNA, to target binding sites on GAM5958 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5958 target RNA into GAM5958 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5958 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5958 target genes. The mRNA of each one of this plurality of GAM5958 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5958 RNA, herein designated GAM RNA, and which when bound by GAM5958 RNA causes inhibition of translation of the GAM5958 target mRNA into a corresponding GAM5958 target protein.

The mechanism of the translational inhibition exerted by GAM5958 RNA, herein designated GAM RNA, on one or more GAM5958 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5958 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5958 RNA, herein designated GAM RNA, of GAM5958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5958 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5958 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5958 RNA correlate with, and may be deduced from, the identity of the GAM5958 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5963 5672 AAGTGTTCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGAGGACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTAGGTCAGA Messenger 5963 (GAM5963) oligonucleotides modulates expression of respective target genes

CAGAGAAGCT whose function and utility is known in the art.

TTCTCTTTCT GAM5963 is a novel bioinformatically detectable regulatory, non protein coding,

GATGGGAAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5963 was detected is

GTCAAAGTGG described with additional reference to Figs. 9-15.

AAATCTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM5963 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5963

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5963

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5963 precursor RNA is designated SEQ ID:5672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5672 is located from position 126883041 to position 126883119 relative to chromosome X on the `-` strand.

GAM5963 precursor RNA folds onto itself, forming GAM5963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5963 precursor RNA, designated SEQ ID NO: 5672, and a schematic representation of a predicted secondary folding of GAM5963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5963 folded precursor RNA yielding a GAM5963 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5963 RNA, hereby incorporated herein.

GAM5963 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5963 target RNA, herein designated GAM TARGET RNA. GAM5963 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5963 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5963 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5963 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5963 RNA, herein designated GAM RNA, to target binding sites on GAM5963 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5963 target RNA into GAM5963 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5963 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5963 target genes. The mRNA of each one of this plurality of GAM5963 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5963 RNA, herein designated GAM RNA, and which when bound by GAM5963 RNA causes inhibition of translation of the GAM5963 target mRNA into a corresponding GAM5963 target protein.

The mechanism of the translational inhibition exerted by GAM5963 RNA, herein designated GAM RNA, on one or more GAM5963 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5963 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5963 RNA, herein designated GAM RNA, of GAM5963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM5963 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5963 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5963 RNA correlate with, and may be deduced from, the identity of the GAM5963 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5971 6005 CACTGTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGTAAGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAATGTTCT Messenger 5971 (GAM5971) oligonucleotides modulates expression of respective target genes
TTTTCAAAAA whose function and utility is known in the art.

TAGTCTGAGC GAM5971 is a novel bioinformatically detectable regulatory, non protein coding,
CAATTGGATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5971 was detected is

TTTTTGTGGA described with additional reference to Figs. 9-15.

ATATTTTTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATTTGCCCT encoded by the human genome.

GCATGTG GAM5971 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5971
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5971
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5971 precursor RNA is designated SEQ ID:6005, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6005 is located from position 10754212 to position 10754308 relative to chromosome 9 on the `-` strand.

GAM5971 precursor RNA folds onto itself, forming GAM5971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5971 precursor RNA, designated SEQ ID NO: 6005, and a schematic representation of a predicted secondary folding of GAM5971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5971 folded precursor RNA yielding a GAM5971 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5971 RNA, hereby incorporated herein.

GAM5971 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5971 target RNA, herein designated GAM TARGET RNA. GAM5971 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5971 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5971 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5971 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5971 RNA, herein designated GAM RNA, to target binding sites on GAM5971 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5971 target RNA into GAM5971 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5971 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5971 target genes. The mRNA of each one of this plurality of GAM5971 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5971 RNA, herein designated GAM RNA, and which when bound by GAM5971 RNA causes inhibition of translation of the GAM5971 target mRNA into a corresponding GAM5971 target protein.

The mechanism of the translational inhibition exerted by GAM5971 RNA, herein designated GAM RNA, on one or more GAM5971 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5971 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5971 RNA, herein designated GAM RNA, of

GAM5971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5971 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5971 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5971 RNA correlate with, and may be deduced from, the identity of the GAM5971 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5973 7222 TGGAGTATTT Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGAGTGACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAAACAACAG Messenger 5973 (GAM5973) oligonucleotides modulates expression of respective target genes
ATGTTCATAC whose function and utility is known in the art.

TCTGCCAGTT GAM5973 is a novel bioinformatically detectable regulatory, non protein coding,
CTGGAGGTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM5973 was detected is

GAAAGTCCAA described with additional reference to Figs. 9-15.

GATCAGGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGGCAGATT encoded by the human genome.

TGGTTGCTGT GAM5973 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5973
TGGGTTCTCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5973
TCTTGGCTCG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CA to the nucleotide sequence of GAM5973 precursor RNA is designated SEQ ID:7222, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7222 is located from position 42645831 to position 42645952 relative to chromosome 22 on the `+` strand.

GAM5973 precursor RNA folds onto itself, forming GAM5973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5973 precursor RNA, designated SEQ ID NO: 7222, and a schematic representation of a predicted secondary folding of GAM5973 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5973 folded precursor RNA yielding a GAM5973 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5973 RNA, hereby incorporated herein.

GAM5973 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5973 target RNA, herein designated GAM TARGET RNA. GAM5973 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5973 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5973 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5973 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5973 RNA, herein designated GAM RNA, to target binding sites on GAM5973 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5973 target RNA into GAM5973 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5973 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5973 target genes. The mRNA of each one of this plurality of GAM5973 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5973 RNA, herein designated GAM RNA, and which when bound by GAM5973 RNA causes inhibition of translation of the GAM5973 target mRNA into a corresponding GAM5973 target protein.

The mechanism of the translational inhibition exerted by GAM5973 RNA, herein designated GAM RNA, on one or more GAM5973 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5973 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM5973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5973 RNA, herein designated GAM RNA, of GAM5973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5973 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5973 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5973 RNA correlate with, and may be deduced from, the identity of the GAM5973 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5990 7241 TGGGGGCACT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTTCTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTGCTCTTT Messenger 5990 (GAM5990) oligonucleotides modulates expression of respective target genes

CTTCTGGAAA whose function and utility is known in the art.

CATTATTCTG GAM5990 is a novel bioinformatically detectable regulatory, non protein coding,

TTCCTTTGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM5990 was detected is

CATGGGCAAG described with additional reference to Figs. 9-15.

GGTCCTGTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTA encoded by the human genome.

GAM5990 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5990

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5990

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5990 precursor RNA is designated SEQ ID:7241, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7241 is located from position 30850318 to position 30850400 relative to chromosome 6 on the `+` strand.

GAM5990 precursor RNA folds onto itself, forming GAM5990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5990 precursor RNA, designated SEQ ID NO: 7241, and a schematic representation of a predicted secondary folding of GAM5990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5990 folded precursor RNA yielding a GAM5990 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM5990 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5990 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM5990 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5990 target RNA, herein designated GAM TARGET RNA. GAM5990 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5990 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5990 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5990 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5990 RNA, herein designated GAM RNA, to target binding sites on GAM5990 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5990 target RNA into GAM5990 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5990 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5990 target genes. The mRNA of each one of this plurality of GAM5990 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5990 RNA, herein designated GAM RNA, and which when bound by GAM5990 RNA causes inhibition of translation of the GAM5990 target mRNA into a corresponding GAM5990 target protein.

The mechanism of the translational inhibition exerted by GAM5990 RNA, herein

designated GAM RNA, on one or more GAM5990 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5990 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5990 RNA, herein designated GAM RNA, of GAM5990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5990 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5990 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5990 RNA correlate with, and may be deduced from, the identity of the GAM5990 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM5998 6129 CCTTGGCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAGGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTCTTGAG Messenger 5998 (GAM5998) oligonucleotides modulates expression of respective target genes
CCTGAGAAGC whose function and utility is known in the art.

AGAGGTGACA GAM5998 is a novel bioinformatically detectable regulatory, non protein coding,
GTACTGGCCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM5998 was detected is

TGGTTCTTAG described with additional reference to Figs. 9-15.

CAGGGGGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCGGGCAGGG encoded by the human genome.

TAGGGG GAM5998 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM5998
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM5998
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5998 precursor RNA is designated SEQ ID:6129, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6129 is located from position 30012813 to position 30012908 relative to chromosome 16

on the `+` strand.

GAM5998 precursor RNA folds onto itself, forming GAM5998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM5998 precursor RNA, designated SEQ ID NO: 6129, and a schematic representation of a predicted secondary folding of GAM5998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM5998 folded precursor RNA yielding a GAM5998 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM5998 RNA, hereby incorporated herein.

GAM5998 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM5998 target RNA, herein designated GAM TARGET RNA. GAM5998 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM5998 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5998 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5998 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM5998 RNA, herein designated GAM RNA, to target binding sites on GAM5998 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5998 target RNA into GAM5998 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM5998 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM5998 target genes. The mRNA of each one of this plurality of GAM5998 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM5998 RNA, herein designated GAM RNA, and which when bound by GAM5998 RNA causes inhibition of translation of the GAM5998 target mRNA into a corresponding GAM5998 target protein.

The mechanism of the translational inhibition exerted by GAM5998 RNA, herein designated GAM RNA, on one or more GAM5998 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM5998 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM5998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM5998 RNA, herein designated GAM RNA, of GAM5998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM5998 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM5998 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM5998 RNA correlate with, and may be deduced from, the identity of the GAM5998 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6014 6740 GGCATGGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCCTTGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTAATGTTT Messenger 6014 (GAM6014) oligonucleotides modulates expression of respective target genes
GCTAATTTAC whose function and utility is known in the art.

GTGGTACAAG GAM6014 is a novel bioinformatically detectable regulatory, non protein coding,
TGCTCCAGTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6014 was detected is

CGGCC described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM6014 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6014

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6014

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6014 precursor RNA is designated SEQ ID:6740, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6740 is located from position 21850242 to position 21850306 relative to chromosome 9 on the `+` strand.

GAM6014 precursor RNA folds onto itself, forming GAM6014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6014 precursor RNA, designated SEQ ID NO: 6740, and a schematic representation of a predicted secondary folding of GAM6014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6014 folded precursor RNA yielding a GAM6014 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6014 RNA, hereby incorporated herein.

GAM6014 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6014 target RNA, herein designated GAM TARGET RNA. GAM6014 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6014 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6014 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6014 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6014 RNA, herein designated GAM RNA, to target binding sites on GAM6014 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6014 target RNA into GAM6014 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6014 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6014 target genes. The mRNA of each one of this plurality of GAM6014 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6014 RNA, herein designated GAM RNA, and which when bound by GAM6014 RNA causes inhibition of translation of the GAM6014 target mRNA into a corresponding GAM6014 target protein.

The mechanism of the translational inhibition exerted by GAM6014 RNA, herein designated GAM RNA, on one or more GAM6014 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6014 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6014 RNA, herein designated GAM RNA, of GAM6014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6014 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6014 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6014 RNA correlate with, and may be deduced from, the identity of the GAM6014 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6024 6285 GAAATGTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATTAAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGTAGTGAG Messenger 6024 (GAM6024) oligonucleotides modulates expression of respective target genes

GCTGGCATTT whose function and utility is known in the art.

ATAGAATCTG GAM6024 is a novel bioinformatically detectable regulatory, non protein coding,

GCTTTCTTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6024 was detected is

ATTGGGTGGA described with additional reference to Figs. 9-15.

AAGCTAGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAACCAGTTT encoded by the human genome.

CTCTCAGCCT GAM6024 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6024
TTTCTCTCCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6024
CAGGTC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6024 precursor RNA is designated SEQ ID:6285, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6285 is located from position 116757829 to position 116757944 relative to chromosome 9 on the `-` strand.

GAM6024 precursor RNA folds onto itself, forming GAM6024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6024 precursor RNA, designated SEQ ID NO: 6285, and a schematic representation of a predicted secondary folding of GAM6024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6024 folded precursor RNA yielding a GAM6024 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6024 RNA, hereby incorporated herein.

GAM6024 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6024 target RNA, herein designated GAM TARGET RNA. GAM6024 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6024 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6024 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6024 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6024 RNA, herein designated GAM RNA, to target binding sites on GAM6024 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6024 target RNA into GAM6024 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6024 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6024 target genes. The mRNA of each one of this plurality of GAM6024 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6024 RNA, herein designated GAM RNA, and which when bound by GAM6024 RNA causes inhibition of translation of the GAM6024 target mRNA into a corresponding GAM6024 target protein.

The mechanism of the translational inhibition exerted by GAM6024 RNA, herein designated GAM RNA, on one or more GAM6024 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6024 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6024 RNA, herein designated GAM RNA, of GAM6024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6024 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6024 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6024 RNA correlate with, and may be deduced from, the identity of the GAM6024 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6051 5706 ACTCTTGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCCTCCACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGAGGACG Messenger 6051 (GAM6051) oligonucleotides modulates expression of respective target genes
TTTCCTGACA whose function and utility is known in the art.

CATTCAACAG GAM6051 is a novel bioinformatically detectable regulatory, non protein coding,
CATCAGCGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6051 was detected is

CAATCAGGAG described with additional reference to Figs. 9-15.

GGAGCTCAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGT encoded by the human genome.

GAM6051 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6051 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6051 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6051 precursor RNA is designated SEQ ID:5706, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5706 is located from position 62941952 to position 62942035 relative to chromosome 14 on the `-` strand.

GAM6051 precursor RNA folds onto itself, forming GAM6051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6051 precursor RNA, designated SEQ ID NO: 5706, and a schematic representation of a predicted secondary folding of GAM6051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6051 folded precursor RNA yielding a GAM6051 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6051 RNA, hereby incorporated herein.

GAM6051 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6051 target RNA, herein designated GAM TARGET RNA. GAM6051 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6051 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6051 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6051 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6051 RNA, herein designated GAM RNA, to target binding sites on GAM6051 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6051 target RNA into GAM6051 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6051 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6051 target genes. The mRNA of each one of this plurality of GAM6051 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6051 RNA, herein designated GAM RNA, and which when bound by GAM6051 RNA causes inhibition of translation of the GAM6051 target mRNA into a corresponding GAM6051 target protein.

The mechanism of the translational inhibition exerted by GAM6051 RNA, herein designated GAM RNA, on one or more GAM6051 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6051 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6051 RNA, herein designated GAM RNA, of GAM6051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6051 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6051 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6051 RNA correlate with, and may be deduced from, the identity of the GAM6051 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6055 6917 GTGGGTGGTG CAGGGGTGGT CTTAGGAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 6055 (GAM6055) oligonucleotides modulates expression of respective target genes

CTTTCCTGAA whose function and utility is known in the art.

GGAGTGGCCA GAM6055 is a novel bioinformatically detectable regulatory, non protein coding, GGGTTCACCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6055 was detected is

ATCTTTCCAC described with additional reference to Figs. 9-15.

CCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6055 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6055

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6055

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6055 precursor RNA is designated SEQ ID:6917, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6917 is located from position 43546131 to position 43546204 relative to chromosome 19 on the `+` strand.

GAM6055 precursor RNA folds onto itself, forming GAM6055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6055 precursor RNA, designated SEQ ID NO: 6917, and a schematic representation of a predicted secondary folding of GAM6055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6055 folded precursor RNA yielding a GAM6055 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6055 RNA, hereby incorporated herein.

GAM6055 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6055 target RNA, herein designated GAM TARGET RNA. GAM6055 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6055 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6055 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6055 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6055 RNA, herein designated GAM RNA, to target binding sites on GAM6055 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6055 target RNA into GAM6055 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6055 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6055 target genes. The mRNA of each one of this plurality of GAM6055 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6055 RNA, herein designated GAM RNA, and which when bound by GAM6055 RNA causes inhibition of translation of the GAM6055 target mRNA into a corresponding GAM6055 target protein.

The mechanism of the translational inhibition exerted by GAM6055 RNA, herein designated GAM RNA, on one or more GAM6055 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6055 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6055 RNA, herein designated GAM RNA, of GAM6055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6055 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6055 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6055 RNA correlate with, and may be deduced from, the identity of the GAM6055 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6083 5994 CACCCCGTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGTAACACG detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCCTGAGGT Messenger 6083 (GAM6083) oligonucleotides modulates expression of respective target genes
CAGCAGTAGA whose function and utility is known in the art.

GGACCAGTAT GAM6083 is a novel bioinformatically detectable regulatory, non protein coding,
TGGTTTTGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6083 was detected is

CCCAGCCTCT described with additional reference to Figs. 9-15.

GCGTGGATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTG encoded by the human genome.

GAM6083 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6083

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6083
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6083 precursor RNA is designated SEQ ID:5994, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5994 is located from position 69517032 to position 69517115 relative to chromosome 11 on the `-` strand.

GAM6083 precursor RNA folds onto itself, forming GAM6083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6083 precursor RNA, designated SEQ ID NO: 5994, and a schematic representation of a predicted secondary folding of GAM6083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6083 folded precursor RNA yielding a GAM6083 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6083 RNA, hereby incorporated herein.

GAM6083 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6083 target RNA, herein designated GAM TARGET RNA. GAM6083 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6083 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6083 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6083 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6083 RNA, herein designated GAM RNA, to target binding sites on GAM6083 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6083 target RNA into GAM6083 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6083 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6083 target genes. The mRNA of each one of this plurality of GAM6083 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6083 RNA, herein designated GAM RNA, and which when bound by GAM6083 RNA causes inhibition of translation of the GAM6083 target mRNA into a corresponding GAM6083 target protein.

The mechanism of the translational inhibition exerted by GAM6083 RNA, herein designated GAM RNA, on one or more GAM6083 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6083 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6083 RNA, herein designated GAM RNA, of GAM6083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6083 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6083 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6083 RNA correlate with, and may be deduced from, the identity of the GAM6083 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6102 7225 TGGCCATGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGTGGCTCG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACTGTAAT Messenger 6102 (GAM6102) oligonucleotides modulates expression of respective target genes
CTCAGCACTT whose function and utility is known in the art.

TCGGAAGCCA GAM6102 is a novel bioinformatically detectable regulatory, non protein coding,
AGGCGGTCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6102 was detected is

ATCACCTGAG described with additional reference to Figs. 9-15.

GTCAGGAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAGACCAGT encoded by the human genome.

CTGGCCA GAM6102 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6102
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6102
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6102 precursor RNA is designated SEQ ID:7225, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7225 is located from position 43773501 to position 43773597 relative to chromosome 7 on the `+` strand.

GAM6102 precursor RNA folds onto itself, forming GAM6102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6102 precursor RNA, designated SEQ ID NO: 7225, and a schematic representation of a predicted secondary folding of GAM6102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6102 folded precursor RNA yielding a GAM6102 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6102 RNA, hereby incorporated herein.

GAM6102 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6102 target RNA, herein designated GAM TARGET RNA. GAM6102 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6102 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6102 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6102 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6102 RNA, herein designated GAM RNA, to target binding sites on GAM6102 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6102 target RNA into GAM6102 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6102 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6102 target genes. The mRNA of each one of this plurality of GAM6102 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6102 RNA, herein designated GAM RNA, and which when bound by GAM6102 RNA causes inhibition of translation of the GAM6102 target mRNA into a corresponding GAM6102 target protein.

The mechanism of the translational inhibition exerted by GAM6102 RNA, herein designated GAM RNA, on one or more GAM6102 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6102 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6102 RNA, herein designated GAM RNA, of GAM6102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM6102 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6102 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6102 RNA correlate with, and may be deduced from, the identity of the GAM6102 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6121 6203 CTGAGGCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAAATTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAACCCAGG Messenger 6121 (GAM6121) oligonucleotides modulates expression of respective target genes
AGGTAGAGGT whose function and utility is known in the art.

TGCAGTGAGT GAM6121 is a novel bioinformatically detectable regulatory, non protein coding,
CAAGATCATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6121 was detected is

CCATTGCACT described with additional reference to Figs. 9-15.

CCAACCTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGACAAGAGC encoded by the human genome.

AAAACTCTGT GAM6121 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6121
CTCAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6121

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6121 precursor RNA is designated SEQ ID:6203, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6203 is located from position 182463 to position 182567 relative to chromosome 18 on the `+` strand.

GAM6121 precursor RNA folds onto itself, forming GAM6121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6121 precursor RNA, designated SEQ ID NO: 6203, and a schematic representation of a predicted secondary folding of GAM6121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6121 folded precursor RNA yielding a GAM6121 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6121 RNA, hereby incorporated herein.

GAM6121 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6121 target RNA, herein designated GAM TARGET RNA. GAM6121 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6121 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6121 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6121 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6121 RNA, herein designated GAM RNA, to target binding sites on GAM6121 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6121 target RNA into GAM6121 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6121 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6121 target genes. The mRNA of each one of this plurality of GAM6121 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6121 RNA, herein designated GAM RNA, and which when bound by GAM6121 RNA causes inhibition of translation of the GAM6121 target mRNA into a corresponding GAM6121 target protein.

The mechanism of the translational inhibition exerted by GAM6121 RNA, herein designated GAM RNA, on one or more GAM6121 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6121 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6121 RNA, herein designated GAM RNA, of

GAM6121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6121 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6121 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6121 RNA correlate with, and may be deduced from, the identity of the GAM6121 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6161 7237 TGGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAAGCATGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCACACCAGG Messenger 6161 (GAM6161) oligonucleotides modulates expression of respective target genes

TGCCCAGACA whose function and utility is known in the art.

TCTGGTTGGC GAM6161 is a novel bioinformatically detectable regulatory, non protein coding,

TTTGGCTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6161 was detected is

TTGTCCTGCA described with additional reference to Figs. 9-15.

GGCACCTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGTCTGGAT encoded by the human genome.

TTGCACACTT GAM6161 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6161

TCCAAGTTGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6161

CCA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6161 precursor RNA is designated SEQ ID:7237, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7237 is located from position 28205840 to position 28205952 relative to chromosome 15 on the `-` strand.

GAM6161 precursor RNA folds onto itself, forming GAM6161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6161 precursor RNA, designated SEQ ID NO: 7237, and a schematic representation of a predicted secondary folding of GAM6161 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6161 folded precursor RNA yielding a GAM6161 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6161 RNA, hereby incorporated herein.

GAM6161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6161 target RNA, herein designated GAM TARGET RNA. GAM6161 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6161 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6161 RNA, herein designated GAM RNA, to target binding sites on GAM6161 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6161 target RNA into GAM6161 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6161 target genes. The mRNA of each one of this plurality of GAM6161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6161 RNA, herein designated GAM RNA, and which when bound by GAM6161 RNA causes inhibition of translation of the GAM6161 target mRNA into a corresponding GAM6161 target protein.

The mechanism of the translational inhibition exerted by GAM6161 RNA, herein designated GAM RNA, on one or more GAM6161 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6161 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM6161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6161 RNA, herein designated GAM RNA, of GAM6161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6161 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6161 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6161 RNA correlate with, and may be deduced from, the identity of the GAM6161 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6172 7032 TCCCTGACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CACCTTTACT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGAAGTCTA Messenger 6172 (GAM6172) oligonucleotides modulates expression of respective target genes

AGGAACAGAC whose function and utility is known in the art.

TGTTTAACCT GAM6172 is a novel bioinformatically detectable regulatory, non protein coding,

GTTTCCAGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6172 was detected is

GTTTCAGGGA described with additional reference to Figs. 9-15.

CTTCTGTATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGTGTAGCA encoded by the human genome.

AGGA GAM6172 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6172

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6172

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6172 precursor RNA is designated SEQ ID:7032, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7032 is located from position 73791102 to position 73791195 relative to chromosome 13 on the `-` strand.

GAM6172 precursor RNA folds onto itself, forming GAM6172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6172 precursor RNA, designated SEQ ID NO: 7032, and a schematic representation of a predicted secondary folding of GAM6172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6172 folded precursor RNA yielding a GAM6172 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6172 RNA, hereby incorporated herein.

GAM6172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6172 target RNA, herein designated GAM TARGET RNA. GAM6172 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6172 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6172 RNA, herein designated GAM RNA, to target binding sites on GAM6172 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6172 target RNA into GAM6172 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6172 target genes. The mRNA of each one of this plurality of GAM6172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6172 RNA, herein designated GAM RNA, and which when bound by GAM6172 RNA causes inhibition of translation of the GAM6172 target mRNA into a corresponding GAM6172 target protein.

The mechanism of the translational inhibition exerted by GAM6172 RNA, herein designated GAM RNA, on one or more GAM6172 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6172 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6172 RNA, herein designated GAM RNA, of GAM6172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6172 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6172 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6172 RNA correlate with, and may be deduced from, the identity of the GAM6172 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6234 7305 TTCTGAACTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGCCAGATC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTAACCTGCT Messenger 6234 (GAM6234) oligonucleotides modulates expression of respective target genes

GGTAAAGCAC whose function and utility is known in the art.

TGGCTGAGGG GAM6234 is a novel bioinformatically detectable regulatory, non protein coding,

TTTAGACTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6234 was detected is

CAAGGAATTT described with additional reference to Figs. 9-15.

GAGGTTGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCCTGCCTT encoded by the human genome.

ATTGCAACCC GAM6234 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6234

AGTGTCTGGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6234

TGCTGAGACC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

AGAG to the nucleotide sequence of GAM6234 precursor RNA is designated SEQ ID:7305, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7305 is located from position 80342962 to position 80343085 relative to chromosome 10

on the `+` strand.

GAM6234 precursor RNA folds onto itself, forming GAM6234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6234 precursor RNA, designated SEQ ID NO: 7305, and a schematic representation of a predicted secondary folding of GAM6234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6234 folded precursor RNA yielding a GAM6234 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6234 RNA, hereby incorporated herein.

GAM6234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6234 target RNA, herein designated GAM TARGET RNA. GAM6234 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6234 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6234 RNA, herein designated GAM RNA, to target binding sites on GAM6234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6234 target RNA into GAM6234 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6234 target genes. The mRNA of each one of this plurality of GAM6234 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM6234 RNA, herein designated GAM RNA, and which when bound by GAM6234 RNA causes inhibition of translation of the GAM6234 target mRNA into a corresponding GAM6234 target protein.

The mechanism of the translational inhibition exerted by GAM6234 RNA, herein designated GAM RNA, on one or more GAM6234 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6234 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6234 RNA, herein designated GAM RNA, of GAM6234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6234 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6234 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6234 RNA correlate with, and may be deduced from, the identity of the GAM6234 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6250 7345 TTTGCGCTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAAAGGCAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGATATAAA Messenger 6250 (GAM6250) oligonucleotides modulates expression of respective target genes

TTAGAACTCT whose function and utility is known in the art.

TCTGAATGGG GAM6250 is a novel bioinformatically detectable regulatory, non protein coding,

CCTTCTATAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6250 was detected is

TTAAATGGGC described with additional reference to Figs. 9-15.

TTTTTCTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGTGTATAT encoded by the human genome.

TTGTAAACTT GAM6250 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6250

GTCTTGAATG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6250

GAAAAAA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6250 precursor RNA is designated SEQ ID:7345, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7345 is located from position 36468581 to position 36468697 relative to chromosome 20 on the `+` strand.

GAM6250 precursor RNA folds onto itself, forming GAM6250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6250 precursor RNA, designated SEQ ID NO: 7345, and a schematic representation of a predicted secondary folding of GAM6250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6250 folded precursor RNA yielding a GAM6250 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6250 RNA, hereby incorporated herein.

GAM6250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6250 target RNA, herein designated GAM TARGET RNA. GAM6250 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6250 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6250 RNA, herein designated GAM RNA, to target binding sites on GAM6250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6250 target RNA into GAM6250 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6250 target genes. The mRNA of each one of this plurality of GAM6250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6250 RNA, herein designated GAM RNA, and which when bound by GAM6250 RNA causes inhibition of translation of the GAM6250 target mRNA into a corresponding GAM6250 target protein.

The mechanism of the translational inhibition exerted by GAM6250 RNA, herein designated GAM RNA, on one or more GAM6250 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6250 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6250 RNA, herein designated GAM RNA, of GAM6250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6250 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6250 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6250 RNA correlate with, and may be deduced from, the identity of the GAM6250 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6265 7349 TTTTGAGATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTATTGAGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTACTAATCT Messenger 6265 (GAM6265) oligonucleotides modulates expression of respective target genes

TGACATATTT whose function and utility is known in the art.

TGGTTGGCAC GAM6265 is a novel bioinformatically detectable regulatory, non protein coding,

CACATTCTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6265 was detected is

GTATAGTGGG described with additional reference to Figs. 9-15.

TTAGTGGTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AATAGTTTGC encoded by the human genome.

AGACTTTGTG GAM6265 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6265 AAACAAAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6265 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6265 precursor RNA is designated SEQ ID:7349, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7349 is located from position 78004551 to position 78004658 relative to chromosome 9 on the `+` strand.

GAM6265 precursor RNA folds onto itself, forming GAM6265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6265 precursor RNA, designated SEQ ID NO: 7349, and a schematic representation of a predicted secondary folding of GAM6265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6265 folded precursor RNA yielding a GAM6265 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6265 RNA, hereby incorporated herein.

GAM6265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6265 target RNA, herein designated GAM TARGET RNA. GAM6265 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6265 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6265 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6265 RNA, herein designated GAM RNA, to target binding sites on GAM6265 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6265 target RNA into GAM6265 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6265 target genes. The mRNA of each one of this plurality of GAM6265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6265 RNA, herein designated GAM RNA, and which when bound by GAM6265 RNA causes inhibition of translation of the GAM6265 target mRNA into a corresponding GAM6265 target protein.

The mechanism of the translational inhibition exerted by GAM6265 RNA, herein designated GAM RNA, on one or more GAM6265 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6265 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6265 RNA, herein designated GAM RNA, of GAM6265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6265 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6265 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6265 RNA correlate with, and may be deduced from, the identity of the GAM6265 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6271 6477 GATTCAAAGC AAGATGGTAG CATTGGAGAG GATGAGATAT GGTCAGATGA GGATATATTT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 6271 (GAM6271) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM6271 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM6271 was detected is

TAAAAGTTGA described with additional reference to Figs. 9-15.

GCTAACAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGCTGAGG encoded by the human genome.

AATC GAM6271 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6271 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6271 precursor RNA is designated SEQ ID:6477, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6477 is located from position 133099410 to position 133099503 relative to chromosome 7 on the `+` strand.

GAM6271 precursor RNA folds onto itself, forming GAM6271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6271 precursor RNA, designated SEQ ID NO: 6477, and a schematic representation of a predicted secondary folding of GAM6271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6271 folded precursor RNA yielding a GAM6271 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6271 RNA, hereby incorporated herein.

GAM6271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6271 target RNA, herein designated GAM TARGET RNA. GAM6271 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6271 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6271 RNA, herein designated GAM RNA, to target binding sites on GAM6271 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6271 target RNA into GAM6271 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6271 target genes. The mRNA of each one of this plurality of GAM6271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6271 RNA, herein designated GAM RNA, and which when bound by GAM6271 RNA causes inhibition of translation of the GAM6271 target mRNA into a corresponding GAM6271 target protein.

The mechanism of the translational inhibition exerted by GAM6271 RNA, herein designated GAM RNA, on one or more GAM6271 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6271 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6271 RNA, herein designated GAM RNA, of GAM6271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6271 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6271 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6271 RNA correlate with, and may be deduced from, the identity of the GAM6271 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6296 7034 TCCCTTCAGA GCCCATGGGT TTCCCATTCC Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 6296 (GAM6296) oligonucleotides modulates expression of respective target genes

CTCCTGTCAG whose function and utility is known in the art.

CCCTGGCCAT GAM6296 is a novel bioinformatically detectable regulatory, non protein coding, GAAATCCTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6296 was detected is

GGATCTGGAG described with additional reference to Figs. 9-15.

GGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6296 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6296

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6296

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6296 precursor RNA is designated SEQ ID:7034, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7034 is located from position 40099114 to position 40099186 relative to chromosome 17 on the `-` strand.

GAM6296 precursor RNA folds onto itself, forming GAM6296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6296 precursor RNA, designated SEQ ID NO: 7034, and a schematic representation of a predicted secondary folding of GAM6296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6296 folded precursor RNA yielding a GAM6296 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6296 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6296 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6296 target RNA, herein designated GAM TARGET RNA. GAM6296 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6296 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM6296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6296 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6296 RNA, herein designated GAM RNA, to target binding sites on GAM6296 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6296 target RNA into GAM6296 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6296 target genes. The mRNA of each one of this plurality of GAM6296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6296 RNA, herein designated GAM RNA, and which when bound by GAM6296 RNA causes inhibition of translation of the GAM6296 target mRNA into a corresponding GAM6296 target protein.

The mechanism of the translational inhibition exerted by GAM6296 RNA, herein designated GAM RNA, on one or more GAM6296 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6296 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6296 RNA, herein designated GAM RNA, of GAM6296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6296 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6296 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6296 RNA correlate with, and may be deduced from, the identity of the GAM6296 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6306 7263 TGTCCCTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGCTGTGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTGTTCAA Messenger 6306 (GAM6306) oligonucleotides modulates expression of respective target genes

ACTCAGGCCT whose function and utility is known in the art.

GTGTGACTCC GAM6306 is a novel bioinformatically detectable regulatory, non protein coding,

ATTGGGGTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6306 was detected is

GAGGTGAAAG described with additional reference to Figs. 9-15.

CATAACATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTACAGAGGG encoded by the human genome.

GACA GAM6306 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6306 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6306 precursor RNA is designated SEQ ID:7263, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7263 is located from position 56453736 to position 56453829 relative to chromosome 12 on the `-` strand.

GAM6306 precursor RNA folds onto itself, forming GAM6306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6306 precursor RNA, designated SEQ ID NO: 7263, and a schematic representation of a predicted secondary folding of GAM6306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6306 folded precursor RNA yielding a GAM6306 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6306 RNA, hereby incorporated herein.

GAM6306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6306 target RNA, herein designated GAM TARGET RNA. GAM6306 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6306 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6306 RNA, herein designated GAM RNA, to target binding sites on GAM6306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6306 target RNA into GAM6306 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6306 target genes. The mRNA of each one of this plurality of GAM6306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6306 RNA, herein designated GAM RNA, and which when bound by GAM6306 RNA causes inhibition of translation of the GAM6306 target mRNA into a corresponding GAM6306 target protein.

The mechanism of the translational inhibition exerted by GAM6306 RNA, herein designated GAM RNA, on one or more GAM6306 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6306 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6306 RNA, herein designated GAM RNA, of GAM6306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6306 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6306 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6306 RNA correlate with, and may be deduced from, the identity of the GAM6306 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6329 6903 GTGCAGTACA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGACAGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTGACAAGT Messenger 6329 (GAM6329) oligonucleotides modulates expression of respective target genes
TCCATCCATA whose function and utility is known in the art.

CCATGGAAGA GAM6329 is a novel bioinformatically detectable regulatory, non protein coding,
GGGTTAAACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6329 was detected is

TGTGGCTGTT described with additional reference to Figs. 9-15.

TTTGCCACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAT encoded by the human genome.

GAM6329 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6329

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6329
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6329 precursor RNA is designated SEQ ID:6903, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6903 is located from position 26729102 to position 26729184 relative to chromosome 11 on the `-` strand.

GAM6329 precursor RNA folds onto itself, forming GAM6329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6329 precursor RNA, designated SEQ ID NO: 6903, and a schematic representation of a predicted secondary folding of GAM6329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6329 folded precursor RNA yielding a GAM6329 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM6329 RNA, hereby incorporated herein.

GAM6329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6329 target RNA, herein designated GAM TARGET RNA. GAM6329 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6329 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6329 RNA, herein designated GAM RNA, to target binding sites on GAM6329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6329 target RNA into GAM6329 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6329 target genes. The mRNA of each one of this plurality of GAM6329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6329 RNA, herein designated GAM RNA, and which when bound by GAM6329 RNA causes inhibition of translation of the GAM6329 target mRNA into a corresponding GAM6329 target protein.

The mechanism of the translational inhibition exerted by GAM6329 RNA, herein designated GAM RNA, on one or more GAM6329 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6329 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6329 RNA, herein designated GAM RNA, of GAM6329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6329 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6329 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6329 RNA correlate with, and may be deduced from, the identity of the GAM6329 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6361 6488 GCAGCAGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGCCAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGCCGGGCC Messenger 6361 (GAM6361) oligonucleotides modulates expression of respective target genes

TGGGGCCTGG whose function and utility is known in the art.

TGTCCGACCG GAM6361 is a novel bioinformatically detectable regulatory, non protein coding,

CAGCCCAGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6361 was detected is

CCCCTCATCG described with additional reference to Figs. 9-15.

CCTGACACTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCCTCTGC encoded by the human genome.

GAM6361 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6361

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6361

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6361 precursor RNA is designated SEQ ID:6488, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6488 is located from position 77134484 to position 77134572 relative to chromosome 17 on the `-` strand.

GAM6361 precursor RNA folds onto itself, forming GAM6361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6361 precursor RNA, designated SEQ ID NO: 6488, and a schematic representation of a predicted secondary folding of GAM6361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6361 folded precursor RNA

yielding a GAM6361 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6361 RNA, hereby incorporated herein.

GAM6361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6361 target RNA, herein designated GAM TARGET RNA. GAM6361 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6361 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6361 RNA, herein designated GAM RNA, to target binding sites on GAM6361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6361 target RNA into GAM6361 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6361 target genes. The mRNA of each one of this plurality of GAM6361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6361 RNA, herein designated GAM RNA, and which when bound by GAM6361 RNA causes inhibition of translation of the GAM6361 target mRNA into a corresponding GAM6361 target protein.

The mechanism of the translational inhibition exerted by GAM6361 RNA, herein designated GAM RNA, on one or more GAM6361 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6361 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6361 RNA, herein designated GAM RNA, of GAM6361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6361 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6361 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6361 RNA correlate with, and may be deduced from, the identity of the GAM6361 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6366 5733 AGAGTATACC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTGCCCGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTGTAGCT Messenger 6366 (GAM6366) oligonucleotides modulates expression of respective target genes

CATGCCTGTA whose function and utility is known in the art.

ATCCCACCAC GAM6366 is a novel bioinformatically detectable regulatory, non protein coding,

TTTGGGAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6366 was detected is

CAAGGCGGGT described with additional reference to Figs. 9-15.

GGATCATTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGGTTAGTAG encoded by the human genome.

TTTGAGACCA GAM6366 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6366

GCTTGGCCAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6366

CATGGGGAAA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

CTCT to the nucleotide sequence of GAM6366 precursor RNA is designated SEQ ID:5733, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5733 is located from position 102138768 to position 102138891 relative to chromosome 14 on the `+` strand.

GAM6366 precursor RNA folds onto itself, forming GAM6366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6366 precursor RNA, designated SEQ ID NO: 5733, and a schematic representation of a predicted secondary folding of GAM6366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6366 folded precursor RNA yielding a GAM6366 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6366 RNA, hereby incorporated herein.

GAM6366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6366 target RNA, herein designated GAM TARGET RNA. GAM6366 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6366 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6366 RNA, herein designated GAM RNA, to target binding sites on GAM6366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6366 target RNA into GAM6366 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6366 target genes. The mRNA of each one of this plurality of GAM6366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6366 RNA, herein designated GAM RNA, and which when bound by GAM6366 RNA causes inhibition of translation of the GAM6366 target mRNA into a corresponding GAM6366 target protein.

The mechanism of the translational inhibition exerted by GAM6366 RNA, herein designated GAM RNA, on one or more GAM6366 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6366 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6366 RNA, herein designated GAM RNA, of GAM6366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6366 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6366 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6366 RNA correlate with, and may be deduced from, the identity of the GAM6366 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6388 6256 CTTCTTGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCAGTGTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCTGATTGC Messenger 6388 (GAM6388) oligonucleotides modulates expression of respective target genes

CCCAGTCTAG whose function and utility is known in the art.

TTTATCGCAA GAM6388 is a novel bioinformatically detectable regulatory, non protein coding,

GGGAATTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6388 was detected is

TTGCGGGGCA described with additional reference to Figs. 9-15.

GTGAGCTCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTGGCAGA encoded by the human genome.

AG GAM6388 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6388

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6388

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6388 precursor RNA is designated SEQ ID:6256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6256 is located from position 9805117 to position 9805208 relative to chromosome 8 on the `+` strand.

GAM6388 precursor RNA folds onto itself, forming GAM6388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6388 precursor RNA, designated SEQ ID NO: 6256, and a schematic representation of a predicted secondary folding of GAM6388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6388 folded precursor RNA yielding a GAM6388 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6388 RNA, hereby incorporated herein.

GAM6388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6388 target RNA, herein designated GAM TARGET RNA. GAM6388 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6388 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6388 RNA, herein designated GAM RNA, to target binding sites on GAM6388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6388 target RNA into GAM6388 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6388 target genes. The mRNA of each one of this plurality of GAM6388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6388 RNA, herein designated GAM RNA, and which when bound by GAM6388 RNA causes inhibition of translation of the GAM6388 target mRNA into a corresponding GAM6388 target protein.

The mechanism of the translational inhibition exerted by GAM6388 RNA, herein designated GAM RNA, on one or more GAM6388 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6388 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6388 RNA, herein designated GAM RNA, of GAM6388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6388 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6388 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6388 RNA correlate with, and may be deduced from, the identity of the GAM6388 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6414 6948 GTTTTGAAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGCGGTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGCCAGAGG Messenger 6414 (GAM6414) oligonucleotides modulates expression of respective target genes
ATGTGTGGGA whose function and utility is known in the art.

GGGGTTTCTC GAM6414 is a novel bioinformatically detectable regulatory, non protein coding,
TAACACTGAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6414 was detected is

TTCTATTCCA described with additional reference to Figs. 9-15.

TGAGCTTTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGGC encoded by the human genome.

GAM6414 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6414

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6414

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6414 precursor RNA is designated SEQ ID:6948, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6948 is located from position 98886813 to position 98886898 relative to chromosome 10 on the `+` strand.

GAM6414 precursor RNA folds onto itself, forming GAM6414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6414 precursor RNA, designated SEQ ID NO: 6948, and a schematic representation of a predicted secondary folding of GAM6414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6414 folded precursor RNA yielding a GAM6414 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6414 RNA, hereby incorporated herein.

GAM6414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6414 target RNA, herein designated GAM TARGET RNA. GAM6414 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6414 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6414 RNA, herein designated GAM RNA, to target binding sites on GAM6414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6414 target RNA into GAM6414 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6414 target genes. The mRNA of each one of this

plurality of GAM6414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6414 RNA, herein designated GAM RNA, and which when bound by GAM6414 RNA causes inhibition of translation of the GAM6414 target mRNA into a corresponding GAM6414 target protein.

The mechanism of the translational inhibition exerted by GAM6414 RNA, herein designated GAM RNA, on one or more GAM6414 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6414 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6414 RNA, herein designated GAM RNA, of GAM6414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6414 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6414 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6414 RNA correlate with, and may be deduced from, the identity of the GAM6414 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6417 6575 GGAAATGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAATTAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGGTAGTGA Messenger 6417 (GAM6417) oligonucleotides modulates expression of respective target genes
GGCTGGCATT whose function and utility is known in the art.

TATAGAATCT GAM6417 is a novel bioinformatically detectable regulatory, non protein coding,
GGCTTTCTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6417 was detected is

TATTGGGTGG described with additional reference to Figs. 9-15.

AAAGCTAGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAACCAGTT encoded by the human genome.

TCTCTCAGCC GAM6417 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6417

TTTTCTCTCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6417

TCAGGTCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6417 precursor RNA is designated SEQ ID:6575, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6575 is located from position 116757828 to position 116757945 relative to chromosome 9 on the `-` strand.

GAM6417 precursor RNA folds onto itself, forming GAM6417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6417 precursor RNA, designated SEQ ID NO: 6575, and a schematic representation of a predicted secondary folding of GAM6417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6417 folded precursor RNA yielding a GAM6417 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6417 RNA, hereby incorporated herein.

GAM6417 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6417 target RNA, herein designated GAM TARGET RNA. GAM6417 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6417 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6417 RNA, herein designated GAM RNA, to target binding sites on GAM6417 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6417 target RNA

into GAM6417 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6417 target genes. The mRNA of each one of this plurality of GAM6417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6417 RNA, herein designated GAM RNA, and which when bound by GAM6417 RNA causes inhibition of translation of the GAM6417 target mRNA into a corresponding GAM6417 target protein.

The mechanism of the translational inhibition exerted by GAM6417 RNA, herein designated GAM RNA, on one or more GAM6417 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6417 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6417 RNA, herein designated GAM RNA, of GAM6417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6417 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6417 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6417 RNA correlate with, and may be deduced from, the identity of the GAM6417 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6431 6755 GGCGTCACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCTGATGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CGGTTGGGAA Messenger 6431 (GAM6431) oligonucleotides modulates expression of respective target genes

GGCAAAACCT whose function and utility is known in the art.

GCCCTGAAAA GAM6431 is a novel bioinformatically detectable regulatory, non protein coding,

GCCTTTGGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6431 was detected is

AGTGATTCTA described with additional reference to Figs. 9-15.

GCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6431 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6431 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6431 precursor RNA is designated SEQ ID:6755, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6755 is located from position 12904884 to position 12904956 relative to chromosome 19 on the `+` strand.

GAM6431 precursor RNA folds onto itself, forming GAM6431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6431 precursor RNA, designated SEQ ID NO: 6755, and a schematic representation of a predicted secondary folding of GAM6431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6431 folded precursor RNA yielding a GAM6431 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6431 RNA, hereby incorporated herein.

GAM6431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6431 target RNA, herein designated GAM TARGET RNA. GAM6431 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6431 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6431 RNA, herein designated GAM RNA, to target binding sites on GAM6431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6431 target RNA into GAM6431 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6431 target genes. The mRNA of each one of this plurality of GAM6431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6431 RNA, herein designated GAM RNA, and which when bound by GAM6431 RNA causes inhibition of translation of the GAM6431 target mRNA into a corresponding GAM6431 target protein.

The mechanism of the translational inhibition exerted by GAM6431 RNA, herein designated GAM RNA, on one or more GAM6431 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6431 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6431 RNA, herein designated GAM RNA, of GAM6431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6431 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6431 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6431 RNA correlate with, and may be deduced from, the identity of the GAM6431 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6440 7026 TCCCCTAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGATTATCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TATCAGCTAC Messenger 6440 (GAM6440) oligonucleotides modulates expression of respective target genes

TGACCCAGTT whose function and utility is known in the art.

AGCTTTCCTA GAM6440 is a novel bioinformatically detectable regulatory, non protein coding,

CTTCACAACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6440 was detected is

GGTTTCTAAT described with additional reference to Figs. 9-15.

GCTTTATGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTGTGAGAG encoded by the human genome.

AAATGGCAAG GAM6440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6440

TTGGGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6440

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6440 precursor RNA is designated SEQ ID:7026, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7026 is located from position 104082529 to position 104082634 relative to chromosome 7 on the `+` strand.

GAM6440 precursor RNA folds onto itself, forming GAM6440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6440 precursor RNA, designated SEQ ID NO: 7026, and a schematic representation of a predicted secondary folding of GAM6440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6440 folded precursor RNA yielding a GAM6440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6440 RNA, hereby incorporated herein.

GAM6440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6440 target RNA, herein designated GAM TARGET RNA. GAM6440 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6440 RNA, herein designated GAM RNA, to target binding sites on GAM6440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6440 target RNA into GAM6440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6440 target genes. The mRNA of each one of this plurality of GAM6440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6440 RNA, herein designated GAM RNA, and which when bound by GAM6440 RNA causes inhibition of translation of the GAM6440 target mRNA into a corresponding GAM6440 target protein.

The mechanism of the translational inhibition exerted by GAM6440 RNA, herein designated GAM RNA, on one or more GAM6440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6440 RNA, herein designated GAM RNA, of GAM6440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6440 RNA correlate with, and may be deduced from, the identity of the GAM6440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6459 5667 AAGCTGGGGG CACTGGCTTC TGCTCTTGCT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 6459 (GAM6459) oligonucleotides modulates expression of respective target genes

CTTTCTTCTG whose function and utility is known in the art.

GAAACATTAT GAM6459 is a novel bioinformatically detectable regulatory, non protein coding,
TCTGTTCCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6459 was detected is

TGGACATGGG described with additional reference to Figs. 9-15.

CAAGGGTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTCCCTAACT encoded by the human genome.

T GAM6459 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6459
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6459
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6459 precursor RNA is designated SEQ ID:5667, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5667 is located from position 30850314 to position 30850404 relative to chromosome 6 on the `+` strand.

GAM6459 precursor RNA folds onto itself, forming GAM6459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6459 precursor RNA, designated SEQ ID NO: 5667, and a schematic representation of a predicted secondary folding of GAM6459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6459 folded precursor RNA yielding a GAM6459 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6459 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6459 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6459 target RNA, herein designated GAM TARGET RNA. GAM6459 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6459 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM6459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6459 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6459 RNA, herein designated GAM RNA, to target binding sites on GAM6459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6459 target RNA into GAM6459 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6459 target genes. The mRNA of each one of this plurality of GAM6459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6459 RNA, herein designated GAM RNA, and which when bound by GAM6459 RNA causes inhibition of translation of the GAM6459 target mRNA into a corresponding GAM6459 target protein.

The mechanism of the translational inhibition exerted by GAM6459 RNA, herein designated GAM RNA, on one or more GAM6459 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6459 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6459 RNA, herein designated GAM RNA, of GAM6459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6459 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6459 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6459 RNA correlate with, and may be deduced from, the identity of the GAM6459 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6466 5788 AGGGCAAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCGCTCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCGTGGCCC Messenger 6466 (GAM6466) oligonucleotides modulates expression of respective target genes

GTGTTCTCTC whose function and utility is known in the art.

CTTTTGTCCC GAM6466 is a novel bioinformatically detectable regulatory, non protein coding,

CATAGTGTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6466 was detected is

CTCCGCCAGG described with additional reference to Figs. 9-15.

AACTTGGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCTGAAGAC encoded by the human genome.

TGTGAATGAG GAM6466 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6466

AGTCATGGGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6466

CTGTGGAACG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

CTCATCCCT to the nucleotide sequence of GAM6466 precursor RNA is designated SEQ ID:5788, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5788 is located from position 78873540 to position 78873668 relative to chromosome 17 on the `+` strand.

GAM6466 precursor RNA folds onto itself, forming GAM6466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6466 precursor RNA, designated SEQ ID NO: 5788, and a schematic representation of a predicted secondary folding of GAM6466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6466 folded precursor RNA yielding a GAM6466 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6466 RNA, hereby incorporated herein.

GAM6466 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM6466 target RNA, herein designated GAM TARGET RNA. GAM6466 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6466 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6466 RNA, herein designated GAM RNA, to target binding sites on GAM6466 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6466 target RNA into GAM6466 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6466 target genes. The mRNA of each one of this plurality of GAM6466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6466 RNA, herein designated GAM RNA, and which when bound by GAM6466 RNA causes inhibition of translation of the GAM6466 target mRNA into a corresponding GAM6466 target protein.

The mechanism of the translational inhibition exerted by GAM6466 RNA, herein designated GAM RNA, on one or more GAM6466 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6466 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6466 RNA, herein designated GAM RNA, of GAM6466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6466 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM6466 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6466 RNA correlate with, and may be deduced from, the identity of the GAM6466 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6467 6179 CTCTGTGATG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTGGGGACC detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTCCTCGG Messenger 6467 (GAM6467) oligonucleotides modulates expression of respective target genes
TCACACCCCA whose function and utility is known in the art.

GTCCTGCTCT GAM6467 is a novel bioinformatically detectable regulatory, non protein coding,
GAAGGTTGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6467 was detected is

GTTTTCCAAA described with additional reference to Figs. 9-15.

CAGAAGGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTAGCTAGAG encoded by the human genome.

GGGAGATAGC GAM6467 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6467
AAGATTCTGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6467
AGTCTGGAAA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
GCCTTCACTT to the nucleotide sequence of GAM6467 precursor RNA is designated SEQ ID:6179, and is

G provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6179 is located from position 23774919 to position 23775049 relative to chromosome 13 on the `+` strand.

GAM6467 precursor RNA folds onto itself, forming GAM6467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6467 precursor RNA, designated SEQ ID NO: 6179, and a schematic representation of a predicted secondary folding of GAM6467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6467 folded precursor RNA yielding a GAM6467 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor

product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6467 RNA, hereby incorporated herein.

GAM6467 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6467 target RNA, herein designated GAM TARGET RNA. GAM6467 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6467 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6467 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6467 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6467 RNA, herein designated GAM RNA, to target binding sites on GAM6467 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6467 target RNA into GAM6467 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6467 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6467 target genes. The mRNA of each one of this plurality of GAM6467 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6467 RNA, herein designated GAM RNA, and which when bound by GAM6467 RNA causes inhibition of translation of the GAM6467 target mRNA into a corresponding GAM6467 target protein.

The mechanism of the translational inhibition exerted by GAM6467 RNA, herein designated GAM RNA, on one or more GAM6467 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6467 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6467 RNA, herein designated GAM RNA, of GAM6467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6467 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6467 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6467 RNA correlate with, and may be deduced from, the identity of the GAM6467 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6506 6866 GTAGTCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTATTCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGGTG Messenger 6506 (GAM6506) oligonucleotides modulates expression of respective target genes
GGAGGATCAC whose function and utility is known in the art.

TTCGGCCCAG GAM6506 is a novel bioinformatically detectable regulatory, non protein coding,
GAGTCTGAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6506 was detected is

CTGGAGTGAG described with additional reference to Figs. 9-15.

CTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM6506 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6506

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6506
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6506 precursor RNA is designated SEQ ID:6866, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6866 is located from position 29270291 to position 29270364 relative to chromosome 17 on the `+` strand.

GAM6506 precursor RNA folds onto itself, forming GAM6506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6506 precursor RNA, designated SEQ ID NO: 6866, and a schematic representation of a predicted secondary folding of GAM6506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6506 folded precursor RNA yielding a GAM6506 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6506 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6506 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6506 target RNA, herein designated GAM TARGET RNA. GAM6506 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6506 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6506 RNA, herein designated GAM RNA, to target binding sites on GAM6506 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6506 target RNA into GAM6506 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6506 target genes. The mRNA of each one of this plurality of GAM6506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6506 RNA, herein designated GAM RNA, and which when bound by GAM6506 RNA causes inhibition of translation of the GAM6506 target mRNA into a corresponding GAM6506 target protein.

The mechanism of the translational inhibition exerted by GAM6506 RNA, herein designated GAM RNA, on one or more GAM6506 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6506 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6506 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6506 RNA, herein designated GAM RNA, of GAM6506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in
Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6506 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6506 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6506 RNA correlate with, and may be deduced from, the identity of the GAM6506 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6509 6106 CCTAGATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATCTGCTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCAAGATAT Messenger 6509 (GAM6509) oligonucleotides modulates expression of respective target genes
TCCCGGCCTC whose function and utility is known in the art.

AGAAGCTGAG GAM6509 is a novel bioinformatically detectable regulatory, non protein coding,
GGGAGAACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6509 was detected is

TCTGTTCTTC described with additional reference to Figs. 9-15.

CCCACCTTCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTTGCATTC encoded by the human genome.

CTCCTTCAGC GAM6509 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6509
ATCTTCTTAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6509
GG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6509 precursor RNA is designated SEQ ID:6106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6106 is located from position 16592351 to position 16592462 relative to chromosome 21 on the `+` strand.

GAM6509 precursor RNA folds onto itself, forming GAM6509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6509 precursor RNA, designated SEQ ID NO: 6106, and a schematic representation of a predicted secondary folding of GAM6509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6509 folded precursor RNA yielding a GAM6509 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6509 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6509 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6509 target RNA, herein designated GAM TARGET RNA. GAM6509 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6509 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6509 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6509 RNA, herein designated GAM RNA, to target binding sites on GAM6509 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6509 target RNA into GAM6509 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6509 target genes. The mRNA of each one of this plurality of GAM6509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6509 RNA, herein designated GAM RNA, and which when bound by GAM6509 RNA causes inhibition of translation of the GAM6509 target mRNA into a corresponding GAM6509 target protein.

The mechanism of the translational inhibition exerted by GAM6509 RNA, herein designated GAM RNA, on one or more GAM6509 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6509 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6509 RNA, herein designated GAM RNA, of GAM6509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6509 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6509 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6509 RNA correlate with, and may be deduced from, the identity of the GAM6509 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6531 7064 TCTCCCAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
AATATTCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GATAGGCTGC Messenger 6531 (GAM6531) oligonucleotides modulates expression of respective target genes
CAGTTGGACT whose function and utility is known in the art.

AAGGAAGCCA GAM6531 is a novel bioinformatically detectable regulatory, non protein coding,
CTCCTGCGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6531 was detected is

ACCCTGGGAG described with additional reference to Figs. 9-15.

A GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM6531 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6531

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6531
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6531 precursor RNA is designated SEQ ID:7064, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7064 is located from position 54026269 to position 54026339 relative to chromosome 8 on the `+` strand.

GAM6531 precursor RNA folds onto itself, forming GAM6531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6531 precursor RNA, designated SEQ ID NO: 7064, and a schematic representation of a predicted secondary folding of GAM6531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6531 folded precursor RNA yielding a GAM6531 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6531 RNA, hereby incorporated herein.

GAM6531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6531 target RNA, herein designated GAM TARGET RNA. GAM6531 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6531 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6531 RNA, herein designated GAM RNA, to target binding sites on GAM6531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6531 target RNA into GAM6531 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6531 target genes. The mRNA of each one of this plurality of GAM6531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6531 RNA, herein

designated GAM RNA, and which when bound by GAM6531 RNA causes inhibition of translation of the GAM6531 target mRNA into a corresponding GAM6531 target protein.

The mechanism of the translational inhibition exerted by GAM6531 RNA, herein designated GAM RNA, on one or more GAM6531 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6531 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6531 RNA, herein designated GAM RNA, of GAM6531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6531 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6531 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6531 RNA correlate with, and may be deduced from, the identity of the GAM6531 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6541 6067 CCCAAGGTTA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTGGTAAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAGAGAGAA Messenger 6541 (GAM6541) oligonucleotides modulates expression of respective target genes
GCCAGAAGCC whose function and utility is known in the art.

TGGGGCCTCC GAM6541 is a novel bioinformatically detectable regulatory, non protein coding,
TGACGGCTCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6541 was detected is

TGCTTCTCTT described with additional reference to Figs. 9-15.

TTTACTAAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTCTGCCA encoded by the human genome.

TGGG GAM6541 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6541
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6541

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6541 precursor RNA is designated SEQ ID:6067, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6067 is located from position 99881835 to position 99881928 relative to chromosome 13 on the `+` strand.

GAM6541 precursor RNA folds onto itself, forming GAM6541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6541 precursor RNA, designated SEQ ID NO: 6067, and a schematic representation of a predicted secondary folding of GAM6541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6541 folded precursor RNA yielding a GAM6541 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6541 RNA, hereby incorporated herein.

GAM6541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6541 target RNA, herein designated GAM TARGET RNA. GAM6541 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6541 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6541 RNA, herein designated GAM RNA, to target binding sites on GAM6541 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6541 target RNA into GAM6541 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6541 target genes. The mRNA of each one of this plurality of GAM6541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6541 RNA, herein designated GAM RNA, and which when bound by GAM6541 RNA causes inhibition of translation of the GAM6541 target mRNA into a corresponding GAM6541 target protein.

The mechanism of the translational inhibition exerted by GAM6541 RNA, herein designated GAM RNA, on one or more GAM6541 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6541 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6541 RNA, herein designated GAM RNA, of GAM6541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6541 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6541 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6541 RNA correlate with, and may be deduced from, the identity of the GAM6541 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6564 6725 GGCAAGATCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGCTCCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGTGGCCCGT Messenger 6564 (GAM6564) oligonucleotides modulates expression of respective target genes

GTTCTCTCCT whose function and utility is known in the art.

TTTGTCCCCA GAM6564 is a novel bioinformatically detectable regulatory, non protein coding,

TAGTGTGACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6564 was detected is

CCGCCAGGAA described with additional reference to Figs. 9-15.

CTTGGAATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGAAGACTG encoded by the human genome.

TGAATGAGAG GAM6564 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6564

TCATGGGTCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6564

GTGGAACGCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

CATCCCTGAC to the nucleotide sequence of GAM6564 precursor RNA is designated SEQ ID:6725, and is

C provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6725 is located from position 78873542 to position 78873672 relative to chromosome 17 on the `+` strand.

GAM6564 precursor RNA folds onto itself, forming GAM6564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6564 precursor RNA, designated SEQ ID NO: 6725, and a schematic representation of a predicted secondary folding of GAM6564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6564 folded precursor RNA yielding a GAM6564 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6564 RNA, hereby incorporated herein.

GAM6564 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6564 target RNA, herein designated GAM TARGET RNA. GAM6564 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6564 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6564 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6564 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6564 RNA, herein designated GAM RNA, to target binding sites on GAM6564 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6564 target RNA into GAM6564 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6564 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6564 target genes. The mRNA of each one of this plurality of GAM6564 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6564 RNA, herein designated GAM RNA, and which when bound by GAM6564 RNA causes inhibition of translation of the GAM6564 target mRNA into a corresponding GAM6564 target protein.

The mechanism of the translational inhibition exerted by GAM6564 RNA, herein designated GAM RNA, on one or more GAM6564 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6564 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6564 RNA, herein designated GAM RNA, of GAM6564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6564 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6564 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6564 RNA correlate with, and may be deduced from, the identity of the GAM6564 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6567 6479 GCAAAGCAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCTTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGATAGTGAT Messenger 6567 (GAM6567) oligonucleotides modulates expression of respective target genes

TTAGCTCAAG whose function and utility is known in the art.

AGGGAGTGAG GAM6567 is a novel bioinformatically detectable regulatory, non protein coding,

ATGTGACTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6567 was detected is

TGCCACATGT described with additional reference to Figs. 9-15.

TAAATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6567 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6567

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6567

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6567 precursor RNA is designated SEQ ID:6479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6479 is located from position 88200970 to position 88201046 relative to chromosome 11 on the `+` strand.

GAM6567 precursor RNA folds onto itself, forming GAM6567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6567 precursor RNA, designated SEQ ID NO: 6479, and a schematic representation of a predicted secondary folding of GAM6567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6567 folded precursor RNA yielding a GAM6567 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6567 RNA, hereby incorporated herein.

GAM6567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6567 target RNA, herein designated GAM TARGET RNA. GAM6567 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6567 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6567 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6567 RNA, herein designated GAM RNA, to target binding sites on GAM6567 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6567 target RNA into GAM6567 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6567 target genes. The mRNA of each one of this plurality of GAM6567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6567 RNA, herein designated GAM RNA, and which when bound by GAM6567 RNA causes inhibition of translation of the GAM6567 target mRNA into a corresponding GAM6567 target protein.

The mechanism of the translational inhibition exerted by GAM6567 RNA, herein designated GAM RNA, on one or more GAM6567 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6567 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6567 RNA, herein designated GAM RNA, of GAM6567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6567 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6567 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6567 RNA correlate with, and may be deduced from, the identity of the GAM6567 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6618 6975 TAGTCTCATC CAGGTATGAC Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTGCCACT Messenger 6618 (GAM6618) oligonucleotides modulates expression of respective target genes

GTGTCTGAAA whose function and utility is known in the art.

TTCCTGAGCA GAM6618 is a novel bioinformatically detectable regulatory, non protein coding, CCGAGGGCCG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6618 was detected is

CTTCAGGCAC described with additional reference to Figs. 9-15.

CAGGCACTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCAACCTGA encoded by the human genome.

GAGCTG GAM6618 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6618 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6618 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6618 precursor RNA is designated SEQ ID:6975, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6975 is located from position 140693627 to position 140693722 relative to chromosome 7 on the `-` strand.

GAM6618 precursor RNA folds onto itself, forming GAM6618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6618 precursor RNA, designated SEQ ID NO: 6975, and a schematic representation of a predicted secondary folding of GAM6618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6618 folded precursor RNA yielding a GAM6618 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6618 RNA, hereby incorporated herein.

GAM6618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6618 target RNA, herein designated GAM TARGET RNA. GAM6618 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6618 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6618 RNA, herein designated GAM RNA, to target binding sites on GAM6618 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6618 target RNA into GAM6618 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6618 target genes. The mRNA of each one of this plurality of GAM6618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6618 RNA, herein designated GAM RNA, and which when bound by GAM6618 RNA causes inhibition of translation of the GAM6618 target mRNA into a corresponding GAM6618 target protein.

The mechanism of the translational inhibition exerted by GAM6618 RNA, herein designated GAM RNA, on one or more GAM6618 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6618 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6618 RNA, herein designated GAM RNA, of GAM6618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6618 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6618 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6618 RNA correlate with, and may be deduced from, the identity of the GAM6618 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6638 6216 CTGCCTAATG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGTGTATG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGCTGTAG Messenger 6638 (GAM6638) oligonucleotides modulates expression of respective target genes

CATTTCTGGC whose function and utility is known in the art.

ACCTGCCAAC GAM6638 is a novel bioinformatically detectable regulatory, non protein coding,

TTGTCAGAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6638 was detected is

TGCCTTTCCC described with additional reference to Figs. 9-15.

TTCCTGGCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGTCTATG encoded by the human genome.

TGGCAG GAM6638 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6638

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6638

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6638 precursor RNA is designated SEQ ID:6216, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6216 is located from position 51855487 to position 51855582 relative to chromosome 3 on the `-` strand.

GAM6638 precursor RNA folds onto itself, forming GAM6638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6638 precursor RNA, designated SEQ ID NO: 6216, and a schematic representation of a predicted secondary folding of GAM6638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6638 folded precursor RNA yielding a GAM6638 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6638 RNA, hereby incorporated herein.

GAM6638 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6638 target RNA, herein designated GAM TARGET RNA. GAM6638 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6638 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6638 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6638 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6638 RNA, herein designated GAM RNA, to target binding sites on GAM6638 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6638 target RNA into GAM6638 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6638 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6638 target genes. The mRNA of each one of this plurality of GAM6638 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6638 RNA, herein designated GAM RNA, and which when bound by GAM6638 RNA causes inhibition of translation of the GAM6638 target mRNA into a corresponding GAM6638 target protein.

The mechanism of the translational inhibition exerted by GAM6638 RNA, herein designated GAM RNA, on one or more GAM6638 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6638 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6638 RNA, herein designated GAM RNA, of GAM6638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6638 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6638 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6638 RNA correlate with, and may be deduced from, the identity of the GAM6638 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6674 5744 AGCAGAGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGGAATGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTCTGCTC Messenger 6674 (GAM6674) oligonucleotides modulates expression of respective target genes

TCACTGAATG whose function and utility is known in the art.

GTGGGGAACC GAM6674 is a novel bioinformatically detectable regulatory, non protein coding,

TTCAACTGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6674 was detected is

TAGCCTGTGC described with additional reference to Figs. 9-15.

T GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6674 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6674

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6674

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6674 precursor RNA is designated SEQ ID:5744, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5744 is located from position 4506790 to position 4506860 relative to chromosome 16 on the `-` strand.

GAM6674 precursor RNA folds onto itself, forming GAM6674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6674 precursor RNA, designated SEQ ID NO: 5744, and a schematic representation of a predicted secondary folding of GAM6674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6674 folded precursor RNA yielding a GAM6674 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM6674 RNA, hereby incorporated herein.

GAM6674 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6674 target RNA, herein designated GAM TARGET RNA. GAM6674 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6674 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6674 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6674 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6674 RNA, herein designated GAM RNA, to target binding sites on GAM6674 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6674 target RNA into GAM6674 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6674 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6674 target genes. The mRNA of each one of this plurality of GAM6674 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6674 RNA, herein designated GAM RNA, and which when bound by GAM6674 RNA causes inhibition of translation of the GAM6674 target mRNA into a corresponding GAM6674 target protein.

The mechanism of the translational inhibition exerted by GAM6674 RNA, herein designated GAM RNA, on one or more GAM6674 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6674 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6674 RNA, herein designated GAM RNA, of GAM6674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6674 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6674 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6674 RNA correlate with, and may be deduced from, the identity of the GAM6674 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6700 5661 AAGAGACTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTAGATGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TTAAATTAAG Messenger 6700 (GAM6700) oligonucleotides modulates expression of respective target genes
GCTCTTGAGA whose function and utility is known in the art.

TTGGGAGATT GAM6700 is a novel bioinformatically detectable regulatory, non protein coding,
ATCCTGGATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6700 was detected is

ATCAGAGTAG described with additional reference to Figs. 9-15.

GCTTGATGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATCACAAGAG encoded by the human genome.

TCCTT GAM6700 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6700
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6700
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6700 precursor RNA is designated SEQ ID:5661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5661 is located from position 156731865 to position 156731959 relative to chromosome 1 on the `+` strand.

GAM6700 precursor RNA folds onto itself, forming GAM6700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6700 precursor RNA, designated SEQ ID NO: 5661, and a schematic representation of a predicted secondary folding of GAM6700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6700 folded precursor RNA

yielding a GAM6700 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6700 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6700 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6700 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6700 target RNA, herein designated GAM TARGET RNA. GAM6700 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6700 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6700 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6700 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6700 RNA, herein designated GAM RNA, to target binding sites on GAM6700 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6700 target RNA into GAM6700 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6700 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6700 target genes. The mRNA of each one of this plurality of GAM6700 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6700 RNA, herein designated GAM RNA, and which when bound by GAM6700 RNA causes inhibition of translation of the GAM6700 target mRNA into a corresponding GAM6700 target protein.

The mechanism of the translational inhibition exerted by GAM6700 RNA, herein designated GAM RNA, on one or more GAM6700 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6700 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6700 RNA, herein designated GAM RNA, of GAM6700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6700 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6700 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6700 RNA correlate with, and may be deduced from, the identity of the GAM6700 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6773 6874 GTCCACTGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTCACTAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTTTGTCC Messenger 6773 (GAM6773) oligonucleotides modulates expression of respective target genes

TCACCCCTGA whose function and utility is known in the art.

AGCAGATAAA GAM6773 is a novel bioinformatically detectable regulatory, non protein coding,

CACATGTAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6773 was detected is

TGGAGGAAAA described with additional reference to Figs. 9-15.

GTGACAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTGGGTTCA encoded by the human genome.

TCAGTGGGC GAM6773 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6773

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6773

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6773 precursor RNA is designated SEQ ID:6874, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6874 is located from position 203719518 to position 203719616 relative to chromosome 1 on the `+` strand.

GAM6773 precursor RNA folds onto itself, forming GAM6773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6773 precursor RNA, designated SEQ ID NO: 6874, and a schematic representation of a predicted secondary folding of GAM6773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6773 folded precursor RNA yielding a GAM6773 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6773 RNA, hereby incorporated herein. Expression of GAM6773 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM6773 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6773 target RNA, herein designated GAM TARGET RNA. GAM6773 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6773 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6773 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6773 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6773 RNA, herein designated GAM RNA, to target binding sites on GAM6773 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6773 target RNA into GAM6773 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6773 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6773 target genes. The mRNA of each one of this plurality of GAM6773 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6773 RNA, herein designated GAM RNA, and which when bound by GAM6773 RNA causes inhibition of translation of the GAM6773 target mRNA into a corresponding GAM6773 target protein.

The mechanism of the translational inhibition exerted by GAM6773 RNA, herein designated GAM RNA, on one or more GAM6773 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6773 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6773 RNA, herein designated GAM RNA, of GAM6773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6773 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6773 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6773 RNA correlate with, and may be deduced from, the identity of the GAM6773 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6774 6210 CTGCAGCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AATAAAATTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CCGAGATGAT Messenger 6774 (GAM6774) oligonucleotides modulates expression of respective target genes

GTTTGGGTTT whose function and utility is known in the art.

GTGCTGGACA GAM6774 is a novel bioinformatically detectable regulatory, non protein coding,

TTCCTGAGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6774 was detected is

GAGCCAGAGG described with additional reference to Figs. 9-15.

TGAGTCTTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTGTTGGG encoded by the human genome.

GAGAGCAG GAM6774 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6774

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6774

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6774 precursor RNA is designated SEQ ID:6210, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6210 is located from position 175687263 to position 175687360 relative to chromosome 5 on the `+` strand.

GAM6774 precursor RNA folds onto itself, forming GAM6774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6774 precursor RNA, designated SEQ ID NO: 6210, and a schematic representation of a predicted secondary folding of GAM6774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6774 folded precursor RNA yielding a GAM6774 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6774 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6774 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6774 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6774 target RNA, herein designated GAM TARGET RNA. GAM6774 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6774 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6774 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6774 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6774 RNA, herein designated GAM RNA, to target binding sites on GAM6774 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6774 target RNA into GAM6774 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6774 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6774 target genes. The mRNA of each one of this plurality of GAM6774 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6774 RNA, herein

designated GAM RNA, and which when bound by GAM6774 RNA causes inhibition of translation of the GAM6774 target mRNA into a corresponding GAM6774 target protein.

The mechanism of the translational inhibition exerted by GAM6774 RNA, herein designated GAM RNA, on one or more GAM6774 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6774 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6774 RNA, herein designated GAM RNA, of GAM6774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6774 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6774 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6774 RNA correlate with, and may be deduced from, the identity of the GAM6774 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6799 6991 TCACCCAGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTCTCTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACAGACAT Messenger 6799 (GAM6799) oligonucleotides modulates expression of respective target genes
GTCCAGTGGA whose function and utility is known in the art.

CCGTAGTGTT GAM6799 is a novel bioinformatically detectable regulatory, non protein coding,
GTGACGGTCG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6799 was detected is

CCCATCTGCG described with additional reference to Figs. 9-15.

CCCAGTACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGGATCATGC encoded by the human genome.

GGAACATGTT GAM6799 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6799
GTCAAAGCTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6799

CAGATTGCCT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
GTGA to the nucleotide sequence of GAM6799 precursor RNA is designated SEQ ID:6991, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6991 is located from position 56320939 to position 56321062 relative to chromosome 12 on the `-` strand.

GAM6799 precursor RNA folds onto itself, forming GAM6799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6799 precursor RNA, designated SEQ ID NO: 6991, and a schematic representation of a predicted secondary folding of GAM6799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6799 folded precursor RNA yielding a GAM6799 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6799 RNA, hereby incorporated herein.

GAM6799 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6799 target RNA, herein designated GAM TARGET RNA. GAM6799 target
RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6799 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6799 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6799 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6799 RNA, herein designated GAM RNA, to target binding sites on GAM6799 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6799 target RNA into GAM6799 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6799 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6799 target genes. The mRNA of each one of this plurality of GAM6799 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6799 RNA, herein designated GAM RNA, and which when bound by GAM6799 RNA causes inhibition of translation of the GAM6799 target mRNA into a corresponding GAM6799 target protein.

The mechanism of the translational inhibition exerted by GAM6799 RNA, herein designated GAM RNA, on one or more GAM6799 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6799 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6799 RNA, herein designated GAM RNA, of GAM6799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6799 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6799 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6799 RNA correlate with, and may be deduced from, the identity of the GAM6799 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6807 6137 CGAGTGATTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAGGTAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TATGTTATTG Messenger 6807 (GAM6807) oligonucleotides modulates expression of respective target genes

GAAAGGTGTG whose function and utility is known in the art.

ATCTATATAG GAM6807 is a novel bioinformatically detectable regulatory, non protein coding,

AACCCTGTAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6807 was detected is

ATGAAAAGGA described with additional reference to Figs. 9-15.

GGAGATGCCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTATCTTGGC encoded by the human genome.

AGGGATGATC GAM6807 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6807
ATGTATTTGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6807
AATAGTAACT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CACAGCATTT to the nucleotide sequence of GAM6807 precursor RNA is designated SEQ ID:6137, and is

G provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6137 is located from position 121833616 to position 121833746 relative to chromosome 10 on the `+` strand.

GAM6807 precursor RNA folds onto itself, forming GAM6807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6807 precursor RNA, designated SEQ ID NO: 6137, and a schematic representation of a predicted secondary folding of GAM6807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6807 folded precursor RNA yielding a GAM6807 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6807 RNA, hereby incorporated herein.

GAM6807 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6807 target RNA, herein designated GAM TARGET RNA. GAM6807 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6807 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6807 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6807 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6807 RNA, herein designated GAM RNA, to target binding sites on GAM6807 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6807 target RNA into GAM6807 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6807 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6807 target genes. The mRNA of each one of this plurality of GAM6807 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6807 RNA, herein designated GAM RNA, and which when bound by GAM6807 RNA causes inhibition of translation of the GAM6807 target mRNA into a corresponding GAM6807 target protein.

The mechanism of the translational inhibition exerted by GAM6807 RNA, herein designated GAM RNA, on one or more GAM6807 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6807 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6807 RNA, herein designated GAM RNA, of GAM6807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6807 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6807 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6807 RNA correlate with, and may be deduced from, the identity of the GAM6807 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6811 6248 CTGTTTCCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TAGGTGCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGATCAGGT Messenger 6811 (GAM6811) oligonucleotides modulates expression of respective target genes
TCCTGATTGG whose function and utility is known in the art.

AGTTCTCTTA GAM6811 is a novel bioinformatically detectable regulatory, non protein coding,
TCTGCTCTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6811 was detected is

TTTGGAGGGC described with additional reference to Figs. 9-15.

TGCCCCATTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGAATCTGT encoded by the human genome.

TTTGTTTTGC GAM6811 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6811

TCAAATACAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6811

TCAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6811 precursor RNA is designated SEQ ID:6248, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6248 is located from position 110102077 to position 110102190 relative to chromosome 13 on the `-` strand.

GAM6811 precursor RNA folds onto itself, forming GAM6811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6811 precursor RNA, designated SEQ ID NO: 6248, and a schematic representation of a predicted secondary folding of GAM6811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6811 folded precursor RNA yielding a GAM6811 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6811 RNA, hereby incorporated herein.

GAM6811 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6811 target RNA, herein designated GAM TARGET RNA. GAM6811 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6811 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6811 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6811 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6811 RNA, herein designated GAM RNA, to target binding sites on GAM6811 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6811 target RNA into GAM6811 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6811 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6811 target genes. The mRNA of each one of this plurality of GAM6811 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6811 RNA, herein designated GAM RNA, and which when bound by GAM6811 RNA causes inhibition of translation of the GAM6811 target mRNA into a corresponding GAM6811 target protein.

The mechanism of the translational inhibition exerted by GAM6811 RNA, herein designated GAM RNA, on one or more GAM6811 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6811 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6811 RNA, herein designated GAM RNA, of GAM6811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6811 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6811 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6811 RNA correlate with, and may be deduced from, the identity of the GAM6811 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6818 6826 GGGTTCTTTT TCCGCTTTCT GAGCCCTTTT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 6818 (GAM6818) oligonucleotides modulates expression of respective target genes

ATACCTTACG whose function and utility is known in the art.

TTTAGAAGGG GAM6818 is a novel bioinformatically detectable regulatory, non protein coding, GAAAATCATC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6818 was detected is

CTCCC described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6818 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6818

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6818

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6818 precursor RNA is designated SEQ ID:6826, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6826 is located from position 122713355 to position 122713419 relative to chromosome 7 on the `-` strand.

GAM6818 precursor RNA folds onto itself, forming GAM6818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6818 precursor RNA, designated SEQ ID NO: 6826, and a schematic representation of a predicted secondary folding of GAM6818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6818 folded precursor RNA yielding a GAM6818 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6818 RNA, hereby incorporated herein.

GAM6818 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6818 target RNA, herein designated GAM TARGET RNA. GAM6818 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6818 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6818 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6818 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6818 RNA, herein designated GAM RNA, to target binding sites on GAM6818 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6818 target RNA into GAM6818 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6818 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6818 target genes. The mRNA of each one of this plurality of GAM6818 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6818 RNA, herein designated GAM RNA, and which when bound by GAM6818 RNA causes inhibition of translation of the GAM6818 target mRNA into a corresponding GAM6818 target protein.

The mechanism of the translational inhibition exerted by GAM6818 RNA, herein designated GAM RNA, on one or more GAM6818 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6818 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6818 RNA, herein designated GAM RNA, of GAM6818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6818 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6818 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6818 RNA correlate with, and may be deduced from, the identity of the GAM6818 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6836 6389 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCATTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAAG Messenger 6836 (GAM6836) oligonucleotides modulates expression of respective target genes

TGGAGGTTGC whose function and utility is known in the art.

AGTGAGCCAA GAM6836 is a novel bioinformatically detectable regulatory, non protein coding,

GATCGTGTCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6836 was detected is

CTGCACTCTA described with additional reference to Figs. 9-15.

GCCTAGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAAAGCGAGA encoded by the human genome.

CTCAGTCTC GAM6836 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6836 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6836 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6836 precursor RNA is designated SEQ ID:6389, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6389 is located from position 71860457 to position 71860555 relative to chromosome 7 on the `-` strand.

GAM6836 precursor RNA folds onto itself, forming GAM6836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6836 precursor RNA, designated SEQ ID NO: 6389, and a schematic representation of a predicted secondary folding of GAM6836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6836 folded precursor RNA yielding a GAM6836 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6836 RNA, hereby incorporated herein.

GAM6836 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6836 target RNA, herein designated GAM TARGET RNA. GAM6836 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6836 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6836 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6836 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6836 RNA, herein designated GAM RNA, to target binding sites on GAM6836 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6836 target RNA into GAM6836 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6836 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6836 target genes. The mRNA of each one of this plurality of GAM6836 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6836 RNA, herein designated GAM RNA, and which when bound by GAM6836 RNA causes inhibition of translation of the GAM6836 target mRNA into a corresponding GAM6836 target protein.

The mechanism of the translational inhibition exerted by GAM6836 RNA, herein designated GAM RNA, on one or more GAM6836 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6836 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6836 RNA, herein designated GAM RNA, of GAM6836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6836 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6836 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6836 RNA correlate with, and may be deduced from, the identity of the GAM6836 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6840 7022 TCCAGTTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGAGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGGCAGGC Messenger 6840 (GAM6840) oligonucleotides modulates expression of respective target genes

TTCTGGGGAA whose function and utility is known in the art.

AGAAAGCCAG GAM6840 is a novel bioinformatically detectable regulatory, non protein coding,

CTGAATTTTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM6840 was detected is

ACTCCATCTC described with additional reference to Figs. 9-15.

CCCAGAAGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTGGG encoded by the human genome.

GAM6840 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6840

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6840

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6840 precursor RNA is designated SEQ ID:7022, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7022 is located from position 40508403 to position 40508488 relative to chromosome 19 on the `+` strand.

GAM6840 precursor RNA folds onto itself, forming GAM6840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6840 precursor RNA, designated SEQ ID NO: 7022, and a schematic representation of a predicted secondary folding of GAM6840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6840 folded precursor RNA yielding a GAM6840 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM6840 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6840 RNA and an

alternative nucleotide sequence thereof, hereby incorporated herein.

GAM6840 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6840 target RNA, herein designated GAM TARGET RNA. GAM6840 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6840 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6840 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6840 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6840 RNA, herein designated GAM RNA, to target binding sites on GAM6840 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6840 target RNA into GAM6840 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6840 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6840 target genes. The mRNA of each one of this plurality of GAM6840 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6840 RNA, herein designated GAM RNA, and which when bound by GAM6840 RNA causes inhibition of translation of the GAM6840 target mRNA into a corresponding GAM6840 target protein.

The mechanism of the translational inhibition exerted by GAM6840 RNA, herein designated GAM RNA, on one or more GAM6840 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6840 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6840 RNA, herein designated GAM RNA, of GAM6840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6840 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6840 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6840 RNA correlate with, and may be deduced from, the identity of the GAM6840 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6842 6993 TCACGTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCAAAGTAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
AAGTGGTTAT Messenger 6842 (GAM6842) oligonucleotides modulates expression of respective target genes
GTTCATATCA whose function and utility is known in the art.

TTTTGAAAGC GAM6842 is a novel bioinformatically detectable regulatory, non protein coding,
TGAGTGGATA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6842 was detected is

GATTTAAATA described with additional reference to Figs. 9-15.

GCAAGAGCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTTCGGAAT encoded by the human genome.

GATGTGTGGA GAM6842 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6842
ACCCAGAATC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6842
ACAGACCCTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
CGATACATGA to the nucleotide sequence of GAM6842 precursor RNA is designated SEQ ID:6993, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6993 is located from position 22646286 to position 22646415 relative to chromosome 18 on the `-` strand.

GAM6842 precursor RNA folds onto itself, forming GAM6842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6842 precursor RNA, designated SEQ ID NO: 6993, and a schematic representation of a predicted secondary folding of GAM6842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6842 folded precursor RNA yielding a GAM6842 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6842 RNA, hereby incorporated herein.

GAM6842 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6842 target RNA, herein designated GAM TARGET RNA. GAM6842 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6842 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6842 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6842 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6842 RNA, herein designated GAM RNA, to target binding sites on GAM6842 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6842 target RNA into GAM6842 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6842 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6842 target genes. The mRNA of each one of this plurality of GAM6842 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6842 RNA, herein designated GAM RNA, and which when bound by GAM6842 RNA causes inhibition of translation of the GAM6842 target mRNA into a corresponding GAM6842 target protein.

The mechanism of the translational inhibition exerted by GAM6842 RNA, herein designated GAM RNA, on one or more GAM6842 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6842 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6842 RNA, herein designated GAM RNA, of GAM6842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6842 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6842 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6842 RNA correlate with, and may be deduced from, the identity of the GAM6842 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6858 5988 CAAGCAGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGGTGCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCATGGATAG Messenger 6858 (GAM6858) oligonucleotides modulates expression of respective target genes

AGCTTTCAAG whose function and utility is known in the art.

AAGTTTGTTC GAM6858 is a novel bioinformatically detectable regulatory, non protein coding,

TAGTTCTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6858 was detected is

CCTGAAACTG described with additional reference to Figs. 9-15.

GACCTCCCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTAGCTTG encoded by the human genome.

GAM6858 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6858

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6858

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6858 precursor RNA is designated SEQ ID:5988, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5988 is located from position 118137371 to position 118137458 relative to chromosome X on the `+` strand.

GAM6858 precursor RNA folds onto itself, forming GAM6858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6858 precursor RNA, designated SEQ ID NO: 5988, and a schematic representation of a predicted secondary folding of GAM6858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6858 folded precursor RNA yielding a GAM6858 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6858 RNA, hereby incorporated herein.

GAM6858 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6858 target RNA, herein designated GAM TARGET RNA. GAM6858 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6858 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6858 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6858 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6858 RNA, herein designated GAM RNA, to target binding sites on GAM6858 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6858 target RNA into GAM6858 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6858 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6858 target genes. The mRNA of each one of this plurality of GAM6858 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6858 RNA, herein designated GAM RNA, and which when bound by GAM6858 RNA causes inhibition of translation of the GAM6858 target mRNA into a corresponding GAM6858 target protein.

The mechanism of the translational inhibition exerted by GAM6858 RNA, herein designated GAM RNA, on one or more GAM6858 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6858 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6858 RNA, herein designated GAM RNA, of GAM6858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6858 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6858 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6858 RNA correlate with, and may be deduced from, the identity of the GAM6858 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6978 6028 CAGGTATGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTGCCACT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTCTGAAA Messenger 6978 (GAM6978) oligonucleotides modulates expression of respective target genes

TTCCTGAGCA whose function and utility is known in the art.

CCGAGGGCCG GAM6978 is a novel bioinformatically detectable regulatory, non protein coding,

CTTCAGGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM6978 was detected is

CAGGCACTTT described with additional reference to Figs. 9-15.

GCCAACCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6978 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6978

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6978

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6978 precursor RNA is designated SEQ ID:6028, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6028 is located from position 140693634 to position 140693712 relative to chromosome 7 on the `-` strand.

GAM6978 precursor RNA folds onto itself, forming GAM6978 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6978 precursor RNA, designated SEQ ID NO: 6028, and a schematic representation of a predicted secondary folding of GAM6978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6978 folded precursor RNA yielding a GAM6978 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6978 RNA, hereby incorporated herein.

GAM6978 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6978 target RNA, herein designated GAM TARGET RNA. GAM6978 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6978 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6978 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6978 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6978 RNA, herein designated GAM RNA, to target binding sites on GAM6978 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6978 target RNA into GAM6978 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6978 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6978 target genes. The mRNA of each one of this plurality of GAM6978 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6978 RNA, herein designated GAM RNA, and which when bound by GAM6978 RNA causes inhibition of translation of the GAM6978 target mRNA into a corresponding GAM6978 target protein.

The mechanism of the translational inhibition exerted by GAM6978 RNA, herein designated GAM RNA, on one or more GAM6978 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6978 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6978 RNA, herein designated GAM RNA, of GAM6978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6978 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6978 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6978 RNA correlate with, and may be deduced from, the identity of the GAM6978 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6982 6040 CATGGGGTCG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTCACTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCCTCAGGG Messenger 6982 (GAM6982) oligonucleotides modulates expression of respective target genes

AAGGCAGTAG whose function and utility is known in the art.

GTTGTATAGT GAM6982 is a novel bioinformatically detectable regulatory, non protein coding,

TATCTTCCGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6982 was detected is

GGGGCAACAT described with additional reference to Figs. 9-15.

CACTGCCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAACCACACA encoded by the human genome.

ACCTACTACC GAM6982 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6982

TCACCCCGCC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6982

AGGCCCGGCC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TTGCACTGCG to the nucleotide sequence of GAM6982 precursor RNA is designated SEQ ID:6040, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6040 is located from position 44721785 to position 44721914 relative to chromosome 22 on the `-` strand.

GAM6982 precursor RNA folds onto itself, forming GAM6982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6982 precursor RNA, designated SEQ ID NO: 6040, and a schematic representation of a predicted secondary folding of GAM6982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6982 folded precursor RNA yielding a GAM6982 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6982 RNA, hereby incorporated herein. Expression of GAM6982 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM6982 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6982 target RNA, herein designated GAM TARGET RNA. GAM6982 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6982 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6982 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6982 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6982 RNA, herein designated GAM RNA, to target binding sites on GAM6982 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6982 target RNA

into GAM6982 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6982 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6982 target genes. The mRNA of each one of this plurality of GAM6982 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6982 RNA, herein designated GAM RNA, and which when bound by GAM6982 RNA causes inhibition of translation of the GAM6982 target mRNA into a corresponding GAM6982 target protein.

The mechanism of the translational inhibition exerted by GAM6982 RNA, herein designated GAM RNA, on one or more GAM6982 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6982 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6982 RNA, herein designated GAM RNA, of GAM6982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6982 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6982 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6982 RNA correlate with, and may be deduced from, the identity of the GAM6982 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6994 7204 TGCTCTGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTAGGCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGCAGTGA Messenger 6994 (GAM6994) oligonucleotides modulates expression of respective target genes

TGCAATTTTG whose function and utility is known in the art.

GCTCACTGCA GAM6994 is a novel bioinformatically detectable regulatory, non protein coding,

ACCTCCACCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM6994 was detected is

CCTGGGTTCA described with additional reference to Figs. 9-15.

AGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM6994 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6994 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6994 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6994 precursor RNA is designated SEQ ID:7204, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7204 is located from position 44650573 to position 44650646 relative to chromosome 19 on the `+` strand.

GAM6994 precursor RNA folds onto itself, forming GAM6994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6994 precursor RNA, designated SEQ ID NO: 7204, and a schematic representation of a predicted secondary folding of GAM6994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6994 folded precursor RNA yielding a GAM6994 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6994 RNA, hereby incorporated herein.

GAM6994 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6994 target RNA, herein designated GAM TARGET RNA. GAM6994 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6994 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6994 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6994 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6994 RNA, herein designated GAM RNA, to target binding sites on GAM6994 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6994 target RNA into GAM6994 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6994 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6994 target genes. The mRNA of each one of this plurality of GAM6994 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6994 RNA, herein designated GAM RNA, and which when bound by GAM6994 RNA causes inhibition of translation of the GAM6994 target mRNA into a corresponding GAM6994 target protein.

The mechanism of the translational inhibition exerted by GAM6994 RNA, herein designated GAM RNA, on one or more GAM6994 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6994 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6994 RNA, herein designated GAM RNA, of GAM6994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6994 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6994 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6994 RNA correlate with, and may be deduced from, the identity of the GAM6994 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM6996 7025 TCCCAGATTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCTGGTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCATTCGG Messenger 6996 (GAM6996) oligonucleotides modulates expression of respective target genes

AGAGCAACAC whose function and utility is known in the art.

CCTGGCCTTA GAM6996 is a novel bioinformatically detectable regulatory, non protein coding,

ACACACTACA micro RNA (miRNA)-like oligonucleotide. The method by which GAM6996 was detected is

TATCTTTGAA described with additional reference to Figs. 9-15.

TTTCACACGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGCAGCCTT encoded by the human genome.

CTGGGA GAM6996 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM6996 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM6996 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM6996 precursor RNA is designated SEQ ID:7025, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7025 is located from position 6197081 to position 6197176 relative to chromosome 17 on the `-` strand.

GAM6996 precursor RNA folds onto itself, forming GAM6996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM6996 precursor RNA, designated SEQ ID NO: 7025, and a schematic representation of a predicted secondary folding of GAM6996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM6996 folded precursor RNA yielding a GAM6996 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM6996 RNA, hereby incorporated herein.

GAM6996 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM6996 target RNA, herein designated GAM TARGET RNA. GAM6996 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM6996 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM6996 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM6996 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM6996 RNA, herein designated GAM RNA, to target binding sites on GAM6996 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM6996 target RNA into GAM6996 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM6996 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM6996 target genes. The mRNA of each one of this plurality of GAM6996 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM6996 RNA, herein designated GAM RNA, and which when bound by GAM6996 RNA causes inhibition of translation of the GAM6996 target mRNA into a corresponding GAM6996 target protein.

The mechanism of the translational inhibition exerted by GAM6996 RNA, herein designated GAM RNA, on one or more GAM6996 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM6996 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM6996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM6996 RNA, herein designated GAM RNA, of GAM6996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM6996 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM6996 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM6996 RNA correlate with, and may be deduced from, the identity of the GAM6996 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7017 6299 GAATAAATAA GCTGCTCTAA TTGCCAAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7017 (GAM7017) oligonucleotides modulates expression of respective target genes

TTCACATGTG whose function and utility is known in the art.

GTTGTATGCA GAM7017 is a novel bioinformatically detectable regulatory, non protein coding,
GCATTACTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7017 was detected is

GAAATTGAAG described with additional reference to Figs. 9-15.

TGTATCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTGATTCTG encoded by the human genome.

CTGTGATGGA GAM7017 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7017
CACTTGTAAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7017
TTTGTTC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7017 precursor RNA is designated SEQ ID:6299, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6299 is located from position 43025637 to position 43025753 relative to chromosome 9 on the `-` strand.

GAM7017 precursor RNA folds onto itself, forming GAM7017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7017 precursor RNA, designated SEQ ID NO: 6299, and a schematic representation of a predicted secondary folding of GAM7017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7017 folded precursor RNA yielding a GAM7017 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7017 RNA, hereby incorporated herein.

GAM7017 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7017 target RNA, herein designated GAM TARGET RNA. GAM7017 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7017 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7017 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7017 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7017 RNA, herein designated GAM RNA, to target binding sites on GAM7017 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7017 target RNA into GAM7017 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7017 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7017 target genes. The mRNA of each one of this plurality of GAM7017 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7017 RNA, herein designated GAM RNA, and which when bound by GAM7017 RNA causes inhibition of translation of the GAM7017 target mRNA into a corresponding GAM7017 target protein.

The mechanism of the translational inhibition exerted by GAM7017 RNA, herein designated GAM RNA, on one or more GAM7017 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7017 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7017 RNA, herein designated GAM RNA, of GAM7017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7017 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7017 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7017 RNA correlate with, and may be deduced from, the identity of the GAM7017 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7022 6822 GGGTGCATGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ACTAGGACCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGAGGCAGA Messenger 7022 (GAM7022) oligonucleotides modulates expression of respective target genes
AATAGTTACC whose function and utility is known in the art.

GAGGGGAAGT GAM7022 is a novel bioinformatically detectable regulatory, non protein coding,
TACAGGCCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7022 was detected is

AGTGTGAGTC described with additional reference to Figs. 9-15.

CCTGTTTGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCTGATGAG encoded by the human genome.

CTTTGAGGTC GAM7022 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7022
CTTGGCCAGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7022
CACTC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7022 precursor RNA is designated SEQ ID:6822, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6822 is located from position 47741101 to position 47741215 relative to chromosome X on the `-` strand.

GAM7022 precursor RNA folds onto itself, forming GAM7022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7022 precursor RNA, designated SEQ ID NO: 6822, and a schematic representation of a predicted secondary folding of GAM7022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7022 folded precursor RNA yielding a GAM7022 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7022 RNA, hereby incorporated herein.

GAM7022 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7022 target RNA, herein designated GAM TARGET RNA. GAM7022 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7022 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7022 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7022 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7022 RNA, herein designated GAM RNA, to target binding sites on GAM7022 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7022 target RNA into GAM7022 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7022 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7022 target genes. The mRNA of each one of this plurality of GAM7022 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7022 RNA, herein designated GAM RNA, and which when bound by GAM7022 RNA causes inhibition of translation of the GAM7022 target mRNA into a corresponding GAM7022 target protein.

The mechanism of the translational inhibition exerted by GAM7022 RNA, herein designated GAM RNA, on one or more GAM7022 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7022 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7022 RNA, herein designated GAM RNA, of GAM7022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7022 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7022 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7022 RNA correlate with, and may be deduced from, the identity of the GAM7022 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7067 6108 CCTCAGCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CATCAGAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCATGCTCG Messenger 7067 (GAM7067) oligonucleotides modulates expression of respective target genes
GAAGAATGCC whose function and utility is known in the art.

TACAGGAATG GAM7067 is a novel bioinformatically detectable regulatory, non protein coding,
AAAACTTAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7067 was detected is

AATTGTGGGA described with additional reference to Figs. 9-15.

AATACTTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAAATATCT encoded by the human genome.

GGTTTCATGG GAM7067 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7067
TATGTAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7067

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7067 precursor RNA is designated SEQ ID:6108, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6108 is located from position 42704752 to position 42704859 relative to chromosome 19 on the `+` strand.

GAM7067 precursor RNA folds onto itself, forming GAM7067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7067 precursor RNA, designated SEQ ID NO: 6108, and a schematic representation of a predicted secondary folding of GAM7067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7067 folded precursor RNA yielding a GAM7067 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7067 RNA, hereby incorporated herein.

GAM7067 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7067 target RNA, herein designated GAM TARGET RNA. GAM7067 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7067 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7067 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7067 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7067 RNA, herein designated GAM RNA, to target binding sites on GAM7067 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7067 target RNA into GAM7067 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7067 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7067 target genes. The mRNA of each one of this plurality of GAM7067 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7067 RNA, herein designated GAM RNA, and which when bound by GAM7067 RNA causes inhibition of translation of the GAM7067 target mRNA into a corresponding GAM7067 target protein.

The mechanism of the translational inhibition exerted by GAM7067 RNA, herein designated GAM RNA, on one or more GAM7067 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7067 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7067 RNA, herein designated GAM RNA, of GAM7067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM7067 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7067 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7067 RNA correlate with, and may be deduced from, the identity of the GAM7067 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7078 6907 GTGCTAGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCACCTATG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGGAGCCAG Messenger 7078 (GAM7078) oligonucleotides modulates expression of respective target genes
CTCTGCCTCC whose function and utility is known in the art.

TGCCCCGAAG GAM7078 is a novel bioinformatically detectable regulatory, non protein coding,
CTCCAGAGAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7078 was detected is

TTCTCCTACA described with additional reference to Figs. 9-15.

ACTGACTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGACAC encoded by the human genome.

GAM7078 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7078

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7078
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7078 precursor RNA is designated SEQ ID:6907, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6907 is located from position 38614091 to position 38614177 relative to chromosome 17 on the `-` strand.

GAM7078 precursor RNA folds onto itself, forming GAM7078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7078 precursor RNA, designated SEQ ID NO: 6907, and a schematic representation of a predicted secondary folding of GAM7078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7078 folded precursor RNA yielding a GAM7078 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7078 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7078 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7078 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7078 target RNA, herein designated GAM TARGET RNA. GAM7078 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7078 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7078 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7078 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7078 RNA, herein designated GAM RNA, to target binding sites on GAM7078 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7078 target RNA into GAM7078 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7078 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7078 target genes. The mRNA of each one of this plurality of GAM7078 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7078 RNA, herein designated GAM RNA, and which when bound by GAM7078 RNA causes inhibition of translation of the GAM7078 target mRNA into a corresponding GAM7078 target protein.

The mechanism of the translational inhibition exerted by GAM7078 RNA, herein designated GAM RNA, on one or more GAM7078 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7078 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7078 RNA, herein designated GAM RNA, of GAM7078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7078 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7078 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7078 RNA correlate with, and may be deduced from, the identity of the GAM7078 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7080 6064 CCATTTTTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAGGTCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGGTTGCA Messenger 7080 (GAM7080) oligonucleotides modulates expression of respective target genes

AACTGGATTT whose function and utility is known in the art.

TTAGACTCTT GAM7080 is a novel bioinformatically detectable regulatory, non protein coding,

CCTGTTGGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7080 was detected is

GTCTCGGACA described with additional reference to Figs. 9-15.

TTTGCTCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCACAGCGG encoded by the human genome.

CCAATTCTTC GAM7080 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7080

AGAGCCACAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7080

AGAACTGG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7080 precursor RNA is designated SEQ ID:6064, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6064 is located from position 1047334 to position 1047441 relative to chromosome 1 on the `-` strand.

GAM7080 precursor RNA folds onto itself, forming GAM7080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7080 precursor RNA, designated SEQ ID NO: 6064, and a

schematic representation of a predicted secondary folding of GAM7080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7080 folded precursor RNA yielding a GAM7080 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7080 RNA, hereby incorporated herein. Expression of GAM7080 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7080 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7080 target RNA, herein designated GAM TARGET RNA. GAM7080 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7080 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7080 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7080 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7080 RNA, herein designated GAM RNA, to target binding sites on GAM7080 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7080 target RNA into GAM7080 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7080 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7080 target genes. The mRNA of each one of this plurality of GAM7080 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7080 RNA, herein designated GAM RNA, and which when bound by GAM7080 RNA causes inhibition of translation of the GAM7080 target mRNA into a corresponding GAM7080 target protein.

The mechanism of the translational inhibition exerted by GAM7080 RNA, herein designated GAM RNA, on one or more GAM7080 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7080 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7080 RNA, herein designated GAM RNA, of GAM7080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7080 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7080 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7080 RNA correlate with, and may be deduced from, the identity of the GAM7080 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7095 7015 TCATCTATCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTAGGCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTATCTTAT Messenger 7095 (GAM7095) oligonucleotides modulates expression of respective target genes

CAGCTACTGA whose function and utility is known in the art.

CCCAGTTAGC GAM7095 is a novel bioinformatically detectable regulatory, non protein coding,

TTTCCTACTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7095 was detected is

CACAACAGGT described with additional reference to Figs. 9-15.

TTCTAATGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTATGTCAGT encoded by the human genome.

GTGAGAGAAA GAM7095 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7095

TGGCAAGTTG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7095

GGAAAATTTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

TGA to the nucleotide sequence of GAM7095 precursor RNA is designated SEQ ID:7015, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7015 is located from position 104082522 to position 104082644 relative to chromosome 7 on the `+` strand.

GAM7095 precursor RNA folds onto itself, forming GAM7095 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7095 precursor RNA, designated SEQ ID NO: 7015, and a schematic representation of a predicted secondary folding of GAM7095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7095 folded precursor RNA yielding a GAM7095 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7095 RNA, hereby incorporated herein.

GAM7095 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7095 target RNA, herein designated GAM TARGET RNA. GAM7095 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7095 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7095 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7095 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7095 RNA, herein designated GAM RNA, to target binding sites on GAM7095 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7095 target RNA into GAM7095 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7095 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7095 target genes. The mRNA of each one of this plurality of GAM7095 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7095 RNA, herein designated GAM RNA, and which when bound by GAM7095 RNA causes inhibition of translation of the GAM7095 target mRNA into a corresponding GAM7095 target protein.

The mechanism of the translational inhibition exerted by GAM7095 RNA, herein designated GAM RNA, on one or more GAM7095 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7095 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7095 RNA, herein designated GAM RNA, of GAM7095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7095 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7095 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7095 RNA correlate with, and may be deduced from, the identity of the GAM7095 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7102 6994 TCACTCTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCCAGGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTGCAGTG Messenger 7102 (GAM7102) oligonucleotides modulates expression of respective target genes

GTACAGCCTC whose function and utility is known in the art.

AGCTCACTGC GAM7102 is a novel bioinformatically detectable regulatory, non protein coding,

AACCTCCACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7102 was detected is

TCCCGGGCTC described with additional reference to Figs. 9-15.

AAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7102 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7102

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7102

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7102 precursor RNA is designated SEQ ID:6994, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6994 is located from position 152542921 to position 152542996 relative to chromosome 1 on the `+` strand.

GAM7102 precursor RNA folds onto itself, forming GAM7102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7102 precursor RNA, designated SEQ ID NO: 6994, and a schematic representation of a predicted secondary folding of GAM7102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7102 folded precursor RNA yielding a GAM7102 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7102 RNA, hereby incorporated herein.

GAM7102 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7102 target RNA, herein designated GAM TARGET RNA. GAM7102 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7102 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7102 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7102 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7102 RNA, herein designated GAM RNA, to target binding sites on GAM7102 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7102 target RNA into GAM7102 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7102 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM7102 target genes. The mRNA of each one of this plurality of GAM7102 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7102 RNA, herein designated GAM RNA, and which when bound by GAM7102 RNA causes inhibition of translation of the GAM7102 target mRNA into a corresponding GAM7102 target protein.

The mechanism of the translational inhibition exerted by GAM7102 RNA, herein designated GAM RNA, on one or more GAM7102 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7102 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7102 RNA, herein designated GAM RNA, of GAM7102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7102 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7102 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7102 RNA correlate with, and may be deduced from, the identity of the GAM7102 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7124 5817 AGTGTCTCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTGCACGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACATTTCATT Messenger 7124 (GAM7124) oligonucleotides modulates expression of respective target genes

TTTCACACAG whose function and utility is known in the art.

GGTCACCAGA GAM7124 is a novel bioinformatically detectable regulatory, non protein coding,

ATACCATCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7124 was detected is

TTTTTTGGTA described with additional reference to Figs. 9-15.

TCACTGTCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGTGATCCT encoded by the human genome.

AGCACCTTCT GAM7124 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7124

GAAATAACGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7124

GAGCTGCCAG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

ATTCT to the nucleotide sequence of GAM7124 precursor RNA is designated SEQ ID:5817, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5817 is located from position 75288695 to position 75288819 relative to chromosome 16 on the `+` strand.

GAM7124 precursor RNA folds onto itself, forming GAM7124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7124 precursor RNA, designated SEQ ID NO: 5817, and a schematic representation of a predicted secondary folding of GAM7124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7124 folded precursor RNA yielding a GAM7124 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7124 RNA, hereby incorporated herein.

GAM7124 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7124 target RNA, herein designated GAM TARGET RNA. GAM7124 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7124 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7124 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7124 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7124 RNA, herein designated GAM RNA, to target binding sites on GAM7124 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7124 target RNA into GAM7124 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7124 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7124 target genes. The mRNA of each one of this plurality of GAM7124 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7124 RNA, herein designated GAM RNA, and which when bound by GAM7124 RNA causes inhibition of translation of the GAM7124 target mRNA into a corresponding GAM7124 target protein.

The mechanism of the translational inhibition exerted by GAM7124 RNA, herein designated GAM RNA, on one or more GAM7124 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7124 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7124 RNA, herein designated GAM RNA, of GAM7124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7124 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7124 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7124 RNA correlate with, and may be deduced from, the identity of the GAM7124 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7135 7216 TGGACTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCTGGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAAATAGTT Messenger 7135 (GAM7135) oligonucleotides modulates expression of respective target genes
ACCGAGGGGA whose function and utility is known in the art.

AGTTACAGGC GAM7135 is a novel bioinformatically detectable regulatory, non protein coding,
CTGAGTGTGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7135 was detected is

GTCCCTGTTT described with additional reference to Figs. 9-15.

GGTTGCTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCTTTGAG encoded by the human genome.

GTCCTTGGCC GAM7135 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7135

A precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7135

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7135 precursor RNA is designated SEQ ID:7216, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7216 is located from position 47741108 to position 47741208 relative to chromosome X on the `-` strand.

GAM7135 precursor RNA folds onto itself, forming GAM7135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7135 precursor RNA, designated SEQ ID NO: 7216, and a schematic representation of a predicted secondary folding of GAM7135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7135 folded precursor RNA yielding a GAM7135 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7135 RNA, hereby incorporated herein.

GAM7135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7135 target RNA, herein designated GAM TARGET RNA. GAM7135 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7135 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7135 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7135 RNA, herein designated GAM RNA, to target binding sites on GAM7135 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7135 target RNA into GAM7135 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7135 target genes. The mRNA of each one of this plurality of GAM7135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7135 RNA, herein designated GAM RNA, and which when bound by GAM7135 RNA causes inhibition of translation of the GAM7135 target mRNA into a corresponding GAM7135 target protein.

The mechanism of the translational inhibition exerted by GAM7135 RNA, herein designated GAM RNA, on one or more GAM7135 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7135 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7135 RNA, herein designated GAM RNA, of GAM7135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7135 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7135 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7135 RNA correlate with, and may be deduced from, the identity of the GAM7135 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7140 6498 GCAGGTCCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTCAGTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGGGCCTT Messenger 7140 (GAM7140) oligonucleotides modulates expression of respective target genes

GGCTGGGATG whose function and utility is known in the art.

CTGAGTTATC GAM7140 is a novel bioinformatically detectable regulatory, non protein coding, CACTGGAGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7140 was detected is

TCGGCAGTAC described with additional reference to Figs. 9-15.

AGGCAGGCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGGCAGTG encoded by the human genome.

GATCCATCGG GAM7140 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7140

AGGTGGCAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7140

T precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7140 precursor RNA is designated SEQ ID:6498, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6498 is located from position 69762447 to position 69762557 relative to chromosome 16 on the `+` strand.

GAM7140 precursor RNA folds onto itself, forming GAM7140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7140 precursor RNA, designated SEQ ID NO: 6498, and a schematic representation of a predicted secondary folding of GAM7140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7140 folded precursor RNA yielding a GAM7140 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7140 RNA, hereby incorporated herein.

GAM7140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7140 target RNA, herein designated GAM TARGET RNA. GAM7140 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7140 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7140 RNA, herein designated GAM RNA, to target binding sites on GAM7140 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7140 target RNA into GAM7140 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7140 target genes. The mRNA of each one of this plurality of GAM7140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7140 RNA, herein designated GAM RNA, and which when bound by GAM7140 RNA causes inhibition of translation of the GAM7140 target mRNA into a corresponding GAM7140 target protein.

The mechanism of the translational inhibition exerted by GAM7140 RNA, herein designated GAM RNA, on one or more GAM7140 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7140 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7140 RNA, herein designated GAM RNA, of GAM7140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7140 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7140 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7140 RNA correlate with, and may be deduced from, the identity of the GAM7140 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7146 5979 ATTATGTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAGTATGTA detected oligonucleotides of the present invention, referred to here as Genomic Address
TATAGTATTT Messenger 7146 (GAM7146) oligonucleotides modulates expression of respective target genes
TTAGTGAAAA whose function and utility is known in the art.

TATTCATATA GAM7146 is a novel bioinformatically detectable regulatory, non protein coding,
AAATATTACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7146 was detected is

TAAATCATTT described with additional reference to Figs. 9-15.

CTACATTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAAAT encoded by the human genome.

GAM7146 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7146

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7146

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7146 precursor RNA is designated SEQ ID:5979, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5979 is located from position 35139835 to position 35139920 relative to chromosome 13 on the `+` strand.

GAM7146 precursor RNA folds onto itself, forming GAM7146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7146 precursor RNA, designated SEQ ID NO: 5979, and a schematic representation of a predicted secondary folding of GAM7146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7146 folded precursor RNA yielding a GAM7146 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7146 RNA, hereby incorporated herein.

GAM7146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7146 target RNA, herein designated GAM TARGET RNA. GAM7146 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7146 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7146 RNA, herein designated GAM RNA, to target binding sites on GAM7146 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7146 target RNA into GAM7146 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7146 target genes. The mRNA of each one of this plurality of GAM7146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7146 RNA, herein designated GAM RNA, and which when bound by GAM7146 RNA causes inhibition of translation of the GAM7146 target mRNA into a corresponding GAM7146 target protein.

The mechanism of the translational inhibition exerted by GAM7146 RNA, herein designated GAM RNA, on one or more GAM7146 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7146 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7146 RNA, herein designated GAM RNA, of GAM7146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7146 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7146 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7146 RNA correlate with, and may be deduced from, the identity of the GAM7146 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7162 5828 AGTTTAAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTCGCAAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGGGTGGC Messenger 7162 (GAM7162) oligonucleotides modulates expression of respective target genes
CTTCAGTCCA whose function and utility is known in the art.

TGAAAGAGAA GAM7162 is a novel bioinformatically detectable regulatory, non protein coding,
CACATCTGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7162 was detected is

CTATCTCAGG described with additional reference to Figs. 9-15.

CTGAGGTCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGCATCCTC encoded by the human genome.

ATCAATAAGC GAM7162 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7162
T precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7162
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7162 precursor RNA is designated SEQ ID:5828, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5828 is located from position 53192373 to position 53192473 relative to chromosome 20 on the `+` strand.

GAM7162 precursor RNA folds onto itself, forming GAM7162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7162 precursor RNA, designated SEQ ID NO: 5828, and a schematic representation of a predicted secondary folding of GAM7162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7162 folded precursor RNA yielding a GAM7162 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7162 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7162 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7162 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7162 target RNA, herein designated GAM TARGET RNA. GAM7162 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7162 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7162 RNA, herein designated GAM RNA, to target binding sites on GAM7162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7162 target RNA into GAM7162 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7162 target genes. The mRNA of each one of this plurality of GAM7162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7162 RNA, herein designated GAM RNA, and which when bound by GAM7162 RNA causes inhibition of translation of the GAM7162 target mRNA into a corresponding GAM7162 target protein.

The mechanism of the translational inhibition exerted by GAM7162 RNA, herein designated GAM RNA, on one or more GAM7162 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7162 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7162 RNA, herein designated GAM RNA, of GAM7162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7162 target RNA, herein designated GAM

TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7162 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7162 RNA correlate with, and may be deduced from, the identity of the GAM7162 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7166 6547 GCTGGGGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGTTTACAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTTTCTAAT Messenger 7166 (GAM7166) oligonucleotides modulates expression of respective target genes
GGAGCCATTA whose function and utility is known in the art.

TCTGTTGGAG GAM7166 is a novel bioinformatically detectable regulatory, non protein coding,
GCATTCATTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7166 was detected is

CCCTCACCAG described with additional reference to Figs. 9-15.

C GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM7166 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7166

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7166
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7166 precursor RNA is designated SEQ ID:6547, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6547 is located from position 109789635 to position 109789705 relative to chromosome 10 on the `-` strand.

GAM7166 precursor RNA folds onto itself, forming GAM7166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7166 precursor RNA, designated SEQ ID NO: 6547, and a schematic representation of a predicted secondary folding of GAM7166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7166 folded precursor RNA yielding a GAM7166 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor

product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7166 RNA, hereby incorporated herein.

GAM7166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7166 target RNA, herein designated GAM TARGET RNA. GAM7166 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7166 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7166 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7166 RNA, herein designated GAM RNA, to target binding sites on GAM7166 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7166 target RNA into GAM7166 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7166 target genes. The mRNA of each one of this plurality of GAM7166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7166 RNA, herein designated GAM RNA, and which when bound by GAM7166 RNA causes inhibition of translation of the GAM7166 target mRNA into a corresponding GAM7166 target protein.

The mechanism of the translational inhibition exerted by GAM7166 RNA, herein designated GAM RNA, on one or more GAM7166 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7166 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7166 RNA, herein designated GAM RNA, of GAM7166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7166 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7166 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7166 RNA correlate with, and may be deduced from, the identity of the GAM7166 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7169 5677 AATGTAAACC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTTAAAGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GATGTGTGTG Messenger 7169 (GAM7169) oligonucleotides modulates expression of respective target genes
GGGCCTTATG whose function and utility is known in the art.

AAGACCAGGA GAM7169 is a novel bioinformatically detectable regulatory, non protein coding,
TTCTGCGGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7169 was detected is

GTCAGGGGAT described with additional reference to Figs. 9-15.

TGCCCCTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GACAGAGACT encoded by the human genome.

AGGGTTTTAG GAM7169 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7169
ACTGAGGCTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7169
CCTGCAGGGT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
GTTCGCATT to the nucleotide sequence of GAM7169 precursor RNA is designated SEQ ID:5677, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5677 is located from position 50572112 to position 50572240 relative to chromosome 16 on the `+` strand.

GAM7169 precursor RNA folds onto itself, forming GAM7169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7169 precursor RNA, designated SEQ ID NO: 5677, and a schematic representation of a predicted secondary folding of GAM7169 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7169 folded precursor RNA yielding a GAM7169 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7169 RNA, hereby incorporated herein.

GAM7169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7169 target RNA, herein designated GAM TARGET RNA. GAM7169 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7169 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7169 RNA, herein designated GAM RNA, to target binding sites on GAM7169 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7169 target RNA into GAM7169 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7169 target genes. The mRNA of each one of this plurality of GAM7169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7169 RNA, herein designated GAM RNA, and which when bound by GAM7169 RNA causes inhibition of translation of the GAM7169 target mRNA into a corresponding GAM7169 target protein.

The mechanism of the translational inhibition exerted by GAM7169 RNA, herein designated GAM RNA, on one or more GAM7169 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7169 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM7169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7169 RNA, herein designated GAM RNA, of GAM7169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7169 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7169 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7169 RNA correlate with, and may be deduced from, the identity of the GAM7169 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7199 6724 GGATTTGGCA AAGAAGGCAG TACAGTTAAT CCTGGCTGCA ACTGCTGGAA AATTTGCTAC ACCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7199 (GAM7199) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM7199 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM7199 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM7199 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7199 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7199 precursor RNA is designated SEQ ID:6724, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6724 is located from position 48078880 to position 48078943 relative to chromosome 13 on the `-` strand.

GAM7199 precursor RNA folds onto itself, forming GAM7199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7199 precursor RNA, designated SEQ ID NO: 6724, and a schematic representation of a predicted secondary folding of GAM7199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7199 folded precursor RNA yielding a GAM7199 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7199 RNA, hereby incorporated herein.

GAM7199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7199 target RNA, herein designated GAM TARGET RNA. GAM7199 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7199 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7199 RNA, herein designated GAM RNA, to target binding sites on GAM7199 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7199 target RNA into GAM7199 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7199 target genes. The mRNA of each one of this plurality of GAM7199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7199 RNA, herein designated GAM RNA, and which when bound by GAM7199 RNA causes inhibition of translation of the GAM7199 target mRNA into a corresponding GAM7199 target protein.

The mechanism of the translational inhibition exerted by GAM7199 RNA, herein designated GAM RNA, on one or more GAM7199 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7199 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7199 RNA, herein designated GAM RNA, of GAM7199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7199 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7199 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7199 RNA correlate with, and may be deduced from, the identity of the GAM7199 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7201 5704 ACTCTATTTT ATTCAAATGG CACTATGATA TGAGTTCAAA AAATTTTTGA AACAGTGTCC TTTGTTTTGA GATGGAGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7201 (GAM7201) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM7201 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM7201 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM7201 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7201 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7201 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7201 precursor RNA is designated SEQ ID:5704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5704 is located from position 27583817 to position 27583894 relative to chromosome 17 on the `+` strand.

GAM7201 precursor RNA folds onto itself, forming GAM7201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7201 precursor RNA, designated SEQ ID NO: 5704, and a schematic representation of a predicted secondary folding of GAM7201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7201 folded precursor RNA yielding a GAM7201 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7201 RNA, hereby incorporated herein.

GAM7201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7201 target RNA, herein designated GAM TARGET RNA. GAM7201 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7201 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7201 RNA, herein designated GAM RNA, to target binding sites on GAM7201 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7201 target RNA into GAM7201 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7201 target genes. The mRNA of each one of this plurality of GAM7201 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7201 RNA, herein

designated GAM RNA, and which when bound by GAM7201 RNA causes inhibition of translation of the GAM7201 target mRNA into a corresponding GAM7201 target protein.

The mechanism of the translational inhibition exerted by GAM7201 RNA, herein designated GAM RNA, on one or more GAM7201 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7201 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7201 RNA, herein designated GAM RNA, of GAM7201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7201 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7201 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7201 RNA correlate with, and may be deduced from, the identity of the GAM7201 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7212 6746 GGCCAGGACT CTTGCAGAAC TGAGACCTGG GAGCTCCTCC CTCACCAGGA AGGGACCCGA GGCAGGCGGC GGGGGTCTCT GAGCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7212 (GAM7212) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM7212 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM7212 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM7212 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7212

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7212

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7212 precursor RNA is designated SEQ ID:6746, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6746 is located from position 45164402 to position 45164486 relative to chromosome 21 on the `-` strand.

GAM7212 precursor RNA folds onto itself, forming GAM7212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7212 precursor RNA, designated SEQ ID NO: 6746, and a schematic representation of a predicted secondary folding of GAM7212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7212 folded precursor RNA yielding a GAM7212 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7212 RNA, hereby incorporated herein.

GAM7212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7212 target RNA, herein designated GAM TARGET RNA. GAM7212 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7212 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7212 RNA, herein designated GAM RNA, to target binding sites on GAM7212 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7212 target RNA into GAM7212 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7212 target genes. The mRNA of each one of this plurality of GAM7212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7212 RNA, herein designated GAM RNA, and which when bound by GAM7212 RNA causes inhibition of translation of the GAM7212 target mRNA into a corresponding GAM7212 target protein.

The mechanism of the translational inhibition exerted by GAM7212 RNA, herein designated GAM RNA, on one or more GAM7212 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7212 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7212 RNA, herein designated GAM RNA, of GAM7212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7212 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7212 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7212 RNA correlate with, and may be deduced from, the identity of the GAM7212 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7241 5965 ATGACTGTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCAGGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTCAGTGT Messenger 7241 (GAM7241) oligonucleotides modulates expression of respective target genes

GAAGAACTAC whose function and utility is known in the art.

GGGTTTCCTG GAM7241 is a novel bioinformatically detectable regulatory, non protein coding,

ATGTTGAAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7241 was detected is

TCAGAATTAG described with additional reference to Figs. 9-15.

CCACACTGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTCTCAGTC encoded by the human genome.

ATGCAT GAM7241 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7241 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7241 precursor RNA is designated SEQ ID:5965, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5965 is located from position 46762982 to position 46763077 relative to chromosome 12 on the `-` strand.

GAM7241 precursor RNA folds onto itself, forming GAM7241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7241 precursor RNA, designated SEQ ID NO: 5965, and a schematic representation of a predicted secondary folding of GAM7241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7241 folded precursor RNA yielding a GAM7241 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7241 RNA, hereby incorporated herein.

GAM7241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7241 target RNA, herein designated GAM TARGET RNA. GAM7241 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7241 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7241 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7241 RNA, herein designated GAM RNA, to target binding sites on GAM7241 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7241 target RNA into GAM7241 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7241 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7241 target genes. The mRNA of each one of this plurality of GAM7241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7241 RNA, herein designated GAM RNA, and which when bound by GAM7241 RNA causes inhibition of translation of the GAM7241 target mRNA into a corresponding GAM7241 target protein.

The mechanism of the translational inhibition exerted by GAM7241 RNA, herein designated GAM RNA, on one or more GAM7241 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7241 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7241 RNA, herein designated GAM RNA, of GAM7241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7241 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7241 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7241 RNA correlate with, and may be deduced from, the identity of the GAM7241 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7250 6026 CAGGGAGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCTGTGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGATGTGG Messenger 7250 (GAM7250) oligonucleotides modulates expression of respective target genes
TTTATAAATT whose function and utility is known in the art.

ACCATTTGGA GAM7250 is a novel bioinformatically detectable regulatory, non protein coding,
AGGAGCTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7250 was detected is

CAGCACAGCA described with additional reference to Figs. 9-15.

GCCTGCAACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACTCTTCCTG encoded by the human genome.

GAM7250 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7250 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7250 precursor RNA is designated SEQ ID:6026, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6026 is located from position 82179628 to position 82179717 relative to chromosome 7 on the `-` strand.

GAM7250 precursor RNA folds onto itself, forming GAM7250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7250 precursor RNA, designated SEQ ID NO: 6026, and a schematic representation of a predicted secondary folding of GAM7250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7250 folded precursor RNA yielding a GAM7250 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7250 RNA, hereby incorporated herein.

GAM7250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7250 target RNA, herein designated GAM TARGET RNA. GAM7250 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7250 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7250 RNA, herein designated GAM RNA, to target binding sites on GAM7250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7250 target RNA into GAM7250 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7250 target genes. The mRNA of each one of this plurality of GAM7250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7250 RNA, herein designated GAM RNA, and which when bound by GAM7250 RNA causes inhibition of translation of the GAM7250 target mRNA into a corresponding GAM7250 target protein.

The mechanism of the translational inhibition exerted by GAM7250 RNA, herein designated GAM RNA, on one or more GAM7250 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7250 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7250 RNA, herein designated GAM RNA, of GAM7250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7250 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7250 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7250 RNA correlate with, and may be deduced from, the identity of the GAM7250 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7255 6273 CTTTGAGATG ACTGGTATTG AATGGAGCAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7255 (GAM7255) oligonucleotides modulates expression of respective target genes

TCTTTGAAAG whose function and utility is known in the art.

GCACCAACCC GAM7255 is a novel bioinformatically detectable regulatory, non protein coding, TTCCTAACTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7255 was detected is

ATGGTGGTCT described with additional reference to Figs. 9-15.

CTTGAAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTCTTCCAA encoded by the human genome.

ATTTGTCTTC GAM7255 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7255

TGAAAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7255

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7255 precursor RNA is designated SEQ ID:6273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6273 is located from position 33981298 to position 33981403 relative to chromosome 15 on the `+` strand.

GAM7255 precursor RNA folds onto itself, forming GAM7255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7255 precursor RNA, designated SEQ ID NO: 6273, and a schematic representation of a predicted secondary folding of GAM7255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7255 folded precursor RNA yielding a GAM7255 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7255 RNA, hereby incorporated herein.

GAM7255 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7255 target RNA, herein designated GAM TARGET RNA. GAM7255 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7255 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7255 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7255 RNA, herein designated GAM RNA, to target binding sites on GAM7255 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7255 target RNA into GAM7255 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7255 target genes. The mRNA of each one of this plurality of GAM7255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7255 RNA, herein designated GAM RNA, and which when bound by GAM7255 RNA causes inhibition of translation of the GAM7255 target mRNA into a corresponding GAM7255 target protein.

The mechanism of the translational inhibition exerted by GAM7255 RNA, herein designated GAM RNA, on one or more GAM7255 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7255 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7255 RNA, herein designated GAM RNA, of GAM7255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7255 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7255 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7255 RNA correlate with, and may be deduced from, the identity of the GAM7255 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7257 6863 GTAGAGGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGTTTCTCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTTGGTCAG Messenger 7257 (GAM7257) oligonucleotides modulates expression of respective target genes
GCTGGTCTTT whose function and utility is known in the art.

AACTCCTGAC GAM7257 is a novel bioinformatically detectable regulatory, non protein coding,
CTCAGGTGAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7257 was detected is

ACGCCCGCCT described with additional reference to Figs. 9-15.

TGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM7257 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7257

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7257
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7257 precursor RNA is designated SEQ ID:6863, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6863 is located from position 159922811 to position 159922884 relative to chromosome 6 on the `-` strand.

GAM7257 precursor RNA folds onto itself, forming GAM7257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7257 precursor RNA, designated SEQ ID NO: 6863, and a schematic representation of a predicted secondary folding of GAM7257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7257 folded precursor RNA yielding a GAM7257 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7257 RNA, hereby incorporated herein.

GAM7257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7257 target RNA, herein designated GAM TARGET RNA. GAM7257 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7257 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7257 RNA, herein designated GAM RNA, to target binding sites on GAM7257 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7257 target RNA into GAM7257 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7257 target genes. The mRNA of each one of this plurality of GAM7257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7257 RNA, herein designated GAM RNA, and which when bound by GAM7257 RNA causes inhibition of translation of the GAM7257 target mRNA into a corresponding GAM7257 target protein.

The mechanism of the translational inhibition exerted by GAM7257 RNA, herein designated GAM RNA, on one or more GAM7257 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7257 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7257 RNA, herein designated GAM RNA, of GAM7257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7257 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7257 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7257 RNA correlate with, and may be deduced from, the identity of the GAM7257 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7260 6193 CTGAATCATG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTGTATAC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGATGTCAG Messenger 7260 (GAM7260) oligonucleotides modulates expression of respective target genes

TGAAGAGGTC whose function and utility is known in the art.

TGGCAGGAAT GAM7260 is a novel bioinformatically detectable regulatory, non protein coding,

GCCTCACTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7260 was detected is

CTTCCTACTG described with additional reference to Figs. 9-15.

ACTGGTACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTTATGATGC encoded by the human genome.

AG GAM7260 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7260

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7260

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7260 precursor RNA is designated SEQ ID:6193, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6193 is located from position 61858740 to position 61858831 relative to chromosome X on the `+` strand.

GAM7260 precursor RNA folds onto itself, forming GAM7260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7260 precursor RNA, designated SEQ ID NO: 6193, and a schematic representation of a predicted secondary folding of GAM7260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7260 folded precursor RNA yielding a GAM7260 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7260 RNA, hereby incorporated herein.

GAM7260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7260 target RNA, herein designated GAM TARGET RNA. GAM7260 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7260 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7260 RNA, herein designated GAM RNA, to target binding sites on GAM7260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7260 target RNA into GAM7260 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7260 target genes. The mRNA of each one of this plurality of GAM7260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7260 RNA, herein designated GAM RNA, and which when bound by GAM7260 RNA causes inhibition of translation of the GAM7260 target mRNA into a corresponding GAM7260 target protein.

The mechanism of the translational inhibition exerted by GAM7260 RNA, herein designated GAM RNA, on one or more GAM7260 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7260 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7260 RNA, herein designated GAM RNA, of GAM7260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM7260 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7260 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7260 RNA correlate with, and may be deduced from, the identity of the GAM7260 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7264 6552 GCTGTCTATT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGAGTCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGCACAGA Messenger 7264 (GAM7264) oligonucleotides modulates expression of respective target genes
CATCTGTCAA whose function and utility is known in the art.

GGAAGAAGGA GAM7264 is a novel bioinformatically detectable regulatory, non protein coding,
TTCTTTGAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7264 was detected is

GTATTTGTGT described with additional reference to Figs. 9-15.

CAGTCAACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CATATATGGA encoded by the human genome.

CCACAACAGA GAM7264 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7264
AAGC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7264

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7264 precursor RNA is designated SEQ ID:6552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6552 is located from position 78654885 to position 78654988 relative to chromosome 11 on the `-` strand.

GAM7264 precursor RNA folds onto itself, forming GAM7264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7264 precursor RNA, designated SEQ ID NO: 6552, and a schematic representation of a predicted secondary folding of GAM7264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7264 folded precursor RNA yielding a GAM7264 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7264 RNA, hereby incorporated herein.

GAM7264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7264 target RNA, herein designated GAM TARGET RNA. GAM7264 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7264 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7264 RNA, herein designated GAM RNA, to target binding sites on GAM7264 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7264 target RNA into GAM7264 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7264 target genes. The mRNA of each one of this plurality of GAM7264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7264 RNA, herein designated GAM RNA, and which when bound by GAM7264 RNA causes inhibition of translation of the GAM7264 target mRNA into a corresponding GAM7264 target protein.

The mechanism of the translational inhibition exerted by GAM7264 RNA, herein designated GAM RNA, on one or more GAM7264 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7264 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7264 RNA, herein designated GAM RNA, of

GAM7264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7264 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7264 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7264 RNA correlate with, and may be deduced from, the identity of the GAM7264 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7272 6095 CCCTTTCAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACAAAGCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCAGGATAG Messenger 7272 (GAM7272) oligonucleotides modulates expression of respective target genes

CCCTGGGCAG whose function and utility is known in the art.

AACTCCTGGG GAM7272 is a novel bioinformatically detectable regulatory, non protein coding,

ATTGACTGGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7272 was detected is

CAGTAATGTA described with additional reference to Figs. 9-15.

GTTGAGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7272 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7272

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7272

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7272 precursor RNA is designated SEQ ID:6095, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6095 is located from position 44585164 to position 44585243 relative to chromosome 20 on the `+` strand.

GAM7272 precursor RNA folds onto itself, forming GAM7272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7272 precursor RNA, designated SEQ ID NO: 6095, and a schematic representation of a predicted secondary folding of GAM7272 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7272 folded precursor RNA yielding a GAM7272 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7272 RNA, hereby incorporated herein.

GAM7272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7272 target RNA, herein designated GAM TARGET RNA. GAM7272 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7272 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7272 RNA, herein designated GAM RNA, to target binding sites on GAM7272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7272 target RNA into GAM7272 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7272 target genes. The mRNA of each one of this plurality of GAM7272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7272 RNA, herein designated GAM RNA, and which when bound by GAM7272 RNA causes inhibition of translation of the GAM7272 target mRNA into a corresponding GAM7272 target protein.

The mechanism of the translational inhibition exerted by GAM7272 RNA, herein designated GAM RNA, on one or more GAM7272 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7272 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM7272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7272 RNA, herein designated GAM RNA, of GAM7272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7272 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7272 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7272 RNA correlate with, and may be deduced from, the identity of the GAM7272 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7302 6114 CCTCCTGTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCAAAACGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAACACTCCT Messenger 7302 (GAM7302) oligonucleotides modulates expression of respective target genes

ATATTTTGTA whose function and utility is known in the art.

GCGCCTTCCA GAM7302 is a novel bioinformatically detectable regulatory, non protein coding,

GAATGGGGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7302 was detected is

GCGGAAACTA described with additional reference to Figs. 9-15.

GTGTTGGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGGAGG encoded by the human genome.

GAM7302 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7302

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7302

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7302 precursor RNA is designated SEQ ID:6114, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6114 is located from position 53161341 to position 53161428 relative to chromosome 15 on the `-` strand.

GAM7302 precursor RNA folds onto itself, forming GAM7302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7302 precursor RNA, designated SEQ ID NO: 6114, and a schematic representation of a predicted secondary folding of GAM7302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7302 folded precursor RNA yielding a GAM7302 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7302 RNA, hereby incorporated herein.

GAM7302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7302 target RNA, herein designated GAM TARGET RNA. GAM7302 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7302 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7302 RNA, herein designated GAM RNA, to target binding sites on GAM7302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7302 target RNA into GAM7302 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7302 target genes. The mRNA of each one of this plurality of GAM7302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7302 RNA, herein designated GAM RNA, and which when bound by GAM7302 RNA causes inhibition of translation of the GAM7302 target mRNA into a corresponding GAM7302 target protein.

The mechanism of the translational inhibition exerted by GAM7302 RNA, herein designated GAM RNA, on one or more GAM7302 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7302 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7302 RNA, herein designated GAM RNA, of GAM7302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7302 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7302 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7302 RNA correlate with, and may be deduced from, the identity of the GAM7302 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7320 6185 CTCTTGACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTTCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGAGGGAC Messenger 7320 (GAM7320) oligonucleotides modulates expression of respective target genes

ATTTTACCTG whose function and utility is known in the art.

CCGGGGACAT GAM7320 is a novel bioinformatically detectable regulatory, non protein coding,

TTCCAATGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7320 was detected is

TGGGGACACT described with additional reference to Figs. 9-15.

TTTGGTTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM7320 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7320

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7320

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7320 precursor RNA is designated SEQ ID:6185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6185 is located from position 69298330 to position 69298411 relative to chromosome 5 on the `-` strand.

GAM7320 precursor RNA folds onto itself, forming GAM7320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7320 precursor RNA, designated SEQ ID NO: 6185, and a schematic representation of a predicted secondary folding of GAM7320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7320 folded precursor RNA yielding a GAM7320 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7320 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7320 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7320 target RNA, herein designated GAM TARGET RNA. GAM7320 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7320 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7320 RNA, herein designated GAM RNA, to target binding sites on GAM7320 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7320 target RNA into GAM7320 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7320 target genes. The mRNA of each one of this plurality of GAM7320 target genes comprises one or more target binding sites, each having

a nucleotide sequence which is at least partly complementary to GAM7320 RNA, herein designated GAM RNA, and which when bound by GAM7320 RNA causes inhibition of translation of the GAM7320 target mRNA into a corresponding GAM7320 target protein.

The mechanism of the translational inhibition exerted by GAM7320 RNA, herein designated GAM RNA, on one or more GAM7320 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7320 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7320 RNA, herein designated GAM RNA, of GAM7320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7320 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7320 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7320 RNA correlate with, and may be deduced from, the identity of the GAM7320 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7331 6452 GAGGTAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AACTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTCAGGAGG Messenger 7331 (GAM7331) oligonucleotides modulates expression of respective target genes
CGGGGGCTGC whose function and utility is known in the art.

AATGAGCTGA GAM7331 is a novel bioinformatically detectable regulatory, non protein coding,
GATCAAGCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7331 was detected is

CTGCACTCCA described with additional reference to Figs. 9-15.

GCCTATGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGAGTGAGA encoded by the human genome.

TTCCATCTC GAM7331 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7331
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7331

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7331 precursor RNA is designated SEQ ID:6452, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6452 is located from position 61512957 to position 61513055 relative to chromosome 20 on the `+` strand.

GAM7331 precursor RNA folds onto itself, forming GAM7331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7331 precursor RNA, designated SEQ ID NO: 6452, and a schematic representation of a predicted secondary folding of GAM7331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7331 folded precursor RNA yielding a GAM7331 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7331 RNA, hereby incorporated herein.

GAM7331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7331 target RNA, herein designated GAM TARGET RNA. GAM7331 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7331 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7331 RNA, herein designated GAM RNA, to target binding sites on GAM7331 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7331 target RNA into GAM7331 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7331 target genes. The mRNA of each one of this plurality of GAM7331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7331 RNA, herein designated GAM RNA, and which when bound by GAM7331 RNA causes inhibition of translation of the GAM7331 target mRNA into a corresponding GAM7331 target protein.

The mechanism of the translational inhibition exerted by GAM7331 RNA, herein designated GAM RNA, on one or more GAM7331 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7331 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7331 RNA, herein designated GAM RNA, of GAM7331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7331 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7331 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7331 RNA correlate with, and may be deduced from, the identity of the GAM7331 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7345 6300 GAATAAATAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGCTCTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCCAAGAA Messenger 7345 (GAM7345) oligonucleotides modulates expression of respective target genes

TTCACATGTG whose function and utility is known in the art.

GTTGTATGCA GAM7345 is a novel bioinformatically detectable regulatory, non protein coding,

GCTTTACTGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7345 was detected is

GAGACTGAAG described with additional reference to Figs. 9-15.

TGTATCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTGATTCTG encoded by the human genome.

CTGTGATGGA GAM7345 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7345

CACTTGTAAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7345

TTT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7345 precursor RNA is designated SEQ ID:6300, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6300 is located from position 62131103 to position 62131215 relative to chromosome 9 on the `-` strand.

GAM7345 precursor RNA folds onto itself, forming GAM7345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7345 precursor RNA, designated SEQ ID NO: 6300, and a schematic representation of a predicted secondary folding of GAM7345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7345 folded precursor RNA yielding a GAM7345 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7345 RNA, hereby incorporated herein.

GAM7345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7345 target RNA, herein designated GAM TARGET RNA. GAM7345 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7345 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7345 RNA, herein designated GAM RNA, to target binding sites on GAM7345 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7345 target RNA into GAM7345 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7345 target genes. The mRNA of each one of this plurality of GAM7345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7345 RNA, herein designated GAM RNA, and which when bound by GAM7345 RNA causes inhibition of translation of the GAM7345 target mRNA into a corresponding GAM7345 target protein.

The mechanism of the translational inhibition exerted by GAM7345 RNA, herein designated GAM RNA, on one or more GAM7345 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7345 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7345 RNA, herein designated GAM RNA, of GAM7345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7345 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7345 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7345 RNA correlate with, and may be deduced from, the identity of the GAM7345 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7349 6240 CTGTCTCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCCTGTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTTCTTA Messenger 7349 (GAM7349) oligonucleotides modulates expression of respective target genes

AGATGTTGTT whose function and utility is known in the art.

ACAATAATCT GAM7349 is a novel bioinformatically detectable regulatory, non protein coding,

ACTATGTGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7349 was detected is

GTGTCTGGAG described with additional reference to Figs. 9-15.

GTGTCTCTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTCTCTGGC encoded by the human genome.

ATTAAGAGAC GAM7349 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7349

AG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7349

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7349 precursor RNA is designated SEQ ID:6240, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6240 is located from position 43372332 to position 43372433 relative to chromosome 12 on the `-` strand.

GAM7349 precursor RNA folds onto itself, forming GAM7349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7349 precursor RNA, designated SEQ ID NO: 6240, and a schematic representation of a predicted secondary folding of GAM7349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7349 folded precursor RNA yielding a GAM7349 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7349 RNA, hereby incorporated herein.

GAM7349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7349 target RNA, herein designated GAM TARGET RNA. GAM7349 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7349 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7349 RNA, herein designated GAM RNA, to target binding sites on GAM7349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7349 target RNA into GAM7349 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7349 target genes. The mRNA of each one of this plurality of GAM7349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7349 RNA, herein designated GAM RNA, and which when bound by GAM7349 RNA causes inhibition of translation of the GAM7349 target mRNA into a corresponding GAM7349 target protein.

The mechanism of the translational inhibition exerted by GAM7349 RNA, herein designated GAM RNA, on one or more GAM7349 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7349 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7349 RNA, herein designated GAM RNA, of GAM7349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7349 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7349 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7349 RNA correlate with, and may be deduced from, the identity of the GAM7349 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7350 6883 GTCCTTTAGT CTCTATTTTT GCTCCTAATT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7350 (GAM7350) oligonucleotides modulates expression of respective target genes

GTTCCTGCAG whose function and utility is known in the art.

GTAGTAGGTT GAM7350 is a novel bioinformatically detectable regulatory, non protein coding,
AACATGTAAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7350 was detected is

GTACTTACAG described with additional reference to Figs. 9-15.

AAGGAAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGAACATGG encoded by the human genome.

CATAGATACT GAM7350 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7350
GAAAGAAAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7350
GC precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7350 precursor RNA is designated SEQ ID:6883, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6883 is located from position 83600201 to position 83600312 relative to chromosome 1 on the `+` strand.

GAM7350 precursor RNA folds onto itself, forming GAM7350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7350 precursor RNA, designated SEQ ID NO: 6883, and a schematic representation of a predicted secondary folding of GAM7350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7350 folded precursor RNA yielding a GAM7350 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7350 RNA, hereby incorporated herein.

GAM7350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7350 target RNA, herein designated GAM TARGET RNA. GAM7350 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7350 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7350 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7350 RNA, herein designated GAM RNA, to target binding sites on GAM7350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7350 target RNA into GAM7350 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7350 target genes. The mRNA of each one of this plurality of GAM7350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7350 RNA, herein designated GAM RNA, and which when bound by GAM7350 RNA causes inhibition of translation of the GAM7350 target mRNA into a corresponding GAM7350 target protein.

The mechanism of the translational inhibition exerted by GAM7350 RNA, herein designated GAM RNA, on one or more GAM7350 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7350 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7350 RNA, herein designated GAM RNA, of GAM7350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7350 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7350 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7350 RNA correlate with, and may be deduced from, the identity of the GAM7350 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7363 5741 AGCAAGGACA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTGTGACC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCCCAGTCC Messenger 7363 (GAM7363) oligonucleotides modulates expression of respective target genes
TCTCTCCATT whose function and utility is known in the art.

TGCAGATCAG GAM7363 is a novel bioinformatically detectable regulatory, non protein coding,
CAAGCTTCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7363 was detected is

TCAGCAAGGA described with additional reference to Figs. 9-15.

GGGGTGGACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATGAAACTGG encoded by the human genome.

GTTCAGCTTG GAM7363 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7363
ATTTGTT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7363

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7363 precursor RNA is designated SEQ ID:5741, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5741 is located from position 97689215 to position 97689321 relative to chromosome 9 on the `+` strand.

GAM7363 precursor RNA folds onto itself, forming GAM7363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7363 precursor RNA, designated SEQ ID NO: 5741, and a schematic representation of a predicted secondary folding of GAM7363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7363 folded precursor RNA yielding a GAM7363 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7363 RNA, hereby incorporated herein.

GAM7363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7363 target RNA, herein designated GAM TARGET RNA. GAM7363 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7363 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7363 RNA, herein designated GAM RNA, to target binding sites on GAM7363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7363 target RNA into GAM7363 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7363 target genes. The mRNA of each one of this plurality of GAM7363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7363 RNA, herein designated GAM RNA, and which when bound by GAM7363 RNA causes inhibition of translation of the GAM7363 target mRNA into a corresponding GAM7363 target protein.

The mechanism of the translational inhibition exerted by GAM7363 RNA, herein designated GAM RNA, on one or more GAM7363 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7363 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7363 RNA, herein designated GAM RNA, of GAM7363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7363 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7363 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7363 RNA correlate with, and may be deduced from, the identity of the GAM7363 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7366 6690 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGGCGGAGG Messenger 7366 (GAM7366) oligonucleotides modulates expression of respective target genes

TTGTGGTGAG whose function and utility is known in the art.

TGAAGATTGC GAM7366 is a novel bioinformatically detectable regulatory, non protein coding,

ACTATTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7366 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAAACTCC encoded by the human genome.

GAM7366 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7366

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7366

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7366 precursor RNA is designated SEQ ID:6690, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6690 is located from position 49033585 to position 49033673 relative to chromosome 12 on the `+` strand.

GAM7366 precursor RNA folds onto itself, forming GAM7366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7366 precursor RNA, designated SEQ ID NO: 6690, and a schematic representation of a predicted secondary folding of GAM7366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7366 folded precursor RNA yielding a GAM7366 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7366 RNA, hereby incorporated herein.

GAM7366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7366 target RNA, herein designated GAM TARGET RNA. GAM7366 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7366 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7366 RNA, herein designated GAM RNA, to target binding sites on GAM7366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7366 target RNA into GAM7366 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7366 target genes. The mRNA of each one of this plurality of GAM7366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7366 RNA, herein designated GAM RNA, and which when bound by GAM7366 RNA causes inhibition of translation of the GAM7366 target mRNA into a corresponding GAM7366 target protein.

The mechanism of the translational inhibition exerted by GAM7366 RNA, herein designated GAM RNA, on one or more GAM7366 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7366 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7366 RNA, herein designated GAM RNA, of GAM7366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM7366 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7366 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7366 RNA correlate with, and may be deduced from, the identity of the GAM7366 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7369 7065 TCTCTCTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCTCATCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATTAATCA Messenger 7369 (GAM7369) oligonucleotides modulates expression of respective target genes
CTTAGTTGCA whose function and utility is known in the art.

AGGGACCAGT GAM7369 is a novel bioinformatically detectable regulatory, non protein coding,
AAATTAACAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7369 was detected is

AATGGTGAAC described with additional reference to Figs. 9-15.

ATTTTCCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTGGTGCT encoded by the human genome.

TTTGCTGGAT GAM7369 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7369
GACTAGTGGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7369
TTCTGCTGGA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
ACAGAGA to the nucleotide sequence of GAM7369 precursor RNA is designated SEQ ID:7065, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7065 is located from position 26088279 to position 26088405 relative to chromosome 13 on the `+` strand.

GAM7369 precursor RNA folds onto itself, forming GAM7369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7369 precursor RNA, designated SEQ ID NO: 7065, and a schematic representation of a predicted secondary folding of GAM7369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7369 folded precursor RNA

yielding a GAM7369 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7369 RNA, hereby incorporated herein.

GAM7369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7369 target RNA, herein designated GAM TARGET RNA. GAM7369 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7369 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7369 RNA, herein designated GAM RNA, to target binding sites on GAM7369 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7369 target RNA into GAM7369 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7369 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7369 target genes. The mRNA of each one of this plurality of GAM7369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7369 RNA, herein designated GAM RNA, and which when bound by GAM7369 RNA causes inhibition of translation of the GAM7369 target mRNA into a corresponding GAM7369 target protein.

The mechanism of the translational inhibition exerted by GAM7369 RNA, herein designated GAM RNA, on one or more GAM7369 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7369 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7369 RNA, herein designated GAM RNA, of GAM7369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7369 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7369 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7369 RNA correlate with, and may be deduced from, the identity of the GAM7369 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7371 6773 GGGAAAGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGTTGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGAGGTCT Messenger 7371 (GAM7371) oligonucleotides modulates expression of respective target genes

GCTGGCAGGC whose function and utility is known in the art.

AGGCAGACAT GAM7371 is a novel bioinformatically detectable regulatory, non protein coding,

TTGGAGCCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7371 was detected is

CTTTCCTGCT described with additional reference to Figs. 9-15.

CAGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7371 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7371

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7371

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7371 precursor RNA is designated SEQ ID:6773, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6773 is located from position 127634676 to position 127634751 relative to chromosome 7 on the `-` strand.

GAM7371 precursor RNA folds onto itself, forming GAM7371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7371 precursor RNA, designated SEQ ID NO: 6773, and a

schematic representation of a predicted secondary folding of GAM7371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7371 folded precursor RNA yielding a GAM7371 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7371 RNA, hereby incorporated herein.

GAM7371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7371 target RNA, herein designated GAM TARGET RNA. GAM7371 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7371 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7371 RNA, herein designated GAM RNA, to target binding sites on GAM7371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7371 target RNA into GAM7371 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7371 target genes. The mRNA of each one of this plurality of GAM7371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7371 RNA, herein designated GAM RNA, and which when bound by GAM7371 RNA causes inhibition of translation of the GAM7371 target mRNA into a corresponding GAM7371 target protein.

The mechanism of the translational inhibition exerted by GAM7371 RNA, herein designated GAM RNA, on one or more GAM7371 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7371 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7371 RNA, herein designated GAM RNA, of GAM7371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7371 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7371 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7371 RNA correlate with, and may be deduced from, the identity of the GAM7371 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7374 6111 CCTCATTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCATTCGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGTTTATT Messenger 7374 (GAM7374) oligonucleotides modulates expression of respective target genes
TAGAACCTGC whose function and utility is known in the art.

CGTGTGCTAG GAM7374 is a novel bioinformatically detectable regulatory, non protein coding,
GGCAGATCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7374 was detected is

GGATACAGCT described with additional reference to Figs. 9-15.

GTGGACAAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGGATGAGG encoded by the human genome.

GAM7374 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7374

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7374

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7374 precursor RNA is designated SEQ ID:6111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6111 is located from position 36127247 to position 36127336 relative to chromosome 20 on the `-` strand.

GAM7374 precursor RNA folds onto itself, forming GAM7374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7374 precursor RNA, designated SEQ ID NO: 6111, and a schematic representation of a predicted secondary folding of GAM7374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7374 folded precursor RNA yielding a GAM7374 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7374 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7374 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7374 target RNA, herein designated GAM TARGET RNA. GAM7374 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7374 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7374 RNA, herein designated GAM RNA, to target binding sites on GAM7374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7374 target RNA into GAM7374 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7374 target genes. The mRNA of each one of this plurality of GAM7374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7374 RNA, herein designated GAM RNA, and which when bound by GAM7374 RNA causes inhibition of translation of the GAM7374 target mRNA into a corresponding GAM7374 target protein.

The mechanism of the translational inhibition exerted by GAM7374 RNA, herein designated GAM RNA, on one or more GAM7374 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7374 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7374 RNA, herein designated GAM RNA, of GAM7374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7374 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7374 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7374 RNA correlate with, and may be deduced from, the identity of the GAM7374 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7400 6713 GGAGGGGAGG ATACAAGAGG AATGATAAAT GGCAAGGAAA ACCACTCACT CTTAATGCTT TTTGTCATAC TCATGTCCTC TTGTCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7400 (GAM7400) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM7400 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM7400 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM7400 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7400 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7400 precursor RNA is designated SEQ ID:6713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6713 is located from position 92806795 to position 92806880 relative to chromosome 13 on the `+` strand.

GAM7400 precursor RNA folds onto itself, forming GAM7400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7400 precursor RNA, designated SEQ ID NO: 6713, and a schematic representation of a predicted secondary folding of GAM7400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7400 folded precursor RNA yielding a GAM7400 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7400 RNA, hereby incorporated herein.

GAM7400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7400 target RNA, herein designated GAM TARGET RNA. GAM7400 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7400 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7400 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7400 RNA, herein designated GAM RNA, to target binding sites on GAM7400 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7400 target RNA into GAM7400 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7400 target genes. The mRNA of each one of this

plurality of GAM7400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7400 RNA, herein designated GAM RNA, and which when bound by GAM7400 RNA causes inhibition of translation of the GAM7400 target mRNA into a corresponding GAM7400 target protein.

The mechanism of the translational inhibition exerted by GAM7400 RNA, herein designated GAM RNA, on one or more GAM7400 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7400 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7400 RNA, herein designated GAM RNA, of GAM7400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7400 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7400 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7400 RNA correlate with, and may be deduced from, the identity of the GAM7400 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7415 6061 CCATCTTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGCATTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTTGGCTGG Messenger 7415 (GAM7415) oligonucleotides modulates expression of respective target genes
GATGCTGAGT whose function and utility is known in the art.

TATCCACTGG GAM7415 is a novel bioinformatically detectable regulatory, non protein coding,
AGCATCGGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7415 was detected is

GTACAGGCAG described with additional reference to Figs. 9-15.

GCACAGAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTGGATCCA encoded by the human genome.

TCGGAGGTGG GAM7415 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7415

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7415

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7415 precursor RNA is designated SEQ ID:6061, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6061 is located from position 69762453 to position 69762552 relative to chromosome 16 on the `+` strand.

GAM7415 precursor RNA folds onto itself, forming GAM7415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7415 precursor RNA, designated SEQ ID NO: 6061, and a schematic representation of a predicted secondary folding of GAM7415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7415 folded precursor RNA yielding a GAM7415 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7415 RNA, hereby incorporated herein.

GAM7415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7415 target RNA, herein designated GAM TARGET RNA. GAM7415 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7415 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7415 RNA, herein designated GAM RNA, to target binding sites on GAM7415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7415 target RNA

into GAM7415 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7415 target genes. The mRNA of each one of this plurality of GAM7415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7415 RNA, herein designated GAM RNA, and which when bound by GAM7415 RNA causes inhibition of translation of the GAM7415 target mRNA into a corresponding GAM7415 target protein.

The mechanism of the translational inhibition exerted by GAM7415 RNA, herein designated GAM RNA, on one or more GAM7415 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7415 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7415 RNA, herein designated GAM RNA, of GAM7415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7415 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7415 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7415 RNA correlate with, and may be deduced from, the identity of the GAM7415 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7440 6162 CTCAGGTCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTAGTGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAGTCAACA Messenger 7440 (GAM7440) oligonucleotides modulates expression of respective target genes
GACAGGGAGG whose function and utility is known in the art.

GAGCTTCCCC GAM7440 is a novel bioinformatically detectable regulatory, non protein coding,
TGTGACTGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7440 was detected is

GTGCGCATAA described with additional reference to Figs. 9-15.

AGACTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7440 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7440 precursor RNA is designated SEQ ID:6162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6162 is located from position 42307485 to position 42307562 relative to chromosome 21 on the `-` strand.

GAM7440 precursor RNA folds onto itself, forming GAM7440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7440 precursor RNA, designated SEQ ID NO: 6162, and a schematic representation of a predicted secondary folding of GAM7440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7440 folded precursor RNA yielding a GAM7440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7440 RNA, hereby incorporated herein.

GAM7440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7440 target RNA, herein designated GAM TARGET RNA. GAM7440 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7440 RNA, herein designated GAM RNA, to target binding sites on GAM7440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7440 target RNA into GAM7440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7440 target genes. The mRNA of each one of this plurality of GAM7440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7440 RNA, herein designated GAM RNA, and which when bound by GAM7440 RNA causes inhibition of translation of the GAM7440 target mRNA into a corresponding GAM7440 target protein.

The mechanism of the translational inhibition exerted by GAM7440 RNA, herein designated GAM RNA, on one or more GAM7440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7440 RNA, herein designated GAM RNA, of GAM7440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7440 RNA correlate with, and may be deduced from, the identity of the GAM7440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7446 5735 AGAGTCTCAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGTTGCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGGAGT Messenger 7446 (GAM7446) oligonucleotides modulates expression of respective target genes
GCAATGGTGT whose function and utility is known in the art.

GACCTCAGGT GAM7446 is a novel bioinformatically detectable regulatory, non protein coding,
CACTGCAACC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7446 was detected is

TCTGCTGCCT described with additional reference to Figs. 9-15.

GGGTTCAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATTCT encoded by the human genome.

GAM7446 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7446 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7446 precursor RNA is designated SEQ ID:5735, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5735 is located from position 45848125 to position 45848210 relative to chromosome 19 on the `+` strand.

GAM7446 precursor RNA folds onto itself, forming GAM7446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7446 precursor RNA, designated SEQ ID NO: 5735, and a schematic representation of a predicted secondary folding of GAM7446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7446 folded precursor RNA yielding a GAM7446 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7446 RNA, hereby incorporated herein. Expression of GAM7446 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7446 target RNA, herein designated GAM TARGET RNA. GAM7446 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7446 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7446 RNA, herein designated GAM RNA, to target binding sites on GAM7446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7446 target RNA into GAM7446 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7446 target genes. The mRNA of each one of this plurality of GAM7446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7446 RNA, herein designated GAM RNA, and which when bound by GAM7446 RNA causes inhibition of translation of the GAM7446 target mRNA into a corresponding GAM7446 target protein.

The mechanism of the translational inhibition exerted by GAM7446 RNA, herein designated GAM RNA, on one or more GAM7446 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7446 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7446 RNA, herein designated GAM RNA, of GAM7446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7446 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7446 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7446 RNA correlate with, and may be deduced from, the identity of the GAM7446 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7449 7217 TGGAGACTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGCTTATTA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGAAACTCC Messenger 7449 (GAM7449) oligonucleotides modulates expression of respective target genes

GTGTTACTCA whose function and utility is known in the art.

TTCCTGGAGT GAM7449 is a novel bioinformatically detectable regulatory, non protein coding, TGGGGGTTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7449 was detected is

TGTAGGCACT described with additional reference to Figs. 9-15.

TTATTTCTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

A encoded by the human genome.

GAM7449 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7449

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7449

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7449 precursor RNA is designated SEQ ID:7217, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7217 is located from position 26847818 to position 26847898 relative to chromosome 7 on the `+` strand.

GAM7449 precursor RNA folds onto itself, forming GAM7449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7449 precursor RNA, designated SEQ ID NO: 7217, and a schematic representation of a predicted secondary folding of GAM7449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7449 folded precursor RNA yielding a GAM7449 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7449 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7449 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7449 target RNA, herein designated GAM TARGET RNA. GAM7449 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7449 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7449 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7449 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7449 RNA, herein designated GAM RNA, to target binding sites on GAM7449 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7449 target RNA into GAM7449 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7449 target genes. The mRNA of each one of this plurality of GAM7449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7449 RNA, herein designated GAM RNA, and which when bound by GAM7449 RNA causes inhibition of translation of the GAM7449 target mRNA into a corresponding GAM7449 target protein.

The mechanism of the translational inhibition exerted by GAM7449 RNA, herein designated GAM RNA, on one or more GAM7449 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7449 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7449 RNA, herein designated GAM RNA, of GAM7449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7449 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7449 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7449 RNA correlate with, and may be deduced from, the identity of the GAM7449 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7464 6554 GCTTACAATT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTGGTACCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTAGCATTT Messenger 7464 (GAM7464) oligonucleotides modulates expression of respective target genes
ATTTTCCCTC whose function and utility is known in the art.

AAGTACCTAG GAM7464 is a novel bioinformatically detectable regulatory, non protein coding,
TAACCTTATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7464 was detected is

AAGGTAGGGA described with additional reference to Figs. 9-15.

GGGTAGATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTACCACAT encoded by the human genome.

TCCTTCAGCT GAM7464 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7464
GTATTGAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7464

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7464 precursor RNA is designated SEQ ID:6554, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6554 is located from position 37872487 to position 37872595 relative to chromosome 8 on the `-` strand.

GAM7464 precursor RNA folds onto itself, forming GAM7464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7464 precursor RNA, designated SEQ ID NO: 6554, and a schematic representation of a predicted secondary folding of GAM7464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7464 folded precursor RNA yielding a GAM7464 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7464 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7464 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7464 target RNA, herein designated GAM TARGET RNA. GAM7464 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7464 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7464 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7464 RNA, herein designated GAM RNA, to target binding sites on GAM7464 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7464 target RNA into GAM7464 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7464 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7464 target genes. The mRNA of each one of this plurality of GAM7464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7464 RNA, herein designated GAM RNA, and which when bound by GAM7464 RNA causes inhibition of translation of the GAM7464 target mRNA into a corresponding GAM7464 target protein.

The mechanism of the translational inhibition exerted by GAM7464 RNA, herein designated GAM RNA, on one or more GAM7464 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7464 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7464 RNA, herein designated GAM RNA, of GAM7464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7464 target RNA, herein designated GAM

TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7464 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7464 RNA correlate with, and may be deduced from, the identity of the GAM7464 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7473 6223 CTGGAGGATT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGGGTGCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCTCGGCAG Messenger 7473 (GAM7473) oligonucleotides modulates expression of respective target genes
GGAACAGGAA whose function and utility is known in the art.

GTAGGAATCC GAM7473 is a novel bioinformatically detectable regulatory, non protein coding,
CAGAAGGGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7473 was detected is

TGGGGGAACC described with additional reference to Figs. 9-15.

CTAACCCTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTCAGTCCA encoded by the human genome.

GTTCACCCCT GAM7473 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7473
CACCTCCAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7473
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7473 precursor RNA is designated SEQ ID:6223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6223 is located from position 3484360 to position 3484468 relative to chromosome 19 on the `-` strand.

GAM7473 precursor RNA folds onto itself, forming GAM7473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7473 precursor RNA, designated SEQ ID NO: 6223, and a schematic representation of a predicted secondary folding of GAM7473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7473 folded precursor RNA yielding a GAM7473 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor

product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7473 RNA, hereby incorporated herein. Expression of GAM7473 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7473 target RNA, herein designated GAM TARGET RNA. GAM7473 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7473 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7473 RNA, herein designated GAM RNA, to target binding sites on GAM7473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7473 target RNA into GAM7473 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7473 target genes. The mRNA of each one of this plurality of GAM7473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7473 RNA, herein designated GAM RNA, and which when bound by GAM7473 RNA causes inhibition of translation of the GAM7473 target mRNA into a corresponding GAM7473 target protein.

The mechanism of the translational inhibition exerted by GAM7473 RNA, herein designated GAM RNA, on one or more GAM7473 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7473 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7473 RNA, herein designated GAM RNA, of GAM7473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7473 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7473 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7473 RNA correlate with, and may be deduced from, the identity of the GAM7473 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7477 6017 CAGCGCGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCGCCACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAATAAATG Messenger 7477 (GAM7477) oligonucleotides modulates expression of respective target genes

TTGCTTGGAG whose function and utility is known in the art.

TGGACCGAGG GAM7477 is a novel bioinformatically detectable regulatory, non protein coding,

CTCTGCAGGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7477 was detected is

ATGCAGGGAG described with additional reference to Figs. 9-15.

GGCCGGGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGCCCCAGGG encoded by the human genome.

TTATTTCTAA GAM7477 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7477

GTTGAGGACA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7477

GGAGGTTGTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

AGTTCTGCTG to the nucleotide sequence of GAM7477 precursor RNA is designated SEQ ID:6017, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6017 is located from position 72048231 to position 72048360 relative to chromosome 7 on the `+` strand.

GAM7477 precursor RNA folds onto itself, forming GAM7477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7477 precursor RNA, designated SEQ ID NO: 6017, and a schematic representation of a predicted secondary folding of GAM7477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7477 folded precursor RNA yielding a GAM7477 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7477 RNA, hereby incorporated herein.

GAM7477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7477 target RNA, herein designated GAM TARGET RNA. GAM7477 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7477 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7477 RNA, herein designated GAM RNA, to target binding sites on GAM7477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7477 target RNA into GAM7477 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7477 target genes. The mRNA of each one of this plurality of GAM7477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7477 RNA, herein designated GAM RNA, and which when bound by GAM7477 RNA causes inhibition of translation of the GAM7477 target mRNA into a corresponding GAM7477 target protein.

The mechanism of the translational inhibition exerted by GAM7477 RNA, herein designated GAM RNA, on one or more GAM7477 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7477 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7477 RNA, herein designated GAM RNA, of GAM7477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7477 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7477 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7477 RNA correlate with, and may be deduced from, the identity of the GAM7477 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7520 6992 TCACCCTGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCTAGGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GACGGAATGC Messenger 7520 (GAM7520) oligonucleotides modulates expression of respective target genes

AGTGAAGTCA whose function and utility is known in the art.

TCATAGTTTA GAM7520 is a novel bioinformatically detectable regulatory, non protein coding,

CTGTAACACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7520 was detected is

GAACTCCTGG described with additional reference to Figs. 9-15.

GCTCAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7520 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7520

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7520

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7520 precursor RNA is designated SEQ ID:6992, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6992 is located from position 42534098 to position 42534177 relative to chromosome 17 on the `+` strand.

GAM7520 precursor RNA folds onto itself, forming GAM7520 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7520 precursor RNA, designated SEQ ID NO: 6992, and a schematic representation of a predicted secondary folding of GAM7520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7520 folded precursor RNA yielding a GAM7520 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7520 RNA, hereby incorporated herein.

GAM7520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7520 target RNA, herein designated GAM TARGET RNA. GAM7520 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7520 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7520 RNA, herein designated GAM RNA, to target binding sites on GAM7520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7520 target RNA into GAM7520 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7520 target genes. The mRNA of each one of this plurality of GAM7520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7520 RNA, herein designated GAM RNA, and which when bound by GAM7520 RNA causes inhibition of translation of the GAM7520 target mRNA into a corresponding GAM7520 target protein.

The mechanism of the translational inhibition exerted by GAM7520 RNA, herein designated GAM RNA, on one or more GAM7520 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7520 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7520 RNA, herein designated GAM RNA, of GAM7520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7520 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7520 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7520 RNA correlate with, and may be deduced from, the identity of the GAM7520 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7530 6557 GCTTCCTCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CACCTTGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTGCTGCTC Messenger 7530 (GAM7530) oligonucleotides modulates expression of respective target genes

CCACACCACA whose function and utility is known in the art.

GTGACTAGCA GAM7530 is a novel bioinformatically detectable regulatory, non protein coding,

GCACATAATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7530 was detected is

GTTTGAATTA described with additional reference to Figs. 9-15.

AAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7530 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7530

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7530

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7530 precursor RNA is designated SEQ ID:6557, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6557 is located from position 3260144 to position 3260217 relative to chromosome 7 on the `-` strand.

GAM7530 precursor RNA folds onto itself, forming GAM7530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7530 precursor RNA, designated SEQ ID NO: 6557, and a schematic representation of a predicted secondary folding of GAM7530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7530 folded precursor RNA yielding a GAM7530 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7530 RNA, hereby incorporated herein. Expression of GAM7530 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7530 target RNA, herein designated GAM TARGET RNA. GAM7530 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7530 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7530 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7530 RNA, herein designated GAM RNA, to target binding sites on GAM7530 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7530 target RNA into GAM7530 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7530 target genes. The mRNA of each one of this plurality of GAM7530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7530 RNA, herein designated GAM RNA, and which when bound by GAM7530 RNA causes inhibition of translation of the GAM7530 target mRNA into a corresponding GAM7530 target protein.

The mechanism of the translational inhibition exerted by GAM7530 RNA, herein designated GAM RNA, on one or more GAM7530 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7530 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7530 RNA, herein designated GAM RNA, of GAM7530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7530 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7530 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7530 RNA correlate with, and may be deduced from, the identity of the GAM7530 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7542 6752 GGCGCTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCAAACAGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTGATGCT Messenger 7542 (GAM7542) oligonucleotides modulates expression of respective target genes

TTGAAGCACC whose function and utility is known in the art.

CTCACTGTAG GAM7542 is a novel bioinformatically detectable regulatory, non protein coding,

ATGAGAGTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7542 was detected is

CTTGCACTGC described with additional reference to Figs. 9-15.

AAACATAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATCACCCGT encoded by the human genome.

GCC GAM7542 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7542 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7542 precursor RNA is designated SEQ ID:6752, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6752 is located from position 129239735 to position 129239827 relative to chromosome 12 on the `+` strand.

GAM7542 precursor RNA folds onto itself, forming GAM7542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7542 precursor RNA, designated SEQ ID NO: 6752, and a schematic representation of a predicted secondary folding of GAM7542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7542 folded precursor RNA yielding a GAM7542 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7542 RNA, hereby incorporated herein.

GAM7542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7542 target RNA, herein designated GAM TARGET RNA. GAM7542 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7542 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7542 RNA, herein designated GAM RNA, to target binding sites on GAM7542 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7542 target RNA into GAM7542 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7542 target genes. The mRNA of each one of this plurality of GAM7542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7542 RNA, herein designated GAM RNA, and which when bound by GAM7542 RNA causes inhibition of translation of the GAM7542 target mRNA into a corresponding GAM7542 target protein.

The mechanism of the translational inhibition exerted by GAM7542 RNA, herein designated GAM RNA, on one or more GAM7542 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7542 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7542 RNA, herein designated GAM RNA, of GAM7542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7542 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7542 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7542 RNA correlate with, and may be deduced from, the identity of the GAM7542 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7546 6119 CCTGCTGTAT GCTAGGCATT GTGCAAGGTG TTAGGGCTGA TGCTTGAGCA CAGTACCTCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7546 (GAM7546) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM7546 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM7546 was detected is

ACATCTGCAG described with additional reference to Figs. 9-15.

TATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM7546 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7546 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7546 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7546 precursor RNA is designated SEQ ID:6119, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6119 is located from position 60900963 to position 60901037 relative to chromosome 17 on the `+` strand.

GAM7546 precursor RNA folds onto itself, forming GAM7546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7546 precursor RNA, designated SEQ ID NO: 6119, and a schematic representation of a predicted secondary folding of GAM7546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7546 folded precursor RNA yielding a GAM7546 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7546 RNA, hereby incorporated herein.

GAM7546 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7546 target RNA, herein designated GAM TARGET RNA. GAM7546 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7546 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7546 RNA, herein designated GAM RNA, to target binding sites on GAM7546 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7546 target RNA into GAM7546 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7546 target genes. The mRNA of each one of this plurality of GAM7546 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7546 RNA, herein designated GAM RNA, and which when bound by GAM7546 RNA causes inhibition of translation of the GAM7546 target mRNA into a corresponding GAM7546 target protein.

The mechanism of the translational inhibition exerted by GAM7546 RNA, herein designated GAM RNA, on one or more GAM7546 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7546 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7546 RNA, herein designated GAM RNA, of GAM7546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7546 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7546 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7546 RNA correlate with, and may be deduced from, the identity of the GAM7546 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7553 5658 AACTGGTCGG TGATTTAGGT AGTTTCCTGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7553 (GAM7553) oligonucleotides modulates expression of respective target genes

TGTTGGGATC whose function and utility is known in the art.

CACCTTTCTC GAM7553 is a novel bioinformatically detectable regulatory, non protein coding, TCGACAGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7553 was detected is

GACACTGCCT described with additional reference to Figs. 9-15.

TCATTACTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTT encoded by the human genome.

GAM7553 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7553 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7553 precursor RNA is designated SEQ ID:5658, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5658 is located from position 26917372 to position 26917455 relative to chromosome 7 on the `-` strand.

GAM7553 precursor RNA folds onto itself, forming GAM7553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7553 precursor RNA, designated SEQ ID NO: 5658, and a schematic representation of a predicted secondary folding of GAM7553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7553 folded precursor RNA yielding a GAM7553 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7553 RNA, hereby incorporated herein. Expression of GAM7553 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7553 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7553 target RNA, herein designated GAM TARGET RNA. GAM7553 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7553 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7553 RNA, herein designated GAM RNA, to target binding sites on GAM7553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7553 target RNA into GAM7553 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7553 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7553 target genes. The mRNA of each one of this plurality of GAM7553 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7553 RNA, herein designated GAM RNA, and which when bound by GAM7553 RNA causes inhibition of translation of the GAM7553 target mRNA into a corresponding GAM7553 target protein.

The mechanism of the translational inhibition exerted by GAM7553 RNA, herein designated GAM RNA, on one or more GAM7553 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7553 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7553 RNA, herein designated GAM RNA, of GAM7553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7553 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7553 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7553 RNA correlate with, and may be deduced from, the identity of the GAM7553 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7559 7274 TGTGGCTCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTCCCTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCACTCTCCC Messenger 7559 (GAM7559) oligonucleotides modulates expression of respective target genes
TATAACTGGC whose function and utility is known in the art.

CTCTCCCTGC GAM7559 is a novel bioinformatically detectable regulatory, non protein coding,
TCAGACCTTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7559 was detected is

CTGGACGAGC described with additional reference to Figs. 9-15.

TGCATGAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGGCAGCTG encoded by the human genome.

CA GAM7559 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7559
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7559
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7559 precursor RNA is designated SEQ ID:7274, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7274 is located from position 49747946 to position 49748037 relative to chromosome 12 on the `+` strand.

GAM7559 precursor RNA folds onto itself, forming GAM7559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7559 precursor RNA, designated SEQ ID NO: 7274, and a schematic representation of a predicted secondary folding of GAM7559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7559 folded precursor RNA yielding a GAM7559 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7559 RNA, hereby incorporated herein.

GAM7559 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7559 target RNA, herein designated GAM TARGET RNA. GAM7559 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7559 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7559 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7559 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7559 RNA, herein designated GAM RNA, to target binding sites on GAM7559 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7559 target RNA into GAM7559 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7559 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7559 target genes. The mRNA of each one of this plurality of GAM7559 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7559 RNA, herein designated GAM RNA, and which when bound by GAM7559 RNA causes inhibition of translation of the GAM7559 target mRNA into a corresponding GAM7559 target protein.

The mechanism of the translational inhibition exerted by GAM7559 RNA, herein designated GAM RNA, on one or more GAM7559 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7559 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7559 RNA, herein designated GAM RNA, of GAM7559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7559 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7559 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7559 RNA correlate with, and may be deduced from, the identity of the GAM7559 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7591 7346 TTTGGAGTAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCAGTATAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTCGTTTAA Messenger 7591 (GAM7591) oligonucleotides modulates expression of respective target genes
AAGAGATTTT whose function and utility is known in the art.

TATAACTTCA GAM7591 is a novel bioinformatically detectable regulatory, non protein coding,
GA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7591 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM7591 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7591

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7591
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7591 precursor RNA is designated SEQ ID:7346, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7346 is located from position 136686979 to position 136687030 relative to chromosome 2 on the `-` strand.

GAM7591 precursor RNA folds onto itself, forming GAM7591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7591 precursor RNA, designated SEQ ID NO: 7346, and a schematic representation of a predicted secondary folding of GAM7591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7591 folded precursor RNA yielding a GAM7591 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7591 RNA, hereby incorporated herein. Expression of GAM7591 RNA

was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7591 target RNA, herein designated GAM TARGET RNA. GAM7591 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7591 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7591 RNA, herein designated GAM RNA, to target binding sites on GAM7591 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7591 target RNA into GAM7591 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7591 target genes. The mRNA of each one of this plurality of GAM7591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7591 RNA, herein designated GAM RNA, and which when bound by GAM7591 RNA causes inhibition of translation of the GAM7591 target mRNA into a corresponding GAM7591 target protein.

The mechanism of the translational inhibition exerted by GAM7591 RNA, herein designated GAM RNA, on one or more GAM7591 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7591 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7591 RNA, herein designated GAM RNA, of GAM7591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7591 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7591 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7591 RNA correlate with, and may be deduced from, the identity of the GAM7591 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7592 6043 CATTAGATTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCATAAGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAAACCCTA Messenger 7592 (GAM7592) oligonucleotides modulates expression of respective target genes
TTGTGAGCTG whose function and utility is known in the art.

CACATGCAAG GAM7592 is a novel bioinformatically detectable regulatory, non protein coding,
GGATCTAGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7592 was detected is

TGTGCGCTCC described with additional reference to Figs. 9-15.

TTATGAGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAATG encoded by the human genome.

GAM7592 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7592

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7592
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7592 precursor RNA is designated SEQ ID:6043, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6043 is located from position 22819631 to position 22819716 relative to chromosome 21 on the `+` strand.

GAM7592 precursor RNA folds onto itself, forming GAM7592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7592 precursor RNA, designated SEQ ID NO: 6043, and a schematic representation of a predicted secondary folding of GAM7592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7592 folded precursor RNA yielding a GAM7592 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7592 RNA, hereby incorporated herein.

GAM7592 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7592 target RNA, herein designated GAM TARGET RNA. GAM7592 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7592 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7592 RNA, herein designated GAM RNA, to target binding sites on GAM7592 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7592 target RNA into GAM7592 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7592 target genes. The mRNA of each one of this plurality of GAM7592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7592 RNA, herein designated GAM RNA, and which when bound by GAM7592 RNA causes inhibition of translation of the GAM7592 target mRNA into a corresponding GAM7592 target protein.

The mechanism of the translational inhibition exerted by GAM7592 RNA, herein designated GAM RNA, on one or more GAM7592 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7592 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7592 RNA, herein designated GAM RNA, of GAM7592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7592 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7592 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7592 RNA correlate with, and may be deduced from, the identity of the GAM7592 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7601 5980 ATTATTCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAAAATCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAATGTCTTT Messenger 7601 (GAM7601) oligonucleotides modulates expression of respective target genes

GAGCTTCTGG whose function and utility is known in the art.

TTGTGTAATG GAM7601 is a novel bioinformatically detectable regulatory, non protein coding,

CTGGGGTTTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7601 was detected is

AAGTCACCAT described with additional reference to Figs. 9-15.

TTGTGGGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCATCAATT encoded by the human genome.

AAT GAM7601 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7601

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7601

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7601 precursor RNA is designated SEQ ID:5980, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5980 is located from position 92812990 to position 92813082 relative to chromosome 11 on the `+` strand.

GAM7601 precursor RNA folds onto itself, forming GAM7601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7601 precursor RNA, designated SEQ ID NO: 5980, and a schematic representation of a predicted secondary folding of GAM7601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7601 folded precursor RNA yielding a GAM7601 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7601 RNA, hereby incorporated herein.

GAM7601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7601 target RNA, herein designated GAM TARGET RNA. GAM7601 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7601 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7601 RNA, herein designated GAM RNA, to target binding sites on GAM7601 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7601 target RNA into GAM7601 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7601 target genes. The mRNA of each one of this plurality of GAM7601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7601 RNA, herein designated GAM RNA, and which when bound by GAM7601 RNA causes inhibition of translation of the GAM7601 target mRNA into a corresponding GAM7601 target protein.

The mechanism of the translational inhibition exerted by GAM7601 RNA, herein designated GAM RNA, on one or more GAM7601 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7601 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7601 RNA, herein designated GAM RNA, of GAM7601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7601 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7601 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7601 RNA correlate with, and may be deduced from, the identity of the GAM7601 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7636 6218 CTGCCTATAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATTCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGATGGTTT Messenger 7636 (GAM7636) oligonucleotides modulates expression of respective target genes

GTATCTCAAA whose function and utility is known in the art.

GGAGTACAGT GAM7636 is a novel bioinformatically detectable regulatory, non protein coding,

GAACGAAACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7636 was detected is

TGTTTAAAGA described with additional reference to Figs. 9-15.

TACACCGGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAAAAAGAG encoded by the human genome.

AAGAGGCAG GAM7636 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7636

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7636

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7636 precursor RNA is designated SEQ ID:6218, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6218 is located from position 88520255 to position 88520353 relative to chromosome 9 on the `+` strand.

GAM7636 precursor RNA folds onto itself, forming GAM7636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7636 precursor RNA, designated SEQ ID NO: 6218, and a schematic representation of a predicted secondary folding of GAM7636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7636 folded precursor RNA yielding a GAM7636 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7636 RNA, hereby incorporated herein.

GAM7636 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7636 target RNA, herein designated GAM TARGET RNA. GAM7636 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7636 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7636 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7636 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7636 RNA, herein designated GAM RNA, to target binding sites on GAM7636 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7636 target RNA into GAM7636 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7636 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7636 target genes. The mRNA of each one of this plurality of GAM7636 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7636 RNA, herein designated GAM RNA, and which when bound by GAM7636 RNA causes inhibition of translation of the GAM7636 target mRNA into a corresponding GAM7636 target protein.

The mechanism of the translational inhibition exerted by GAM7636 RNA, herein designated GAM RNA, on one or more GAM7636 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7636 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7636 RNA, herein designated GAM RNA, of GAM7636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7636 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7636 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7636 RNA correlate with, and may be deduced from, the identity of the GAM7636 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7654 6226 CTGGATTCCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAAGCTCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTTTGGCAC Messenger 7654 (GAM7654) oligonucleotides modulates expression of respective target genes
TGAATCATAT whose function and utility is known in the art.

ACAATCTCGT GAM7654 is a novel bioinformatically detectable regulatory, non protein coding,
AGTTTGGATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7654 was detected is

GCTGTGTGTG described with additional reference to Figs. 9-15.

ACTGCAGACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTAGACAGC encoded by the human genome.

AGGGCCCACA GAM7654 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7654
TCACAG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7654
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7654 precursor RNA is designated SEQ ID:6226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:6226 is located from position 102859212 to position 102859317 relative to chromosome 10 on the `-` strand.

GAM7654 precursor RNA folds onto itself, forming GAM7654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7654 precursor RNA, designated SEQ ID NO: 6226, and a schematic representation of a predicted secondary folding of GAM7654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7654 folded precursor RNA yielding a GAM7654 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7654 RNA, hereby incorporated herein.

GAM7654 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7654 target RNA, herein designated GAM TARGET RNA. GAM7654 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7654 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7654 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7654 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7654 RNA, herein designated GAM RNA, to target binding sites on GAM7654 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7654 target RNA into GAM7654 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7654 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7654 target genes. The mRNA of each one of this

plurality of GAM7654 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7654 RNA, herein designated GAM RNA, and which when bound by GAM7654 RNA causes inhibition of translation of the GAM7654 target mRNA into a corresponding GAM7654 target protein.

The mechanism of the translational inhibition exerted by GAM7654 RNA, herein designated GAM RNA, on one or more GAM7654 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7654 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7654 RNA, herein designated GAM RNA, of GAM7654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7654 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7654 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7654 RNA correlate with, and may be deduced from, the identity of the GAM7654 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7663 6078 CCCCGAGGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGACTGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCAGTCCCC Messenger 7663 (GAM7663) oligonucleotides modulates expression of respective target genes

AGCACCCTTG whose function and utility is known in the art.

TCCAGATGGG GAM7663 is a novel bioinformatically detectable regulatory, non protein coding,

GACCAGGAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7663 was detected is

TGGGTGAAGA described with additional reference to Figs. 9-15.

TATTTGGGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGAGCTCTG encoded by the human genome.

TGCTGGTTGC GAM7663 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7663

CCCCGAGGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7663 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7663 precursor RNA is designated SEQ ID:6078, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6078 is located from position 68334837 to position 68334946 relative to chromosome 11 on the `+` strand.

GAM7663 precursor RNA folds onto itself, forming GAM7663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7663 precursor RNA, designated SEQ ID NO: 6078, and a schematic representation of a predicted secondary folding of GAM7663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7663 folded precursor RNA yielding a GAM7663 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7663 RNA, hereby incorporated herein.

GAM7663 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7663 target RNA, herein designated GAM TARGET RNA. GAM7663 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7663 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7663 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7663 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7663 RNA, herein designated GAM RNA, to target binding sites on GAM7663 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7663 target RNA

into GAM7663 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7663 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7663 target genes. The mRNA of each one of this plurality of GAM7663 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7663 RNA, herein designated GAM RNA, and which when bound by GAM7663 RNA causes inhibition of translation of the GAM7663 target mRNA into a corresponding GAM7663 target protein.

The mechanism of the translational inhibition exerted by GAM7663 RNA, herein designated GAM RNA, on one or more GAM7663 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7663 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7663 RNA, herein designated GAM RNA, of GAM7663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7663 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7663 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7663 RNA correlate with, and may be deduced from, the identity of the GAM7663 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7700 5950 ATACTTACTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCATATTATA detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGCTCTAAG Messenger 7700 (GAM7700) oligonucleotides modulates expression of respective target genes

AGTGTAGAGT whose function and utility is known in the art.

TATATGATGT GAM7700 is a novel bioinformatically detectable regulatory, non protein coding,
GCTAGTGAAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7700 was detected is

TGT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7700 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7700 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7700 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7700 precursor RNA is designated SEQ ID:5950, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5950 is located from position 101882286 to position 101882348 relative to chromosome 8 on the `+` strand.

GAM7700 precursor RNA folds onto itself, forming GAM7700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7700 precursor RNA, designated SEQ ID NO: 5950, and a schematic representation of a predicted secondary folding of GAM7700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7700 folded precursor RNA yielding a GAM7700 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7700 RNA, hereby incorporated herein.

GAM7700 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7700 target RNA, herein designated GAM TARGET RNA. GAM7700 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7700 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7700 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7700 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7700 RNA, herein designated GAM RNA, to target binding sites on GAM7700 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7700 target RNA into GAM7700 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7700 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7700 target genes. The mRNA of each one of this plurality of GAM7700 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7700 RNA, herein designated GAM RNA, and which when bound by GAM7700 RNA causes inhibition of translation of the GAM7700 target mRNA into a corresponding GAM7700 target protein.

The mechanism of the translational inhibition exerted by GAM7700 RNA, herein designated GAM RNA, on one or more GAM7700 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7700 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7700 RNA, herein designated GAM RNA, of GAM7700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7700 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7700 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7700 RNA correlate with, and may be deduced from, the identity of the GAM7700 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7707 6191 CTGAAAGTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTGCTGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACGCCTGGGC Messenger 7707 (GAM7707) oligonucleotides modulates expression of respective target genes

ACATACTGCA whose function and utility is known in the art.

TCATTTACAA GAM7707 is a novel bioinformatically detectable regulatory, non protein coding,

AACTGTAGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7707 was detected is

CACCTGTTGT described with additional reference to Figs. 9-15.

GTGTGCAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGATTTCTT encoded by the human genome.

ATAGATTTTT GAM7707 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7707

AG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7707

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7707 precursor RNA is designated SEQ ID:6191, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6191 is located from position 68168613 to position 68168714 relative to chromosome 9 on the `+` strand.

GAM7707 precursor RNA folds onto itself, forming GAM7707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7707 precursor RNA, designated SEQ ID NO: 6191, and a schematic representation of a predicted secondary folding of GAM7707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7707 folded precursor RNA yielding a GAM7707 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7707 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7707 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7707 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7707 target RNA, herein designated GAM TARGET RNA. GAM7707 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7707 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7707 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7707 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7707 RNA, herein designated GAM RNA, to target binding sites on GAM7707 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7707 target RNA into GAM7707 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7707 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7707 target genes. The mRNA of each one of this plurality of GAM7707 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7707 RNA, herein designated GAM RNA, and which when bound by GAM7707 RNA causes inhibition of translation of the GAM7707 target mRNA into a corresponding GAM7707 target protein.

The mechanism of the translational inhibition exerted by GAM7707 RNA, herein designated GAM RNA, on one or more GAM7707 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7707 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7707 RNA, herein designated GAM RNA, of GAM7707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7707 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7707 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7707 RNA correlate with, and may be deduced from, the identity of the GAM7707 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7729 7226 TGGCCTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGCTTCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCCCATCT Messenger 7729 (GAM7729) oligonucleotides modulates expression of respective target genes

GTAAGATAGG whose function and utility is known in the art.

AATAACACAT GAM7729 is a novel bioinformatically detectable regulatory, non protein coding, CTCACAGGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7729 was detected is

CATGGAGAGG described with additional reference to Figs. 9-15.

CTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7729 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7729

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7729

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7729 precursor RNA is designated SEQ ID:7226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7226 is located from position 37886140 to position 37886212 relative to chromosome 22 on the `-` strand.

GAM7729 precursor RNA folds onto itself, forming GAM7729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7729 precursor RNA, designated SEQ ID NO: 7226, and a schematic representation of a predicted secondary folding of GAM7729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7729 folded precursor RNA yielding a GAM7729 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7729 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7729 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7729 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7729 target RNA, herein designated GAM TARGET RNA. GAM7729 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7729 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM7729 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7729 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7729 RNA, herein designated GAM RNA, to target binding sites on GAM7729 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7729 target RNA into GAM7729 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7729 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7729 target genes. The mRNA of each one of this plurality of GAM7729 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7729 RNA, herein designated GAM RNA, and which when bound by GAM7729 RNA causes inhibition of translation of the GAM7729 target mRNA into a corresponding GAM7729 target protein.

The mechanism of the translational inhibition exerted by GAM7729 RNA, herein designated GAM RNA, on one or more GAM7729 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7729 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7729 RNA, herein designated GAM RNA, of GAM7729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7729 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7729 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7729 RNA correlate with, and may be deduced from, the identity of the GAM7729 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7776 6393 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 7776 (GAM7776) oligonucleotides modulates expression of respective target genes

CGGAGGTTGT whose function and utility is known in the art.

GGTGAGCGAA GAM7776 is a novel bioinformatically detectable regulatory, non protein coding,

GATCGTGCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7776 was detected is

TTGCACTCCA described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCAAA encoded by the human genome.

ACTCTGTCTC GAM7776 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7776

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7776

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7776 precursor RNA is designated SEQ ID:6393, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6393 is located from position 120997504 to position 120997603 relative to chromosome X on the `+` strand.

GAM7776 precursor RNA folds onto itself, forming GAM7776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7776 precursor RNA, designated SEQ ID NO: 6393, and a schematic representation of a predicted secondary folding of GAM7776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7776 folded precursor RNA yielding a GAM7776 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7776 RNA, hereby incorporated herein. Expression of GAM7776 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7776 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM7776 target RNA, herein designated GAM TARGET RNA. GAM7776 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7776 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7776 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7776 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7776 RNA, herein designated GAM RNA, to target binding sites on GAM7776 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7776 target RNA into GAM7776 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7776 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7776 target genes. The mRNA of each one of this plurality of GAM7776 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7776 RNA, herein designated GAM RNA, and which when bound by GAM7776 RNA causes inhibition of translation of the GAM7776 target mRNA into a corresponding GAM7776 target protein.

The mechanism of the translational inhibition exerted by GAM7776 RNA, herein designated GAM RNA, on one or more GAM7776 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7776 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7776 RNA, herein designated GAM RNA, of GAM7776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7776 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM7776 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7776 RNA correlate with, and may be deduced from, the identity of the GAM7776 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7777 5743 AGCAGACTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGTTGACC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAATTTGTT Messenger 7777 (GAM7777) oligonucleotides modulates expression of respective target genes

AGATTGCTAT whose function and utility is known in the art.

TACAATGCTG GAM7777 is a novel bioinformatically detectable regulatory, non protein coding,

ATTATATTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7777 was detected is

ATAGCAATTA described with additional reference to Figs. 9-15.

CTGACATAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTTATACTTT encoded by the human genome.

GGGCAATGGC GAM7777 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7777

T precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7777

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7777 precursor RNA is designated SEQ ID:5743, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5743 is located from position 96304357 to position 96304457 relative to chromosome 11 on the `-` strand.

GAM7777 precursor RNA folds onto itself, forming GAM7777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7777 precursor RNA, designated SEQ ID NO: 5743, and a schematic representation of a predicted secondary folding of GAM7777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7777 folded precursor RNA yielding a GAM7777 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7777 RNA, hereby incorporated herein.

GAM7777 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7777 target RNA, herein designated GAM TARGET RNA. GAM7777 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7777 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7777 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7777 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7777 RNA, herein designated GAM RNA, to target binding sites on GAM7777 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7777 target RNA into GAM7777 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7777 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7777 target genes. The mRNA of each one of this plurality of GAM7777 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7777 RNA, herein designated GAM RNA, and which when bound by GAM7777 RNA causes inhibition of translation of the GAM7777 target mRNA into a corresponding GAM7777 target protein.

The mechanism of the translational inhibition exerted by GAM7777 RNA, herein designated GAM RNA, on one or more GAM7777 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7777 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7777 RNA, herein designated GAM RNA, of GAM7777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7777 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7777 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7777 RNA correlate with, and may be deduced from, the identity of the GAM7777 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7784 6867 GTAGTTACCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGCCTTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGAGCTAT Messenger 7784 (GAM7784) oligonucleotides modulates expression of respective target genes
TTGTTTTGGT whose function and utility is known in the art.

TTGCTGAAAC GAM7784 is a novel bioinformatically detectable regulatory, non protein coding,
TAGTCCAAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7784 was detected is

CAGGAAATTT described with additional reference to Figs. 9-15.

AACAGACAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CACAGCCAAA encoded by the human genome.

GAGTGTCATG GAM7784 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7784
TGAATTAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7784

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7784 precursor RNA is designated SEQ ID:6867, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6867 is located from position 107796034 to position 107796141 relative to chromosome 13 on the `+` strand.

GAM7784 precursor RNA folds onto itself, forming GAM7784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7784 precursor RNA, designated SEQ ID NO: 6867, and a schematic representation of a predicted secondary folding of GAM7784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7784 folded precursor RNA yielding a GAM7784 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7784 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7784 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7784 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7784 target RNA, herein designated GAM TARGET RNA. GAM7784 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7784 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7784 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7784 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7784 RNA, herein designated GAM RNA, to target binding sites on GAM7784 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7784 target RNA into GAM7784 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7784 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7784 target genes. The mRNA of each one of this plurality of GAM7784 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7784 RNA, herein designated GAM RNA, and which when bound by GAM7784 RNA causes inhibition of translation of the GAM7784 target mRNA into a corresponding GAM7784 target protein.

The mechanism of the translational inhibition exerted by GAM7784 RNA, herein designated GAM RNA, on one or more GAM7784 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7784 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7784 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7784 RNA, herein designated GAM RNA, of GAM7784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7784 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7784 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7784 RNA correlate with, and may be deduced from, the identity of the GAM7784 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7817 6139 CGCTCTTTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCAGGCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGCAGTGG Messenger 7817 (GAM7817) oligonucleotides modulates expression of respective target genes

CATGATCTCA whose function and utility is known in the art.

GCTCACTGCA GAM7817 is a novel bioinformatically detectable regulatory, non protein coding,

ACCTCCATCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7817 was detected is

CCTGGGTTCA described with additional reference to Figs. 9-15.

AGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7817 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7817

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7817

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7817 precursor RNA is designated SEQ ID:6139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6139 is located from position 101053737 to position 101053810 relative to chromosome 14 on the `+` strand.

GAM7817 precursor RNA folds onto itself, forming GAM7817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7817 precursor RNA, designated SEQ ID NO: 6139, and a schematic representation of a predicted secondary folding of GAM7817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7817 folded precursor RNA yielding a GAM7817 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7817 RNA, hereby incorporated herein.

GAM7817 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7817 target RNA, herein designated GAM TARGET RNA. GAM7817 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7817 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7817 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7817 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7817 RNA, herein designated GAM RNA, to target binding sites on GAM7817 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7817 target RNA into GAM7817 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7817 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7817 target genes. The mRNA of each one of this plurality of GAM7817 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7817 RNA, herein designated GAM RNA, and which when bound by GAM7817 RNA causes inhibition of translation of the GAM7817 target mRNA into a corresponding GAM7817 target protein.

The mechanism of the translational inhibition exerted by GAM7817 RNA, herein designated GAM RNA, on one or more GAM7817 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7817 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7817 RNA, herein designated GAM RNA, of GAM7817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7817 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7817 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7817 RNA correlate with, and may be deduced from, the identity of the GAM7817 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7837 7303 TTCTATGTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

TACCCTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCTGGTTGA Messenger 7837 (GAM7837) oligonucleotides modulates expression of respective target genes
GGGGTGGGGG whose function and utility is known in the art.

AATCAGAAAA GAM7837 is a novel bioinformatically detectable regulatory, non protein coding,
GTAGGTTTAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7837 was detected is

ATTTAACATT described with additional reference to Figs. 9-15.

TTTCTTAACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACATTCACTT encoded by the human genome.

CTTAAAAAGG GAM7837 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7837
AACAAGAAGT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7837
GTAAATAAGT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
ATGTATAGAG to the nucleotide sequence of GAM7837 precursor RNA is designated SEQ ID:7303, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7303 is located from position 29387505 to position 29387634 relative to chromosome 12 on the `+` strand.

GAM7837 precursor RNA folds onto itself, forming GAM7837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7837 precursor RNA, designated SEQ ID NO: 7303, and a schematic representation of a predicted secondary folding of GAM7837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7837 folded precursor RNA yielding a GAM7837 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7837 RNA, hereby incorporated herein.

GAM7837 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7837 target RNA, herein designated GAM TARGET RNA. GAM7837 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7837 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7837 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7837 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7837 RNA, herein designated GAM RNA, to target binding sites on GAM7837 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7837 target RNA into GAM7837 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7837 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7837 target genes. The mRNA of each one of this plurality of GAM7837 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7837 RNA, herein

designated GAM RNA, and which when bound by GAM7837 RNA causes inhibition of translation of the GAM7837 target mRNA into a corresponding GAM7837 target protein.

The mechanism of the translational inhibition exerted by GAM7837 RNA, herein designated GAM RNA, on one or more GAM7837 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7837 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7837 RNA, herein designated GAM RNA, of GAM7837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7837 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7837 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7837 RNA correlate with, and may be deduced from, the identity of the GAM7837 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7845 5732 AGAGGTGTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTAGGCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCTGCCCT Messenger 7845 (GAM7845) oligonucleotides modulates expression of respective target genes
CCCTGGACTG whose function and utility is known in the art.

CCTGACCTCG GAM7845 is a novel bioinformatically detectable regulatory, non protein coding,
CTCCAAGGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7845 was detected is

CAGGGGAAGG described with additional reference to Figs. 9-15.

TTCTGAGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGTGTGAAA encoded by the human genome.

ATGCTTGGAA GAM7845 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7845
TGTCCCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7845

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7845 precursor RNA is designated SEQ ID:5732, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5732 is located from position 68013714 to position 68013820 relative to chromosome 11 on the `+` strand.

GAM7845 precursor RNA folds onto itself, forming GAM7845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7845 precursor RNA, designated SEQ ID NO: 5732, and a schematic representation of a predicted secondary folding of GAM7845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7845 folded precursor RNA yielding a GAM7845 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7845 RNA, hereby incorporated herein.

GAM7845 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7845 target RNA, herein designated GAM TARGET RNA. GAM7845 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7845 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7845 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7845 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7845 RNA, herein designated GAM RNA, to target binding sites on GAM7845 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7845 target RNA into GAM7845 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7845 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7845 target genes. The mRNA of each one of this plurality of GAM7845 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7845 RNA, herein designated GAM RNA, and which when bound by GAM7845 RNA causes inhibition of translation of the GAM7845 target mRNA into a corresponding GAM7845 target protein.

The mechanism of the translational inhibition exerted by GAM7845 RNA, herein designated GAM RNA, on one or more GAM7845 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7845 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7845 RNA, herein designated GAM RNA, of GAM7845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7845 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7845 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7845 RNA correlate with, and may be deduced from, the identity of the GAM7845 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7854 7232 TGGGATTACA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACATGAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTGTGCCCA Messenger 7854 (GAM7854) oligonucleotides modulates expression of respective target genes

GCCAGGGCTG whose function and utility is known in the art.

TGTGTTATGT GAM7854 is a novel bioinformatically detectable regulatory, non protein coding,

AGTGACAGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7854 was detected is

CACTGATACA described with additional reference to Figs. 9-15.

GCTCTCTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGACTTAGG encoded by the human genome.

AACCAAGTTT GAM7854 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7854
GACCCCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7854
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7854 precursor RNA is designated SEQ ID:7232, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7232 is located from position 52841049 to position 52841155 relative to chromosome 19 on the `-` strand.

GAM7854 precursor RNA folds onto itself, forming GAM7854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7854 precursor RNA, designated SEQ ID NO: 7232, and a schematic representation of a predicted secondary folding of GAM7854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7854 folded precursor RNA yielding a GAM7854 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7854 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7854 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7854 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7854 target RNA, herein designated GAM TARGET RNA. GAM7854 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7854 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7854 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7854 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7854 RNA, herein designated GAM RNA, to target binding sites on GAM7854 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7854 target RNA into GAM7854 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7854 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7854 target genes. The mRNA of each one of this plurality of GAM7854 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7854 RNA, herein designated GAM RNA, and which when bound by GAM7854 RNA causes inhibition of translation of the GAM7854 target mRNA into a corresponding GAM7854 target protein.

The mechanism of the translational inhibition exerted by GAM7854 RNA, herein designated GAM RNA, on one or more GAM7854 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7854 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7854 RNA, herein designated GAM RNA, of GAM7854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7854 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7854 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7854 RNA correlate with, and may be deduced from, the identity of the GAM7854 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7865 6126 CCTTCAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTGTAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TATCGGGGTG Messenger 7865 (GAM7865) oligonucleotides modulates expression of respective target genes

GAGAGATAAG whose function and utility is known in the art.

CCAAGTATCC GAM7865 is a novel bioinformatically detectable regulatory, non protein coding,

AGATAACCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7865 was detected is

GGCATAAGGC described with additional reference to Figs. 9-15.

AGAATATTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGTACTATG encoded by the human genome.

AGAGGTACAA GAM7865 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7865

AGGGGAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7865

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7865 precursor RNA is designated SEQ ID:6126, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6126 is located from position 102246140 to position 102246247 relative to chromosome 10 on the `+` strand.

GAM7865 precursor RNA folds onto itself, forming GAM7865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7865 precursor RNA, designated SEQ ID NO: 6126, and a schematic representation of a predicted secondary folding of GAM7865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7865 folded precursor RNA yielding a GAM7865 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7865 RNA, hereby incorporated herein.

GAM7865 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7865 target RNA, herein designated GAM TARGET RNA. GAM7865 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7865 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7865 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7865 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7865 RNA, herein designated GAM RNA, to target binding sites on GAM7865 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7865 target RNA into GAM7865 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7865 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7865 target genes. The mRNA of each one of this plurality of GAM7865 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7865 RNA, herein designated GAM RNA, and which when bound by GAM7865 RNA causes inhibition of translation of the GAM7865 target mRNA into a corresponding GAM7865 target protein.

The mechanism of the translational inhibition exerted by GAM7865 RNA, herein designated GAM RNA, on one or more GAM7865 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7865 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7865 RNA, herein designated GAM RNA, of GAM7865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7865 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7865 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7865 RNA correlate with, and may be deduced from, the identity of the GAM7865 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7884 6934 GTGTTTTGCA CTGTAATACC TCGGTCGTAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 7884 (GAM7884) oligonucleotides modulates expression of respective target genes

CAAAGTGCCG whose function and utility is known in the art.

TGGGACCGAA GAM7884 is a novel bioinformatically detectable regulatory, non protein coding, GTATTATGGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7884 was detected is

GCAGTGACTT described with additional reference to Figs. 9-15.

GACGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7884 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7884

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7884

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7884 precursor RNA is designated SEQ ID:6934, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6934 is located from position 102447082 to position 102447156 relative to chromosome 12 on the `+` strand.

GAM7884 precursor RNA folds onto itself, forming GAM7884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7884 precursor RNA, designated SEQ ID NO: 6934, and a schematic representation of a predicted secondary folding of GAM7884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7884 folded precursor RNA yielding a GAM7884 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7884 RNA, hereby incorporated herein.

GAM7884 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7884 target RNA, herein designated GAM TARGET RNA. GAM7884 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7884 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7884 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7884 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7884 RNA, herein designated GAM RNA, to target binding sites on GAM7884 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7884 target RNA into GAM7884 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7884 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7884 target genes. The mRNA of each one of this plurality of GAM7884 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7884 RNA, herein designated GAM RNA, and which when bound by GAM7884 RNA causes inhibition of translation of the GAM7884 target mRNA into a corresponding GAM7884 target protein.

The mechanism of the translational inhibition exerted by GAM7884 RNA, herein designated GAM RNA, on one or more GAM7884 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7884 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7884 RNA, herein designated GAM RNA, of GAM7884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7884 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7884 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7884 RNA correlate with, and may be deduced from, the identity of the GAM7884 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7889 6250 CTTACCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TATCCTATTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTCATACCT Messenger 7889 (GAM7889) oligonucleotides modulates expression of respective target genes

AAGGCAGTGA whose function and utility is known in the art.

TGGTTTCTCA GAM7889 is a novel bioinformatically detectable regulatory, non protein coding,

GACCTCTTAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7889 was detected is

ATTGAGAAGA described with additional reference to Figs. 9-15.

TGTGGCATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGTAAG encoded by the human genome.

GAM7889 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7889 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7889 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7889 precursor RNA is designated SEQ ID:6250, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6250 is located from position 50175600 to position 50175686 relative to chromosome 20 on the `-` strand.

GAM7889 precursor RNA folds onto itself, forming GAM7889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7889 precursor RNA, designated SEQ ID NO: 6250, and a schematic representation of a predicted secondary folding of GAM7889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7889 folded precursor RNA yielding a GAM7889 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7889 RNA, hereby incorporated herein.

GAM7889 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7889 target RNA, herein designated GAM TARGET RNA. GAM7889 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7889 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7889 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7889 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7889 RNA, herein designated GAM RNA, to target binding sites on GAM7889 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7889 target RNA into GAM7889 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7889 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7889 target genes. The mRNA of each one of this plurality of GAM7889 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7889 RNA, herein designated GAM RNA, and which when bound by GAM7889 RNA causes inhibition of translation of the GAM7889 target mRNA into a corresponding GAM7889 target protein.

The mechanism of the translational inhibition exerted by GAM7889 RNA, herein designated GAM RNA, on one or more GAM7889 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7889 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7889 RNA, herein designated GAM RNA, of GAM7889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7889 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7889 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7889 RNA correlate with, and may be deduced from, the identity of the GAM7889 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7898 7347 TTTTAGCATG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTTGTAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCAAACAGTT Messenger 7898 (GAM7898) oligonucleotides modulates expression of respective target genes
TGTAATAGCA whose function and utility is known in the art.

ATGACGTGTT GAM7898 is a novel bioinformatically detectable regulatory, non protein coding,
ATTTATTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7898 was detected is

GCATTGTTTG described with additional reference to Figs. 9-15.

TAATAGCAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATACTGGAA encoded by the human genome.

GAM7898 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7898

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7898

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7898 precursor RNA is designated SEQ ID:7347, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7347 is located from position 47657707 to position 47657795 relative to chromosome 11 on the `+` strand.

GAM7898 precursor RNA folds onto itself, forming GAM7898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7898 precursor RNA, designated SEQ ID NO: 7347, and a schematic representation of a predicted secondary folding of GAM7898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7898 folded precursor RNA yielding a GAM7898 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7898 RNA, hereby incorporated herein.

GAM7898 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7898 target RNA, herein designated GAM TARGET RNA. GAM7898 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7898 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7898 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7898 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7898 RNA, herein designated GAM RNA, to target binding sites on GAM7898 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7898 target RNA into GAM7898 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7898 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7898 target genes. The mRNA of each one of this plurality of GAM7898 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7898 RNA, herein designated GAM RNA, and which when bound by GAM7898 RNA causes inhibition of translation of the GAM7898 target mRNA into a corresponding GAM7898 target protein.

The mechanism of the translational inhibition exerted by GAM7898 RNA, herein designated GAM RNA, on one or more GAM7898 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7898 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7898 RNA, herein designated GAM RNA, of GAM7898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM7898 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7898 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7898 RNA correlate with, and may be deduced from, the identity of the GAM7898 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7902 7301 TTCCCTGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCTTTAACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTTGAAAAA Messenger 7902 (GAM7902) oligonucleotides modulates expression of respective target genes
AGTTGATGCT whose function and utility is known in the art.

GTTTTATTTG GAM7902 is a novel bioinformatically detectable regulatory, non protein coding,
AAAAATCGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM7902 was detected is

AAGACTATTA described with additional reference to Figs. 9-15.

AAAGGCAAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGGGA encoded by the human genome.

GAM7902 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7902

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7902
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7902 precursor RNA is designated SEQ ID:7301, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7301 is located from position 29022047 to position 29022132 relative to chromosome 10 on the `+` strand.

GAM7902 precursor RNA folds onto itself, forming GAM7902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7902 precursor RNA, designated SEQ ID NO: 7301, and a schematic representation of a predicted secondary folding of GAM7902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7902 folded precursor RNA yielding a GAM7902 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7902 RNA, hereby incorporated herein.

GAM7902 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7902 target RNA, herein designated GAM TARGET RNA. GAM7902 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7902 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7902 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7902 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7902 RNA, herein designated GAM RNA, to target binding sites on GAM7902 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7902 target RNA into GAM7902 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7902 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7902 target genes. The mRNA of each one of this plurality of GAM7902 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7902 RNA, herein designated GAM RNA, and which when bound by GAM7902 RNA causes inhibition of translation of the GAM7902 target mRNA into a corresponding GAM7902 target protein.

The mechanism of the translational inhibition exerted by GAM7902 RNA, herein designated GAM RNA, on one or more GAM7902 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7902 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7902 RNA, herein designated GAM RNA, of

GAM7902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7902 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7902 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7902 RNA correlate with, and may be deduced from, the identity of the GAM7902 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7911 6296 GAAGCTACCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTTTAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTCCTTCAG Messenger 7911 (GAM7911) oligonucleotides modulates expression of respective target genes

CCCTAGCTGC whose function and utility is known in the art.

TTTTATTCTG GAM7911 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTTTATTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7911 was detected is

AAACAAAAAG described with additional reference to Figs. 9-15.

AGGGGGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGAAGGAA encoded by the human genome.

ACTAGTTTTC GAM7911 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7911

TGTACAAAGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7911

CTTT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7911 precursor RNA is designated SEQ ID:6296, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6296 is located from position 25092986 to position 25093099 relative to chromosome 8 on the `+` strand.

GAM7911 precursor RNA folds onto itself, forming GAM7911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7911 precursor RNA, designated SEQ ID NO: 6296, and a schematic representation of a predicted secondary folding of GAM7911 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7911 folded precursor RNA yielding a GAM7911 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7911 RNA, hereby incorporated herein.

GAM7911 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7911 target RNA, herein designated GAM TARGET RNA. GAM7911 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7911 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7911 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7911 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7911 RNA, herein designated GAM RNA, to target binding sites on GAM7911 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7911 target RNA into GAM7911 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7911 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7911 target genes. The mRNA of each one of this plurality of GAM7911 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7911 RNA, herein designated GAM RNA, and which when bound by GAM7911 RNA causes inhibition of translation of the GAM7911 target mRNA into a corresponding GAM7911 target protein.

The mechanism of the translational inhibition exerted by GAM7911 RNA, herein designated GAM RNA, on one or more GAM7911 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7911 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM7911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7911 RNA, herein designated GAM RNA, of GAM7911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7911 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7911 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7911 RNA correlate with, and may be deduced from, the identity of the GAM7911 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7915 5822 AGTTCAGACA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCTAGACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCGTCAGA Messenger 7915 (GAM7915) oligonucleotides modulates expression of respective target genes

CTCAGTTTCA whose function and utility is known in the art.

AAAGAGAATG GAM7915 is a novel bioinformatically detectable regulatory, non protein coding,

TGTGGGAGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM7915 was detected is

CAGTCTTTGT described with additional reference to Figs. 9-15.

CCGACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7915 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7915

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7915

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7915 precursor RNA is designated SEQ ID:5822, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5822 is located from position 14497507 to position 14497582 relative to chromosome 4 on the `-` strand.

GAM7915 precursor RNA folds onto itself, forming GAM7915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7915 precursor RNA, designated SEQ ID NO: 5822, and a schematic representation of a predicted secondary folding of GAM7915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7915 folded precursor RNA yielding a GAM7915 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM7915 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7915 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM7915 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7915 target RNA, herein designated GAM TARGET RNA. GAM7915 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7915 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7915 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7915 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7915 RNA, herein designated GAM RNA, to target binding sites on GAM7915 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7915 target RNA into GAM7915 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7915 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7915 target genes. The mRNA of each one of this plurality of GAM7915 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7915 RNA, herein designated GAM RNA, and which when bound by GAM7915 RNA causes inhibition of translation of the GAM7915 target mRNA into a corresponding GAM7915 target protein.

The mechanism of the translational inhibition exerted by GAM7915 RNA, herein

designated GAM RNA, on one or more GAM7915 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7915 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7915 RNA, herein designated GAM RNA, of GAM7915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7915 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7915 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7915 RNA correlate with, and may be deduced from, the identity of the GAM7915 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7933 6769 GGCTTCCTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCACCTTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CACTGCTGCT Messenger 7933 (GAM7933) oligonucleotides modulates expression of respective target genes

CCCACACCAC whose function and utility is known in the art.

AGTGACTAGC GAM7933 is a novel bioinformatically detectable regulatory, non protein coding,

AGCACATAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7933 was detected is

GGTTTGAATT described with additional reference to Figs. 9-15.

AAAGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM7933 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7933

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7933

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7933 precursor RNA is designated SEQ ID:6769, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6769 is located from position 3260143 to position 3260218 relative to chromosome 7 on

the `-` strand.

GAM7933 precursor RNA folds onto itself, forming GAM7933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7933 precursor RNA, designated SEQ ID NO: 6769, and a schematic representation of a predicted secondary folding of GAM7933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7933 folded precursor RNA yielding a GAM7933 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7933 RNA, hereby incorporated herein. Expression of GAM7933 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM7933 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7933 target RNA, herein designated GAM TARGET RNA. GAM7933 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7933 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7933 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7933 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7933 RNA, herein designated GAM RNA, to target binding sites on GAM7933 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7933 target RNA into GAM7933 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7933 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM7933 target genes. The mRNA of each one of this plurality of GAM7933 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7933 RNA, herein designated GAM RNA, and which when bound by GAM7933 RNA causes inhibition of translation of the GAM7933 target mRNA into a corresponding GAM7933 target protein.

The mechanism of the translational inhibition exerted by GAM7933 RNA, herein designated GAM RNA, on one or more GAM7933 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7933 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7933 RNA, herein designated GAM RNA, of GAM7933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7933 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7933 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7933 RNA correlate with, and may be deduced from, the identity of the GAM7933 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7954 6709 GGAGGACCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCAAAGTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGGTGCAGG Messenger 7954 (GAM7954) oligonucleotides modulates expression of respective target genes

GGTGGTCTTA whose function and utility is known in the art.

GGAGGGCTTT GAM7954 is a novel bioinformatically detectable regulatory, non protein coding,

CCTGAAGGAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7954 was detected is

TGGCCAGGGT described with additional reference to Figs. 9-15.

TCACCCATCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCCACCCAC encoded by the human genome.

GGACCCATCC GAM7954 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7954

TCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7954 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7954 precursor RNA is designated SEQ ID:6709, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6709 is located from position 43546115 to position 43546217 relative to chromosome 19 on the `+` strand.

GAM7954 precursor RNA folds onto itself, forming GAM7954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7954 precursor RNA, designated SEQ ID NO: 6709, and a schematic representation of a predicted secondary folding of GAM7954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7954 folded precursor RNA yielding a GAM7954 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7954 RNA, hereby incorporated herein.

GAM7954 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7954 target RNA, herein designated GAM TARGET RNA. GAM7954 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7954 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7954 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7954 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7954 RNA, herein designated GAM RNA, to target binding sites on GAM7954 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7954 target RNA

into GAM7954 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7954 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7954 target genes. The mRNA of each one of this plurality of GAM7954 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7954 RNA, herein designated GAM RNA, and which when bound by GAM7954 RNA causes inhibition of translation of the GAM7954 target mRNA into a corresponding GAM7954 target protein.

The mechanism of the translational inhibition exerted by GAM7954 RNA, herein designated GAM RNA, on one or more GAM7954 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7954 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7954 RNA, herein designated GAM RNA, of GAM7954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7954 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7954 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7954 RNA correlate with, and may be deduced from, the identity of the GAM7954 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7966 6070 CCCAGAACAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGACCTCTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAACATGTA Messenger 7966 (GAM7966) oligonucleotides modulates expression of respective target genes

AGCACCTAGA whose function and utility is known in the art.

CCATGGTTTC GAM7966 is a novel bioinformatically detectable regulatory, non protein coding,

CCATCCTTAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM7966 was detected is

CATTGTTAAC described with additional reference to Figs. 9-15.

ATTTTGGCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATAGTTCTT encoded by the human genome.

TGTTGTGTGG GAM7966 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7966 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7966 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7966 precursor RNA is designated SEQ ID:6070, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6070 is located from position 67546633 to position 67546732 relative to chromosome 14 on the `-` strand.

GAM7966 precursor RNA folds onto itself, forming GAM7966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7966 precursor RNA, designated SEQ ID NO: 6070, and a schematic representation of a predicted secondary folding of GAM7966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7966 folded precursor RNA yielding a GAM7966 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7966 RNA, hereby incorporated herein.

GAM7966 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7966 target RNA, herein designated GAM TARGET RNA. GAM7966 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7966 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7966 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7966 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7966 RNA, herein designated GAM RNA, to target binding sites on GAM7966 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7966 target RNA into GAM7966 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7966 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7966 target genes. The mRNA of each one of this plurality of GAM7966 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7966 RNA, herein designated GAM RNA, and which when bound by GAM7966 RNA causes inhibition of translation of the GAM7966 target mRNA into a corresponding GAM7966 target protein.

The mechanism of the translational inhibition exerted by GAM7966 RNA, herein designated GAM RNA, on one or more GAM7966 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7966 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7966 RNA, herein designated GAM RNA, of GAM7966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7966 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7966 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7966 RNA correlate with, and may be deduced from, the identity of the GAM7966 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM7980 5999 CACGCGTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGGTCACC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGCTTAGGA Messenger 7980 (GAM7980) oligonucleotides modulates expression of respective target genes
AGCTCACAAG whose function and utility is known in the art.

GTCCTCATCA GAM7980 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGGAGGTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM7980 was detected is

TTTCCCTGTG described with additional reference to Figs. 9-15.

AGTGCCCTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCCTAGGCT encoded by the human genome.

TTCTTACGTG GAM7980 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM7980

TG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM7980

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7980 precursor RNA is designated SEQ ID:5999, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5999 is located from position 55163316 to position 55163417 relative to chromosome 15 on the `+` strand.

GAM7980 precursor RNA folds onto itself, forming GAM7980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM7980 precursor RNA, designated SEQ ID NO: 5999, and a schematic representation of a predicted secondary folding of GAM7980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM7980 folded precursor RNA yielding a GAM7980 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM7980 RNA, hereby incorporated herein.

GAM7980 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM7980 target RNA, herein designated GAM TARGET RNA. GAM7980 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM7980 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7980 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7980 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM7980 RNA, herein designated GAM RNA, to target binding sites on GAM7980 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7980 target RNA into GAM7980 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM7980 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM7980 target genes. The mRNA of each one of this plurality of GAM7980 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7980 RNA, herein designated GAM RNA, and which when bound by GAM7980 RNA causes inhibition of translation of the GAM7980 target mRNA into a corresponding GAM7980 target protein.

The mechanism of the translational inhibition exerted by GAM7980 RNA, herein designated GAM RNA, on one or more GAM7980 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM7980 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM7980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM7980 RNA, herein designated GAM RNA, of GAM7980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM7980 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM7980 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM7980 RNA correlate with, and may be deduced from, the identity of the GAM7980 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8013 6539 GCTCTTGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCAGGCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTGCAGTGG Messenger 8013 (GAM8013) oligonucleotides modulates expression of respective target genes

CATGATCTCA whose function and utility is known in the art.

GCTCACTGCA GAM8013 is a novel bioinformatically detectable regulatory, non protein coding, ACCTCTGCCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8013 was detected is

CCTGGGTTCA described with additional reference to Figs. 9-15.

AGCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8013 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8013

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8013

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8013 precursor RNA is designated SEQ ID:6539, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6539 is located from position 36439313 to position 36439388 relative to chromosome 21 on the `+` strand.

GAM8013 precursor RNA folds onto itself, forming GAM8013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8013 precursor RNA, designated SEQ ID NO: 6539, and a schematic representation of a predicted secondary folding of GAM8013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8013 folded precursor RNA yielding a GAM8013 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM8013 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8013 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM8013 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8013 target RNA, herein designated GAM TARGET RNA. GAM8013 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8013 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM8013 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8013 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8013 RNA, herein designated GAM RNA, to target binding sites on GAM8013 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8013 target RNA into GAM8013 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8013 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8013 target genes. The mRNA of each one of this plurality of GAM8013 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8013 RNA, herein designated GAM RNA, and which when bound by GAM8013 RNA causes inhibition of translation of the GAM8013 target mRNA into a corresponding GAM8013 target protein.

The mechanism of the translational inhibition exerted by GAM8013 RNA, herein designated GAM RNA, on one or more GAM8013 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8013 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8013 RNA, herein designated GAM RNA, of GAM8013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8013 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8013 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8013 RNA correlate with, and may be deduced from, the identity of the GAM8013 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8026 7255 TGGTTCATAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TATTCCTTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGATGTTGAA Messenger 8026 (GAM8026) oligonucleotides modulates expression of respective target genes

CGATGGGCTG whose function and utility is known in the art.

GATTGTTTTG GAM8026 is a novel bioinformatically detectable regulatory, non protein coding,

GAACCTTGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8026 was detected is

CCAGCAGAGC described with additional reference to Figs. 9-15.

CCATGTGTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGAAGAAAA encoded by the human genome.

CATTTGCTTA GAM8026 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8026

CAGCTTATGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8026

CTA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8026 precursor RNA is designated SEQ ID:7255, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7255 is located from position 58074215 to position 58074327 relative to chromosome 19 on the `-` strand.

GAM8026 precursor RNA folds onto itself, forming GAM8026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8026 precursor RNA, designated SEQ ID NO: 7255, and a schematic representation of a predicted secondary folding of GAM8026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8026 folded precursor RNA yielding a GAM8026 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM8026 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8026 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM8026 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8026 target RNA, herein designated GAM TARGET RNA. GAM8026 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8026 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8026 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8026 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8026 RNA, herein designated GAM RNA, to target binding sites on GAM8026 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8026 target RNA into GAM8026 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8026 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8026 target genes. The mRNA of each one of this plurality of GAM8026 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8026 RNA, herein designated GAM RNA, and which when bound by GAM8026 RNA causes inhibition of translation of the GAM8026 target mRNA into a corresponding GAM8026 target protein.

The mechanism of the translational inhibition exerted by GAM8026 RNA, herein designated GAM RNA, on one or more GAM8026 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8026 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8026 RNA, herein designated GAM RNA, of GAM8026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8026 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8026 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8026 RNA correlate with, and may be deduced from, the identity of the GAM8026 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8031 6529 GCTATCAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGCTATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGAGCACT Messenger 8031 (GAM8031) oligonucleotides modulates expression of respective target genes

CTATCATGTT whose function and utility is known in the art.

TTTAGGTGTA GAM8031 is a novel bioinformatically detectable regulatory, non protein coding,

TATTGTGTAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8031 was detected is

TCAGGATAGC described with additional reference to Figs. 9-15.

ATTAAAAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACTGATGGC encoded by the human genome.

GAM8031 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8031

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8031

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8031 precursor RNA is designated SEQ ID:6529, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6529 is located from position 26287592 to position 26287680 relative to chromosome 12 on the `+` strand.

GAM8031 precursor RNA folds onto itself, forming GAM8031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8031 precursor RNA, designated SEQ ID NO: 6529, and a schematic representation of a predicted secondary folding of GAM8031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8031 folded precursor RNA yielding a GAM8031 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM8031 RNA, hereby incorporated herein.

GAM8031 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8031 target RNA, herein designated GAM TARGET RNA. GAM8031 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8031 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8031 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8031 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8031 RNA, herein designated GAM RNA, to target binding sites on GAM8031 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8031 target RNA into GAM8031 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8031 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8031 target genes. The mRNA of each one of this plurality of GAM8031 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8031 RNA, herein designated GAM RNA, and which when bound by GAM8031 RNA causes inhibition of translation of the GAM8031 target mRNA into a corresponding GAM8031 target protein.

The mechanism of the translational inhibition exerted by GAM8031 RNA, herein designated GAM RNA, on one or more GAM8031 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8031 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8031 RNA, herein designated GAM RNA, of GAM8031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8031 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8031 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8031 RNA correlate with, and may be deduced from, the identity of the GAM8031 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8047 5705 ACTCTTAAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTTAGAAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTACAGCAT Messenger 8047 (GAM8047) oligonucleotides modulates expression of respective target genes
CTAGCTTCTC whose function and utility is known in the art.

TAGATCAATA GAM8047 is a novel bioinformatically detectable regulatory, non protein coding,
ATCACAGAGG micro RNA (miRNA)-like oligonucleotide. The method by which GAM8047 was detected is

CTTAAGTGCT described with additional reference to Figs. 9-15.

GACCTCATAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGATAAAGAG encoded by the human genome.

T GAM8047 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8047
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8047
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8047 precursor RNA is designated SEQ ID:5705, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5705 is located from position 136594089 to position 136594179 relative to chromosome X on the `+` strand.

GAM8047 precursor RNA folds onto itself, forming GAM8047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8047 precursor RNA, designated SEQ ID NO: 5705, and a schematic representation of a predicted secondary folding of GAM8047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8047 folded precursor RNA

yielding a GAM8047 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8047 RNA, hereby incorporated herein. Expression of GAM8047 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8047 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8047 target RNA, herein designated GAM TARGET RNA. GAM8047 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8047 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8047 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8047 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8047 RNA, herein designated GAM RNA, to target binding sites on GAM8047 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8047 target RNA into GAM8047 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8047 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8047 target genes. The mRNA of each one of this plurality of GAM8047 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8047 RNA, herein designated GAM RNA, and which when bound by GAM8047 RNA causes inhibition of translation of the GAM8047 target mRNA into a corresponding GAM8047 target protein.

The mechanism of the translational inhibition exerted by GAM8047 RNA, herein designated GAM RNA, on one or more GAM8047 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8047 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8047 RNA, herein designated GAM RNA, of GAM8047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8047 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8047 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8047 RNA correlate with, and may be deduced from, the identity of the GAM8047 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8100 6982 TATGAGGGAC ATGAACACCT GCAGATTTTG GGGTCCACAG GGGTCCTGGA ATTAATTCCC TGTGGATACT GAGAGATGAC TGGACATCCA TTCTCCATG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 8100 (GAM8100) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM8100 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM8100 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM8100 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8100 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8100 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8100 precursor RNA is designated SEQ ID:6982, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6982 is located from position 10904327 to position 10904425 relative to chromosome 18 on the `-` strand.

GAM8100 precursor RNA folds onto itself, forming GAM8100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8100 precursor RNA, designated SEQ ID NO: 6982, and a schematic representation of a predicted secondary folding of GAM8100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8100 folded precursor RNA yielding a GAM8100 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8100 RNA, hereby incorporated herein.

GAM8100 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8100 target RNA, herein designated GAM TARGET RNA. GAM8100 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8100 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8100 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8100 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8100 RNA, herein designated GAM RNA, to target binding sites on GAM8100 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8100 target RNA into GAM8100 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8100 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8100 target genes. The mRNA of each one of this plurality of GAM8100 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8100 RNA, herein designated GAM RNA, and which when bound by GAM8100 RNA causes inhibition of translation of the GAM8100 target mRNA into a corresponding GAM8100 target protein.

The mechanism of the translational inhibition exerted by GAM8100 RNA, herein designated GAM RNA, on one or more GAM8100 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8100 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8100 RNA, herein designated GAM RNA, of GAM8100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8100 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8100 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8100 RNA correlate with, and may be deduced from, the identity of the GAM8100 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8109 6310 GACAGGATTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTACAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTCATTTC Messenger 8109 (GAM8109) oligonucleotides modulates expression of respective target genes

CTTCATGATT whose function and utility is known in the art.

AGGAATACTA GAM8109 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTGAAATG micro RNA (miRNA)-like oligonucleotide. The method by which GAM8109 was detected is

AGAGACCTGT described with additional reference to Figs. 9-15.

ACTGTATCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TT encoded by the human genome.

GAM8109 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8109

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8109

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8109 precursor RNA is designated SEQ ID:6310, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6310 is located from position 48231664 to position 48231745 relative to chromosome 15 on the `+` strand.

GAM8109 precursor RNA folds onto itself, forming GAM8109 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8109 precursor RNA, designated SEQ ID NO: 6310, and a schematic representation of a predicted secondary folding of GAM8109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8109 folded precursor RNA yielding a GAM8109 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8109 RNA, hereby incorporated herein.

GAM8109 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8109 target RNA, herein designated GAM TARGET RNA. GAM8109 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8109 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8109 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8109 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8109 RNA, herein designated GAM RNA, to target binding sites on GAM8109 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8109 target RNA into GAM8109 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8109 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8109 target genes. The mRNA of each one of this plurality of GAM8109 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8109 RNA, herein designated GAM RNA, and which when bound by GAM8109 RNA causes inhibition of translation of the GAM8109 target mRNA into a corresponding GAM8109 target protein.

The mechanism of the translational inhibition exerted by GAM8109 RNA, herein designated GAM RNA, on one or more GAM8109 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8109 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8109 RNA, herein designated GAM RNA, of GAM8109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8109 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8109 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8109 RNA correlate with, and may be deduced from, the identity of the GAM8109 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8145 6589 GGACCAGACT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGTGACAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGAATGTA Messenger 8145 (GAM8145) oligonucleotides modulates expression of respective target genes

GAGGAATTAT whose function and utility is known in the art.

TCAATGTTCA GAM8145 is a novel bioinformatically detectable regulatory, non protein coding,

GGATCAACAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8145 was detected is

GATCTCCTCA described with additional reference to Figs. 9-15.

CTCTAGGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATCC encoded by the human genome.

GAM8145 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8145

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8145

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8145 precursor RNA is designated SEQ ID:6589, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6589 is located from position 90807704 to position 90807788 relative to chromosome 10 on the `+` strand.

GAM8145 precursor RNA folds onto itself, forming GAM8145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8145 precursor RNA, designated SEQ ID NO: 6589, and a schematic representation of a predicted secondary folding of GAM8145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8145 folded precursor RNA yielding a GAM8145 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8145 RNA, hereby incorporated herein. Expression of GAM8145 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8145 target RNA, herein designated GAM TARGET RNA. GAM8145 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8145 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8145 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8145 RNA, herein designated GAM RNA, to target binding sites on GAM8145 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8145 target RNA into GAM8145 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8145 target genes. The mRNA of each one of this plurality of GAM8145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8145 RNA, herein designated GAM RNA, and which when bound by GAM8145 RNA causes inhibition of translation of the GAM8145 target mRNA into a corresponding GAM8145 target protein.

The mechanism of the translational inhibition exerted by GAM8145 RNA, herein designated GAM RNA, on one or more GAM8145 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8145 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8145 RNA, herein designated GAM RNA, of GAM8145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8145 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8145 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8145 RNA correlate with, and may be deduced from, the identity of the GAM8145 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8164 6811 GGGGCAGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

GGATGGAAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGGAGATCCC Messenger 8164 (GAM8164) oligonucleotides modulates expression of respective target genes

AGGTTCCCGG whose function and utility is known in the art.

AATACTCCGG GAM8164 is a novel bioinformatically detectable regulatory, non protein coding,

CTGGGGCCTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8164 was detected is

CGGGCTTCTC described with additional reference to Figs. 9-15.

CTGTCCCCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTACCCC encoded by the human genome.

GAM8164 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8164 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8164 precursor RNA is designated SEQ ID:6811, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6811 is located from position 76816710 to position 76816797 relative to chromosome 17 on the `-` strand.

GAM8164 precursor RNA folds onto itself, forming GAM8164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8164 precursor RNA, designated SEQ ID NO: 6811, and a schematic representation of a predicted secondary folding of GAM8164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8164 folded precursor RNA yielding a GAM8164 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8164 RNA, hereby incorporated herein.

GAM8164 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8164 target RNA, herein designated GAM TARGET RNA. GAM8164 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8164 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8164 RNA, herein designated GAM RNA, to target binding sites on GAM8164 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8164 target RNA into GAM8164 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8164 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8164 target genes. The mRNA of each one of this plurality of GAM8164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8164 RNA, herein designated GAM RNA, and which when bound by GAM8164 RNA causes inhibition of translation of the GAM8164 target mRNA into a corresponding GAM8164 target protein.

The mechanism of the translational inhibition exerted by GAM8164 RNA, herein designated GAM RNA, on one or more GAM8164 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8164 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8164 RNA, herein designated GAM RNA, of GAM8164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8164 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8164 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8164 RNA correlate with, and may be deduced from, the identity of the GAM8164 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8206 6320 GAGAATCACT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGGAGGT Messenger 8206 (GAM8206) oligonucleotides modulates expression of respective target genes

TGCAGTGAGC whose function and utility is known in the art.

CAAGATCGTG GAM8206 is a novel bioinformatically detectable regulatory, non protein coding,

CCATTGCACT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8206 was detected is

CCAGCCTGGG described with additional reference to Figs. 9-15.

TAACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGACTC encoded by the human genome.

GAM8206 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8206 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8206 precursor RNA is designated SEQ ID:6320, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6320 is located from position 107994686 to position 107994771 relative to chromosome 11 on the `+` strand.

GAM8206 precursor RNA folds onto itself, forming GAM8206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8206 precursor RNA, designated SEQ ID NO: 6320, and a schematic representation of a predicted secondary folding of GAM8206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8206 folded precursor RNA yielding a GAM8206 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8206 RNA, hereby incorporated herein.

GAM8206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8206 target RNA, herein designated GAM TARGET RNA. GAM8206 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8206 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8206 RNA, herein designated GAM RNA, to target binding sites on GAM8206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8206 target RNA into GAM8206 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8206 target genes. The mRNA of each one of this plurality of GAM8206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8206 RNA, herein designated GAM RNA, and which when bound by GAM8206 RNA causes inhibition of translation of the GAM8206 target mRNA into a corresponding GAM8206 target protein.

The mechanism of the translational inhibition exerted by GAM8206 RNA, herein designated GAM RNA, on one or more GAM8206 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8206 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8206 RNA, herein designated GAM RNA, of GAM8206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8206 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8206 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8206 RNA correlate with, and may be deduced from, the identity of the GAM8206 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8276 5717 AGAATCGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACCCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCGGAGGTT Messenger 8276 (GAM8276) oligonucleotides modulates expression of respective target genes

GCAGTGAGCC whose function and utility is known in the art.

AGGATCACGC GAM8276 is a novel bioinformatically detectable regulatory, non protein coding, CACTGTACTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8276 was detected is

CACCCTGGGC described with additional reference to Figs. 9-15.

GACAGAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACT encoded by the human genome.

GAM8276 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8276 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8276 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8276 precursor RNA is designated SEQ ID:5717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5717 is located from position 61627070 to position 61627153 relative to chromosome 19 on the `-` strand.

GAM8276 precursor RNA folds onto itself, forming GAM8276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8276 precursor RNA, designated SEQ ID NO: 5717, and a schematic representation of a predicted secondary folding of GAM8276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8276 folded precursor RNA yielding a GAM8276 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8276 RNA, hereby incorporated herein.

GAM8276 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8276 target RNA, herein designated GAM TARGET RNA. GAM8276 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8276 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8276 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8276 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8276 RNA, herein designated GAM RNA, to target binding sites on GAM8276 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8276 target RNA into GAM8276 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8276 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8276 target genes. The mRNA of each one of this plurality of GAM8276 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8276 RNA, herein designated GAM RNA, and which when bound by GAM8276 RNA causes inhibition of translation of the GAM8276 target mRNA into a corresponding GAM8276 target protein.

The mechanism of the translational inhibition exerted by GAM8276 RNA, herein designated GAM RNA, on one or more GAM8276 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8276 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8276 RNA, herein designated GAM RNA, of GAM8276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8276 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8276 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8276 RNA correlate with, and may be deduced from, the identity of the GAM8276 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8285 6051 CCAGAGGCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGACCATGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGTAGACAG Messenger 8285 (GAM8285) oligonucleotides modulates expression of respective target genes

TGGCAACATA whose function and utility is known in the art.

GTCATCCCCA GAM8285 is a novel bioinformatically detectable regulatory, non protein coding,

AGATGCTAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8285 was detected is

CTTCTGCTGG described with additional reference to Figs. 9-15.

AACTGTCATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGTTATCATG encoded by the human genome.

GTCAATGTAA GAM8285 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8285

ACCTGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8285

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8285 precursor RNA is designated SEQ ID:6051, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6051 is located from position 158626692 to position 158626797 relative to chromosome 1 on the `+` strand.

GAM8285 precursor RNA folds onto itself, forming GAM8285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8285 precursor RNA, designated SEQ ID NO: 6051, and a schematic representation of a predicted secondary folding of GAM8285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8285 folded precursor RNA yielding a GAM8285 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8285 RNA, hereby incorporated herein. Expression of GAM8285 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8285 target RNA, herein designated GAM TARGET RNA. GAM8285 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8285 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8285 RNA, herein designated GAM RNA, to target binding sites on GAM8285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8285 target RNA into GAM8285 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8285 target genes. The mRNA of each one of this plurality of GAM8285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8285 RNA, herein designated GAM RNA, and which when bound by GAM8285 RNA causes inhibition of translation of the GAM8285 target mRNA into a corresponding GAM8285 target protein.

The mechanism of the translational inhibition exerted by GAM8285 RNA, herein designated GAM RNA, on one or more GAM8285 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8285 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8285 RNA, herein designated GAM RNA, of GAM8285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8285 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8285 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8285 RNA correlate with, and may be deduced from, the identity of the GAM8285 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8288 7243 TGGGGTGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTTCTGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTGTTGGGA Messenger 8288 (GAM8288) oligonucleotides modulates expression of respective target genes

AGGCTCGGTG whose function and utility is known in the art.

GTCCATTTTC GAM8288 is a novel bioinformatically detectable regulatory, non protein coding,

ACCAGTTAAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8288 was detected is

GAATATGAGG described with additional reference to Figs. 9-15.

CCAGCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8288 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8288

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8288

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8288 precursor RNA is designated SEQ ID:7243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7243 is located from position 54931946 to position 54932023 relative to chromosome 18 on the `+` strand.

GAM8288 precursor RNA folds onto itself, forming GAM8288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8288 precursor RNA, designated SEQ ID NO: 7243, and a schematic representation of a predicted secondary folding of GAM8288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8288 folded precursor RNA yielding a GAM8288 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the

nucleotide sequence of GAM8288 RNA, hereby incorporated herein.

GAM8288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8288 target RNA, herein designated GAM TARGET RNA. GAM8288 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8288 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8288 RNA, herein designated GAM RNA, to target binding sites on GAM8288 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8288 target RNA into GAM8288 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8288 target genes. The mRNA of each one of this plurality of GAM8288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8288 RNA, herein designated GAM RNA, and which when bound by GAM8288 RNA causes inhibition of translation of the GAM8288 target mRNA into a corresponding GAM8288 target protein.

The mechanism of the translational inhibition exerted by GAM8288 RNA, herein designated GAM RNA, on one or more GAM8288 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8288 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8288 RNA, herein designated GAM RNA, of GAM8288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8288 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8288 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8288 RNA correlate with, and may be deduced from, the identity of the GAM8288 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8311 6622 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTAACCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTGGAGG Messenger 8311 (GAM8311) oligonucleotides modulates expression of respective target genes

TTGCAGGGAG whose function and utility is known in the art.

CCGAGATCGC GAM8311 is a novel bioinformatically detectable regulatory, non protein coding,

ACCACTGCAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8311 was detected is

TCCAGCCTGG described with additional reference to Figs. 9-15.

GTGACAAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM8311 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8311

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8311

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8311 precursor RNA is designated SEQ ID:6622, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6622 is located from position 96904480 to position 96904567 relative to chromosome 15 on the `+` strand.

GAM8311 precursor RNA folds onto itself, forming GAM8311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8311 precursor RNA, designated SEQ ID NO: 6622, and a schematic representation of a predicted secondary folding of GAM8311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8311 folded precursor RNA

yielding a GAM8311 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8311 RNA, hereby incorporated herein.

GAM8311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8311 target RNA, herein designated GAM TARGET RNA. GAM8311 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8311 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8311 RNA, herein designated GAM RNA, to target binding sites on GAM8311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8311 target RNA into GAM8311 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8311 target genes. The mRNA of each one of this plurality of GAM8311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8311 RNA, herein designated GAM RNA, and which when bound by GAM8311 RNA causes inhibition of translation of the GAM8311 target mRNA into a corresponding GAM8311 target protein.

The mechanism of the translational inhibition exerted by GAM8311 RNA, herein designated GAM RNA, on one or more GAM8311 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8311 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8311 RNA, herein designated GAM RNA, of GAM8311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8311 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8311 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8311 RNA correlate with, and may be deduced from, the identity of the GAM8311 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8339 6102 CCTAAAACAT Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGTGAAGAT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGGCTACAG Messenger 8339 (GAM8339) oligonucleotides modulates expression of respective target genes

TGCTTTTCTC whose function and utility is known in the art.

ATGACATGGA GAM8339 is a novel bioinformatically detectable regulatory, non protein coding,

GCCTTGTTGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8339 was detected is

TTGTTCACTC described with additional reference to Figs. 9-15.

ATTCTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8339 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8339

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8339

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8339 precursor RNA is designated SEQ ID:6102, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6102 is located from position 107487845 to position 107487922 relative to chromosome X on the `+` strand.

GAM8339 precursor RNA folds onto itself, forming GAM8339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8339 precursor RNA, designated SEQ ID NO: 6102, and a

schematic representation of a predicted secondary folding of GAM8339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8339 folded precursor RNA yielding a GAM8339 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8339 RNA, hereby incorporated herein.

GAM8339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8339 target RNA, herein designated GAM TARGET RNA. GAM8339 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8339 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8339 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8339 RNA, herein designated GAM RNA, to target binding sites on GAM8339 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8339 target RNA into GAM8339 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8339 target genes. The mRNA of each one of this plurality of GAM8339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8339 RNA, herein designated GAM RNA, and which when bound by GAM8339 RNA causes inhibition of translation of the GAM8339 target mRNA into a corresponding GAM8339 target protein.

The mechanism of the translational inhibition exerted by GAM8339 RNA, herein designated GAM RNA, on one or more GAM8339 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8339 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8339 RNA, herein designated GAM RNA, of GAM8339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8339 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8339 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8339 RNA correlate with, and may be deduced from, the identity of the GAM8339 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8349 6859 GTAAATCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGATACCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACTCTTAAA Messenger 8349 (GAM8349) oligonucleotides modulates expression of respective target genes
CCTTTAGAAA whose function and utility is known in the art.

TGCTACAGCA GAM8349 is a novel bioinformatically detectable regulatory, non protein coding,
TCTAGCTTCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8349 was detected is

CTAGATCAAT described with additional reference to Figs. 9-15.

AATCACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTTAAGTGC encoded by the human genome.

TGACCTCATA GAM8349 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8349
AAGATAAAGA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8349
GTTCCCATGA precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
TTTAC to the nucleotide sequence of GAM8349 precursor RNA is designated SEQ ID:6859, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6859 is located from position 136594068 to position 136594192 relative to chromosome X on the `+` strand.

GAM8349 precursor RNA folds onto itself, forming GAM8349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8349 precursor RNA, designated SEQ ID NO: 6859, and a schematic representation of a predicted secondary folding of GAM8349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8349 folded precursor RNA yielding a GAM8349 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8349 RNA, hereby incorporated herein. Expression of GAM8349 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8349 target RNA, herein designated GAM TARGET RNA. GAM8349 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8349 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8349 RNA, herein designated GAM RNA, to target binding sites on GAM8349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8349 target RNA into GAM8349 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8349 target genes. The mRNA of each one of this plurality of GAM8349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8349 RNA, herein designated GAM RNA, and which when bound by GAM8349 RNA causes inhibition of translation of the GAM8349 target mRNA into a corresponding GAM8349 target protein.

The mechanism of the translational inhibition exerted by GAM8349 RNA, herein designated GAM RNA, on one or more GAM8349 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8349 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8349 RNA, herein designated GAM RNA, of GAM8349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8349 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8349 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8349 RNA correlate with, and may be deduced from, the identity of the GAM8349 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8362 6532 GCTCACACAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAAGTCTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAAAGCTTA Messenger 8362 (GAM8362) oligonucleotides modulates expression of respective target genes

GGAATGGAAG whose function and utility is known in the art.

TAGGTTGTCC GAM8362 is a novel bioinformatically detectable regulatory, non protein coding,

CCTCCTAGTC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8362 was detected is

ATGGGATCTC described with additional reference to Figs. 9-15.

TCCAACTCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGACAATCT encoded by the human genome.

TGCTTTACGT GAM8362 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8362

GCTGATGAAC precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8362

ATGCTCTGTG precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar

AGC to the nucleotide sequence of GAM8362 precursor RNA is designated SEQ ID:6532, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6532 is located from position 43562099 to position 43562221 relative to chromosome 15 on the `+` strand.

GAM8362 precursor RNA folds onto itself, forming GAM8362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8362 precursor RNA, designated SEQ ID NO: 6532, and a schematic representation of a predicted secondary folding of GAM8362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8362 folded precursor RNA yielding a GAM8362 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8362 RNA, hereby incorporated herein.

GAM8362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8362 target RNA, herein designated GAM TARGET RNA. GAM8362 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8362 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8362 RNA, herein designated GAM RNA, to target binding sites on GAM8362 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8362 target RNA into GAM8362 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8362 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM8362 target genes. The mRNA of each one of this plurality of GAM8362 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8362 RNA, herein designated GAM RNA, and which when bound by GAM8362 RNA causes inhibition of translation of the GAM8362 target mRNA into a corresponding GAM8362 target protein.

The mechanism of the translational inhibition exerted by GAM8362 RNA, herein designated GAM RNA, on one or more GAM8362 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8362 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8362 RNA, herein designated GAM RNA, of GAM8362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8362 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8362 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8362 RNA correlate with, and may be deduced from, the identity of the GAM8362 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8380 7233 TGGGCAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAGAAAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAGACTGTGG Messenger 8380 (GAM8380) oligonucleotides modulates expression of respective target genes
GAGGTGACTG whose function and utility is known in the art.

TTACAGATCG GAM8380 is a novel bioinformatically detectable regulatory, non protein coding,
GAAAACTCTG micro RNA (miRNA)-like oligonucleotide. The method by which GAM8380 was detected is

ATTGAACCAT described with additional reference to Figs. 9-15.

TCACTTTATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCCAGTAAA encoded by the human genome.

CTTTCTCAAC GAM8380 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8380

CCCA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8380 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8380 precursor RNA is designated SEQ ID:7233, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7233 is located from position 23784450 to position 23784553 relative to chromosome 3 on the `-` strand.

GAM8380 precursor RNA folds onto itself, forming GAM8380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8380 precursor RNA, designated SEQ ID NO: 7233, and a schematic representation of a predicted secondary folding of GAM8380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8380 folded precursor RNA yielding a GAM8380 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM8380 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8380 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM8380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8380 target RNA, herein designated GAM TARGET RNA. GAM8380 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8380 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8380 RNA, herein designated GAM RNA, to target binding sites on GAM8380 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8380 target RNA into GAM8380 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8380 target genes. The mRNA of each one of this plurality of GAM8380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8380 RNA, herein designated GAM RNA, and which when bound by GAM8380 RNA causes inhibition of translation of the GAM8380 target mRNA into a corresponding GAM8380 target protein.

The mechanism of the translational inhibition exerted by GAM8380 RNA, herein designated GAM RNA, on one or more GAM8380 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8380 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8380 RNA, herein designated GAM RNA, of GAM8380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8380 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8380 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8380 RNA correlate with, and may be deduced from, the identity of the GAM8380 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8386 6770 GGCTTGGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

GACCCCAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAGCCCATC Messenger 8386 (GAM8386) oligonucleotides modulates expression of respective target genes

ACCTTCTTTT whose function and utility is known in the art.

TGGGGTTTGG GAM8386 is a novel bioinformatically detectable regulatory, non protein coding,

GGCTTGGCC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8386 was detected is

described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM8386 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8386 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8386 precursor RNA is designated SEQ ID:6770, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6770 is located from position 18386080 to position 18386138 relative to chromosome 19 on the `+` strand.

GAM8386 precursor RNA folds onto itself, forming GAM8386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8386 precursor RNA, designated SEQ ID NO: 6770, and a schematic representation of a predicted secondary folding of GAM8386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8386 folded precursor RNA yielding a GAM8386 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8386 RNA, hereby incorporated herein.

GAM8386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8386 target RNA, herein designated GAM TARGET RNA. GAM8386 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8386 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8386 RNA, herein designated GAM RNA, to target binding sites on GAM8386 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8386 target RNA into GAM8386 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8386 target genes. The mRNA of each one of this plurality of GAM8386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8386 RNA, herein designated GAM RNA, and which when bound by GAM8386 RNA causes inhibition of translation of the GAM8386 target mRNA into a corresponding GAM8386 target protein.

The mechanism of the translational inhibition exerted by GAM8386 RNA, herein designated GAM RNA, on one or more GAM8386 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8386 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8386 RNA, herein designated GAM RNA, of GAM8386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8386 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8386 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8386 RNA correlate with, and may be deduced from, the identity of the GAM8386 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8396 7018 TCCACAGTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GATCTCTTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGTTCCCTC Messenger 8396 (GAM8396) oligonucleotides modulates expression of respective target genes
CACACTCTTC whose function and utility is known in the art.

TTTTGCTCCT GAM8396 is a novel bioinformatically detectable regulatory, non protein coding, CTTCCTGTAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8396 was detected is

TTCAGAGTGG described with additional reference to Figs. 9-15.

TTAAGATCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGAAGTCAGA encoded by the human genome.

CAAGCTATGG GAM8396 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8396

G precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8396

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8396 precursor RNA is designated SEQ ID:7018, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7018 is located from position 113370917 to position 113371017 relative to chromosome 9 on the `-` strand.

GAM8396 precursor RNA folds onto itself, forming GAM8396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8396 precursor RNA, designated SEQ ID NO: 7018, and a schematic representation of a predicted secondary folding of GAM8396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8396 folded precursor RNA yielding a GAM8396 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8396 RNA, hereby incorporated herein. Expression of GAM8396 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8396 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8396 target RNA, herein designated GAM TARGET RNA. GAM8396 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8396 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8396 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8396 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8396 RNA, herein designated GAM RNA, to target binding sites on GAM8396 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8396 target RNA into GAM8396 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8396 target genes. The mRNA of each one of this plurality of GAM8396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8396 RNA, herein designated GAM RNA, and which when bound by GAM8396 RNA causes inhibition of translation of the GAM8396 target mRNA into a corresponding GAM8396 target protein.

The mechanism of the translational inhibition exerted by GAM8396 RNA, herein designated GAM RNA, on one or more GAM8396 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8396 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8396 RNA, herein designated GAM RNA, of GAM8396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8396 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8396 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8396 RNA correlate with, and may be deduced from, the identity of the GAM8396 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8439 7299 TTCCATGGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGGGCCATG detected oligonucleotides of the present invention, referred to here as Genomic Address
ACAGGGAGAT Messenger 8439 (GAM8439) oligonucleotides modulates expression of respective target genes
AGGCCACACC whose function and utility is known in the art.

TTTCCCAGGT GAM8439 is a novel bioinformatically detectable regulatory, non protein coding,
GGAACCTGCA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8439 was detected is

GATGGAG described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM8439 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8439 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8439 precursor RNA is designated SEQ ID:7299, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7299 is located from position 77528891 to position 77528957 relative to chromosome X on the `+` strand.

GAM8439 precursor RNA folds onto itself, forming GAM8439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8439 precursor RNA, designated SEQ ID NO: 7299, and a schematic representation of a predicted secondary folding of GAM8439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8439 folded precursor RNA yielding a GAM8439 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8439 RNA, hereby incorporated herein.

GAM8439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8439 target RNA, herein designated GAM TARGET RNA. GAM8439 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated

region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8439 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8439 RNA, herein designated GAM RNA, to target binding sites on GAM8439 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8439 target RNA into GAM8439 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8439 target genes. The mRNA of each one of this plurality of GAM8439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8439 RNA, herein designated GAM RNA, and which when bound by GAM8439 RNA causes inhibition of translation of the GAM8439 target mRNA into a corresponding GAM8439 target protein.

The mechanism of the translational inhibition exerted by GAM8439 RNA, herein designated GAM RNA, on one or more GAM8439 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8439 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8439 RNA, herein designated GAM RNA, of GAM8439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8439 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8439 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8439 RNA correlate with, and may be deduced from, the identity of the GAM8439 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8447 7252 TGGTGGCATA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCGTGTAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCAGCTACT Messenger 8447 (GAM8447) oligonucleotides modulates expression of respective target genes
TGGGAGGCTG whose function and utility is known in the art.

AGGCAGGAGA GAM8447 is a novel bioinformatically detectable regulatory, non protein coding,
ATTGCTTGAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8447 was detected is

CCCAGGAGGT described with additional reference to Figs. 9-15.

GGAGGTTACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGAGCAGAG encoded by the human genome.

ATTGCACCA GAM8447 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8447
precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8447
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8447 precursor RNA is designated SEQ ID:7252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7252 is located from position 26678132 to position 26678230 relative to chromosome 15 on the `+` strand.

GAM8447 precursor RNA folds onto itself, forming GAM8447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8447 precursor RNA, designated SEQ ID NO: 7252, and a schematic representation of a predicted secondary folding of GAM8447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8447 folded precursor RNA yielding a GAM8447 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM8447 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8447 RNA and an

alternative nucleotide sequence thereof, hereby incorporated herein.

GAM8447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8447 target RNA, herein designated GAM TARGET RNA. GAM8447 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8447 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8447 RNA, herein designated GAM RNA, to target binding sites on GAM8447 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8447 target RNA into GAM8447 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8447 target genes. The mRNA of each one of this plurality of GAM8447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8447 RNA, herein designated GAM RNA, and which when bound by GAM8447 RNA causes inhibition of translation of the GAM8447 target mRNA into a corresponding GAM8447 target protein.

The mechanism of the translational inhibition exerted by GAM8447 RNA, herein designated GAM RNA, on one or more GAM8447 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8447 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8447 RNA, herein designated GAM RNA, of GAM8447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8447 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8447 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8447 RNA correlate with, and may be deduced from, the identity of the GAM8447 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8452 6073 CCCAGCCCAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTGAATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGATTAAAGG Messenger 8452 (GAM8452) oligonucleotides modulates expression of respective target genes

AGGCTGAATT whose function and utility is known in the art.

GCAGAGCCTC GAM8452 is a novel bioinformatically detectable regulatory, non protein coding,

CTTTCATCAA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8452 was detected is

ATTCGAGTTT described with additional reference to Figs. 9-15.

TGAATTGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGG encoded by the human genome.

GAM8452 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8452

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8452

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8452 precursor RNA is designated SEQ ID:6073, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6073 is located from position 10844836 to position 10844919 relative to chromosome 1 on the `+` strand.

GAM8452 precursor RNA folds onto itself, forming GAM8452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8452 precursor RNA, designated SEQ ID NO: 6073, and a schematic representation of a predicted secondary folding of GAM8452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8452 folded precursor RNA

yielding a GAM8452 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8452 RNA, hereby incorporated herein.

GAM8452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8452 target RNA, herein designated GAM TARGET RNA. GAM8452 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8452 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8452 RNA, herein designated GAM RNA, to target binding sites on GAM8452 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8452 target RNA into GAM8452 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8452 target genes. The mRNA of each one of this plurality of GAM8452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8452 RNA, herein designated GAM RNA, and which when bound by GAM8452 RNA causes inhibition of translation of the GAM8452 target mRNA into a corresponding GAM8452 target protein.

The mechanism of the translational inhibition exerted by GAM8452 RNA, herein designated GAM RNA, on one or more GAM8452 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8452 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8452 RNA, herein designated GAM RNA, of GAM8452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8452 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8452 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8452 RNA correlate with, and may be deduced from, the identity of the GAM8452 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8473 6312 GACCAGCCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGGTTTAC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGGGACGCA Messenger 8473 (GAM8473) oligonucleotides modulates expression of respective target genes

GGAACTGCCG whose function and utility is known in the art.

TTTTAAAGCT GAM8473 is a novel bioinformatically detectable regulatory, non protein coding,

GGGCTGAGTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8473 was detected is

GGTC described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8473 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8473

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8473

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8473 precursor RNA is designated SEQ ID:6312, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6312 is located from position 3585727 to position 3585790 relative to chromosome 16 on the `+` strand.

GAM8473 precursor RNA folds onto itself, forming GAM8473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8473 precursor RNA, designated SEQ ID NO: 6312, and a

schematic representation of a predicted secondary folding of GAM8473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8473 folded precursor RNA yielding a GAM8473 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8473 RNA, hereby incorporated herein.

GAM8473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8473 target RNA, herein designated GAM TARGET RNA. GAM8473 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8473 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8473 RNA, herein designated GAM RNA, to target binding sites on GAM8473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8473 target RNA into GAM8473 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8473 target genes. The mRNA of each one of this plurality of GAM8473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8473 RNA, herein designated GAM RNA, and which when bound by GAM8473 RNA causes inhibition of translation of the GAM8473 target mRNA into a corresponding GAM8473 target protein.

The mechanism of the translational inhibition exerted by GAM8473 RNA, herein designated GAM RNA, on one or more GAM8473 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8473 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8473 RNA, herein designated GAM RNA, of GAM8473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8473 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8473 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8473 RNA correlate with, and may be deduced from, the identity of the GAM8473 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8489 6553 GCTGTTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTATGGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTCTGCCCT Messenger 8489 (GAM8489) oligonucleotides modulates expression of respective target genes
TGTCAGAGGA whose function and utility is known in the art.

AGGCTTCCTC GAM8489 is a novel bioinformatically detectable regulatory, non protein coding,
ATCACAAGGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8489 was detected is

AGGGCAGGTG described with additional reference to Figs. 9-15.

TCTGTGCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGC encoded by the human genome.

GAM8489 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8489

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8489

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8489 precursor RNA is designated SEQ ID:6553, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6553 is located from position 49193542 to position 49193626 relative to chromosome 15 on the `+` strand.

GAM8489 precursor RNA folds onto itself, forming GAM8489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8489 precursor RNA, designated SEQ ID NO: 6553, and a schematic representation of a predicted secondary folding of GAM8489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8489 folded precursor RNA yielding a GAM8489 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM8489 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8489 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM8489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8489 target RNA, herein designated GAM TARGET RNA. GAM8489 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8489 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8489 RNA, herein designated GAM RNA, to target binding sites on GAM8489 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8489 target RNA into GAM8489 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8489 target genes. The mRNA of each one of this plurality of GAM8489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8489 RNA, herein designated GAM RNA, and which when bound by GAM8489 RNA causes inhibition of translation of the GAM8489 target mRNA into a corresponding GAM8489 target protein.

The mechanism of the translational inhibition exerted by GAM8489 RNA, herein designated GAM RNA, on one or more GAM8489 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8489 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8489 RNA, herein designated GAM RNA, of GAM8489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8489 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8489 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8489 RNA correlate with, and may be deduced from, the identity of the GAM8489 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8506 7337 TTGGTTAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGGAACCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTAAATGAC Messenger 8506 (GAM8506) oligonucleotides modulates expression of respective target genes

GCACTATGTG whose function and utility is known in the art.

ATTCCTGTGT GAM8506 is a novel bioinformatically detectable regulatory, non protein coding,

CATATAGAAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8506 was detected is

GTTCTATGAT described with additional reference to Figs. 9-15.

TCTTAGCCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8506 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8506

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8506

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8506 precursor RNA is designated SEQ ID:7337, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ

ID:7337 is located from position 80296015 to position 80296094 relative to chromosome 14 on the `+` strand.

GAM8506 precursor RNA folds onto itself, forming GAM8506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8506 precursor RNA, designated SEQ ID NO: 7337, and a schematic representation of a predicted secondary folding of GAM8506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8506 folded precursor RNA yielding a GAM8506 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8506 RNA, hereby incorporated herein.

GAM8506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8506 target RNA, herein designated GAM TARGET RNA. GAM8506 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8506 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8506 RNA, herein designated GAM RNA, to target binding sites on GAM8506 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8506 target RNA into GAM8506 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8506 target genes. The mRNA of each one of this

plurality of GAM8506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8506 RNA, herein designated GAM RNA, and which when bound by GAM8506 RNA causes inhibition of translation of the GAM8506 target mRNA into a corresponding GAM8506 target protein.

The mechanism of the translational inhibition exerted by GAM8506 RNA, herein designated GAM RNA, on one or more GAM8506 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8506 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8506 RNA, herein designated GAM RNA, of GAM8506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8506 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8506 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8506 RNA correlate with, and may be deduced from, the identity of the GAM8506 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8531 7188 TGATAGCAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGCTTCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCCTCAGGA Messenger 8531 (GAM8531) oligonucleotides modulates expression of respective target genes
CAGGTTTGTG whose function and utility is known in the art.

GCAAGGAAGA GAM8531 is a novel bioinformatically detectable regulatory, non protein coding,
AAGCAGAAGT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8531 was detected is

TGCTTTCA described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM8531 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8531

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM8531

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8531 precursor RNA is designated SEQ ID:7188, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7188 is located from position 80266794 to position 80266861 relative to chromosome 12 on the `+` strand.

GAM8531 precursor RNA folds onto itself, forming GAM8531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8531 precursor RNA, designated SEQ ID NO: 7188, and a schematic representation of a predicted secondary folding of GAM8531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8531 folded precursor RNA yielding a GAM8531 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8531 RNA, hereby incorporated herein.

GAM8531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8531 target RNA, herein designated GAM TARGET RNA. GAM8531 target

RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8531 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8531 RNA, herein designated GAM RNA, to target binding sites on GAM8531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8531 target RNA

into GAM8531 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8531 target genes. The mRNA of each one of this plurality of GAM8531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8531 RNA, herein designated GAM RNA, and which when bound by GAM8531 RNA causes inhibition of translation of the GAM8531 target mRNA into a corresponding GAM8531 target protein.

The mechanism of the translational inhibition exerted by GAM8531 RNA, herein designated GAM RNA, on one or more GAM8531 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8531 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8531 RNA, herein designated GAM RNA, of GAM8531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8531 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8531 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8531 RNA correlate with, and may be deduced from, the identity of the GAM8531 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8539 6962 TACTTGGGAT Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGTTAGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAGCCTGCA Messenger 8539 (GAM8539) oligonucleotides modulates expression of respective target genes
AAGCAAGTGG whose function and utility is known in the art.

CTTGGAGAGA GAM8539 is a novel bioinformatically detectable regulatory, non protein coding,
TAGTGATTTA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8539 was detected is

GCTCAAGAGG described with additional reference to Figs. 9-15.

GAGTGAGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGACTGTTGC encoded by the human genome.

CACATGTTAA GAM8539 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8539
ATGCTTTTCT precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8539
GGGCCTGATT precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar
ATTTAAGGGA to the nucleotide sequence of GAM8539 precursor RNA is designated SEQ ID:6962, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6962 is located from position 88200943 to position 88201072 relative to chromosome 11 on the `+` strand.

GAM8539 precursor RNA folds onto itself, forming GAM8539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8539 precursor RNA, designated SEQ ID NO: 6962, and a schematic representation of a predicted secondary folding of GAM8539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8539 folded precursor RNA yielding a GAM8539 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8539 RNA, hereby incorporated herein.

GAM8539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8539 target RNA, herein designated GAM TARGET RNA. GAM8539 target RNA
comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8539 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8539 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8539 RNA, herein designated GAM RNA, to target binding sites on GAM8539 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8539 target RNA into GAM8539 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8539 target genes. The mRNA of each one of this plurality of GAM8539 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8539 RNA, herein designated GAM RNA, and which when bound by GAM8539 RNA causes inhibition of translation of the GAM8539 target mRNA into a corresponding GAM8539 target protein.

The mechanism of the translational inhibition exerted by GAM8539 RNA, herein designated GAM RNA, on one or more GAM8539 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8539 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8539 RNA, herein designated GAM RNA, of GAM8539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8539 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8539 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8539 RNA correlate with, and may be deduced from, the identity of the GAM8539 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8542 6913 GTGGCGTTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCCTTAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTAGGTGA Messenger 8542 (GAM8542) oligonucleotides modulates expression of respective target genes

CCCAGGGTGG whose function and utility is known in the art.

CTTTGCTTTG GAM8542 is a novel bioinformatically detectable regulatory, non protein coding, GCAAGGGAGA micro RNA (miRNA)-like oligonucleotide. The method by which GAM8542 was detected is

AGTCAC described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8542 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8542

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8542

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8542 precursor RNA is designated SEQ ID:6913, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6913 is located from position 25177054 to position 25177119 relative to chromosome 16 on the `-` strand.

GAM8542 precursor RNA folds onto itself, forming GAM8542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8542 precursor RNA, designated SEQ ID NO: 6913, and a schematic representation of a predicted secondary folding of GAM8542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8542 folded precursor RNA yielding a GAM8542 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8542 RNA, hereby incorporated herein.

GAM8542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8542 target RNA, herein designated GAM TARGET RNA. GAM8542 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8542 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8542 RNA, herein designated GAM RNA, to target binding sites on GAM8542 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8542 target RNA into GAM8542 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8542 target genes. The mRNA of each one of this plurality of GAM8542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8542 RNA, herein designated GAM RNA, and which when bound by GAM8542 RNA causes inhibition of translation of the GAM8542 target mRNA into a corresponding GAM8542 target protein.

The mechanism of the translational inhibition exerted by GAM8542 RNA, herein designated GAM RNA, on one or more GAM8542 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8542 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8542 RNA, herein designated GAM RNA, of GAM8542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8542 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8542 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8542 RNA correlate with, and may be deduced from, the identity of the GAM8542 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8563 5691 ACATGTCATA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAGCCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address TACTGAACTC Messenger 8563 (GAM8563) oligonucleotides modulates expression of respective target genes AGCCACATAT whose function and utility is known in the art.

GGAAGTTTGA GAM8563 is a novel bioinformatically detectable regulatory, non protein coding, AGTGGGTCCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8563 was detected is

CGAAATGCAT described with additional reference to Figs. 9-15.

GT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8563 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8563

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8563

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8563 precursor RNA is designated SEQ ID:5691, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5691 is located from position 81283739 to position 81283810 relative to chromosome 8 on the `-` strand.

GAM8563 precursor RNA folds onto itself, forming GAM8563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8563 precursor RNA, designated SEQ ID NO: 5691, and a schematic representation of a predicted secondary folding of GAM8563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8563 folded precursor RNA yielding a GAM8563 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8563 RNA, hereby incorporated herein.

GAM8563 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8563 target RNA, herein designated GAM TARGET RNA. GAM8563 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8563 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8563 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8563 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8563 RNA, herein designated GAM RNA, to target binding sites on GAM8563 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8563 target RNA into GAM8563 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8563 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8563 target genes. The mRNA of each one of this plurality of GAM8563 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8563 RNA, herein designated GAM RNA, and which when bound by GAM8563 RNA causes inhibition of translation of the GAM8563 target mRNA into a corresponding GAM8563 target protein.

The mechanism of the translational inhibition exerted by GAM8563 RNA, herein designated GAM RNA, on one or more GAM8563 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8563 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8563 RNA, herein designated GAM RNA, of GAM8563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8563 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8563 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8563 RNA correlate with, and may be deduced from, the identity of the GAM8563 target gene inhibited

thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8598 7350 TTTTGGCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGCTCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TAACAGAGTG Messenger 8598 (GAM8598) oligonucleotides modulates expression of respective target genes
TTTGAGGGAC whose function and utility is known in the art.

AACTTTCACA GAM8598 is a novel bioinformatically detectable regulatory, non protein coding,
TTTGAGTTTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8598 was detected is

TCCAAAATTA described with additional reference to Figs. 9-15.

AAGGTTGTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGAGTCACA encoded by the human genome.

GTATCTATTG GAM8598 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8598
TCAAAA precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8598

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8598 precursor RNA is designated SEQ ID:7350, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7350 is located from position 31954902 to position 31955007 relative to chromosome 21 on the `+` strand.

GAM8598 precursor RNA folds onto itself, forming GAM8598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8598 precursor RNA, designated SEQ ID NO: 7350, and a schematic representation of a predicted secondary folding of GAM8598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8598 folded precursor RNA yielding a GAM8598 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8598 RNA, hereby incorporated herein.

GAM8598 target gene, herein designated GAM TARGET GENE, encodes a corresponding

messenger RNA, GAM8598 target RNA, herein designated GAM TARGET RNA. GAM8598 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8598 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8598 RNA, herein designated GAM RNA, to target binding sites on GAM8598 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8598 target RNA into GAM8598 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8598 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8598 target genes. The mRNA of each one of this plurality of GAM8598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8598 RNA, herein designated GAM RNA, and which when bound by GAM8598 RNA causes inhibition of translation of the GAM8598 target mRNA into a corresponding GAM8598 target protein.

The mechanism of the translational inhibition exerted by GAM8598 RNA, herein designated GAM RNA, on one or more GAM8598 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8598 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8598 RNA, herein designated GAM RNA, of GAM8598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8598 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target

binding sites to GAM8598 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8598 RNA correlate with, and may be deduced from, the identity of the GAM8598 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8601 6954 TAAATTGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGACAGAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGAGCTAG Messenger 8601 (GAM8601) oligonucleotides modulates expression of respective target genes

GAAGTGGTAT whose function and utility is known in the art.

ATTTAATTTC GAM8601 is a novel bioinformatically detectable regulatory, non protein coding,

TAGATTTCAG micro RNA (miRNA)-like oligonucleotide. The method by which GAM8601 was detected is

GGCTGGAGTG described with additional reference to Figs. 9-15.

GTGGAGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM8601 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8601

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8601

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8601 precursor RNA is designated SEQ ID:6954, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6954 is located from position 114561400 to position 114561477 relative to chromosome 9 on the `+` strand.

GAM8601 precursor RNA folds onto itself, forming GAM8601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8601 precursor RNA, designated SEQ ID NO: 6954, and a schematic representation of a predicted secondary folding of GAM8601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8601 folded precursor RNA yielding a GAM8601 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8601 RNA, hereby incorporated herein.

GAM8601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8601 target RNA, herein designated GAM TARGET RNA. GAM8601 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8601 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8601 RNA, herein designated GAM RNA, to target binding sites on GAM8601 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8601 target RNA into GAM8601 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8601 target genes. The mRNA of each one of this plurality of GAM8601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8601 RNA, herein designated GAM RNA, and which when bound by GAM8601 RNA causes inhibition of translation of the GAM8601 target mRNA into a corresponding GAM8601 target protein.

The mechanism of the translational inhibition exerted by GAM8601 RNA, herein designated GAM RNA, on one or more GAM8601 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8601 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8601 RNA, herein designated GAM RNA, of GAM8601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8601 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8601 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8601 RNA correlate with, and may be deduced from, the identity of the GAM8601 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8631 7028 TCCCGGAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TATGGTCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAGAAGATC Messenger 8631 (GAM8631) oligonucleotides modulates expression of respective target genes
CCTGCTCTGA whose function and utility is known in the art.

GTCACTGCCA GAM8631 is a novel bioinformatically detectable regulatory, non protein coding,
AGCTCTAGCT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8631 was detected is

ATGTGACTTT described with additional reference to Figs. 9-15.

GAACAGGGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCTGTCCC encoded by the human genome.

TATCTATAAA GAM8631 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8631
ATAAACGGGG precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8631
precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8631 precursor RNA is designated SEQ ID:7028, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7028 is located from position 30319063 to position 30319172 relative to chromosome 17 on the `+` strand.

GAM8631 precursor RNA folds onto itself, forming GAM8631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8631 precursor RNA, designated SEQ ID NO: 7028, and a schematic representation of a predicted secondary folding of GAM8631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8631 folded precursor RNA yielding a GAM8631 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8631 RNA, hereby incorporated herein.

GAM8631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8631 target RNA, herein designated GAM TARGET RNA. GAM8631 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8631 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8631 RNA, herein designated GAM RNA, to target binding sites on GAM8631 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8631 target RNA into GAM8631 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8631 target genes. The mRNA of each one of this plurality of GAM8631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8631 RNA, herein designated GAM RNA, and which when bound by GAM8631 RNA causes inhibition of translation of the GAM8631 target mRNA into a corresponding GAM8631 target protein.

The mechanism of the translational inhibition exerted by GAM8631 RNA, herein designated GAM RNA, on one or more GAM8631 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8631 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8631 RNA, herein designated GAM RNA, of GAM8631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8631 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8631 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8631 RNA correlate with, and may be deduced from, the identity of the GAM8631 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8636 6453 GAGGTAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTTAACTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGCACCCTG Messenger 8636 (GAM8636) oligonucleotides modulates expression of respective target genes

TGAGGTAGGT whose function and utility is known in the art.

GCTTTAACTG GAM8636 is a novel bioinformatically detectable regulatory, non protein coding,

TGTGCACATT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8636 was detected is

GTGAGGTAGG described with additional reference to Figs. 9-15.

TGCTGAAACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTTC encoded by the human genome.

GAM8636 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8636

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8636

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8636 precursor RNA is designated SEQ ID:6453, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6453 is located from position 93614982 to position 93615066 relative to chromosome 14 on the `+` strand.

GAM8636 precursor RNA folds onto itself, forming GAM8636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8636 precursor RNA, designated SEQ ID NO: 6453, and a schematic representation of a predicted secondary folding of GAM8636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8636 folded precursor RNA yielding a GAM8636 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8636 RNA, hereby incorporated herein.

GAM8636 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8636 target RNA, herein designated GAM TARGET RNA. GAM8636 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8636 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8636 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8636 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8636 RNA, herein designated GAM RNA, to target binding sites on GAM8636 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8636 target RNA into GAM8636 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8636 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8636 target genes. The mRNA of each one of this plurality of GAM8636 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8636 RNA, herein designated GAM RNA, and which when bound by GAM8636 RNA causes inhibition of translation of the GAM8636 target mRNA into a corresponding GAM8636 target protein.

The mechanism of the translational inhibition exerted by GAM8636 RNA, herein designated GAM RNA, on one or more GAM8636 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8636 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8636 RNA, herein designated GAM RNA, of GAM8636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8636 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8636 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8636 RNA correlate with, and may be deduced from, the identity of the GAM8636 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8647 6968 TAGCACCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCCCTGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTGGAACA Messenger 8647 (GAM8647) oligonucleotides modulates expression of respective target genes

GAAGCAGCTT whose function and utility is known in the art.

CCTTCAGAGA GAM8647 is a novel bioinformatically detectable regulatory, non protein coding,

AGACTGCAGC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8647 was detected is

TCCCAAGGAC described with additional reference to Figs. 9-15.

ACAAGCTGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGATGCTA encoded by the human genome.

GAM8647 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8647

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8647

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8647 precursor RNA is designated SEQ ID:6968, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6968 is located from position 30002913 to position 30003001 relative to chromosome 16 on the `-` strand.

GAM8647 precursor RNA folds onto itself, forming GAM8647 folded precursor RNA,

herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8647 precursor RNA, designated SEQ ID NO: 6968, and a schematic representation of a predicted secondary folding of GAM8647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8647 folded precursor RNA yielding a GAM8647 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8647 RNA, hereby incorporated herein.

GAM8647 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8647 target RNA, herein designated GAM TARGET RNA. GAM8647 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8647 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8647 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8647 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8647 RNA, herein designated GAM RNA, to target binding sites on GAM8647 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8647 target RNA into GAM8647 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8647 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8647 target genes. The mRNA of each one of this plurality of GAM8647 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8647 RNA, herein designated GAM RNA, and which when bound by GAM8647 RNA causes inhibition of translation of the GAM8647 target mRNA into a corresponding GAM8647 target protein.

The mechanism of the translational inhibition exerted by GAM8647 RNA, herein designated GAM RNA, on one or more GAM8647 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8647 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8647 RNA, herein designated GAM RNA, of GAM8647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8647 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8647 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8647 RNA correlate with, and may be deduced from, the identity of the GAM8647 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8665 7134 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGGAG Messenger 8665 (GAM8665) oligonucleotides modulates expression of respective target genes

GCAAGAGGTT whose function and utility is known in the art.

GCAGTGAGCT GAM8665 is a novel bioinformatically detectable regulatory, non protein coding,

GAGATCATAC micro RNA (miRNA)-like oligonucleotide. The method by which GAM8665 was detected is

CACTGCACTC described with additional reference to Figs. 9-15.

TGGCCTGGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACAGAGCGA encoded by the human genome.

GACTGTCTCA GAM8665 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8665

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8665

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8665 precursor RNA is designated SEQ ID:7134, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7134 is located from position 10301954 to position 10302053 relative to chromosome 11 on the `+` strand.

GAM8665 precursor RNA folds onto itself, forming GAM8665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8665 precursor RNA, designated SEQ ID NO: 7134, and a schematic representation of a predicted secondary folding of GAM8665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8665 folded precursor RNA yielding a GAM8665 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8665 RNA, hereby incorporated herein.

GAM8665 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8665 target RNA, herein designated GAM TARGET RNA. GAM8665 target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8665 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8665 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8665 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8665 RNA, herein designated GAM RNA, to target binding sites on GAM8665 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8665 target RNA into GAM8665 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8665 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM8665 target genes. The mRNA of each one of this plurality of GAM8665 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8665 RNA, herein designated GAM RNA, and which when bound by GAM8665 RNA causes inhibition of translation of the GAM8665 target mRNA into a corresponding GAM8665 target protein.

The mechanism of the translational inhibition exerted by GAM8665 RNA, herein designated GAM RNA, on one or more GAM8665 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8665 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8665 RNA, herein designated GAM RNA, of GAM8665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8665 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8665 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8665 RNA correlate with, and may be deduced from, the identity of the GAM8665 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8678 6897 GTGAGATGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCCAGGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCGTCTTGAG Messenger 8678 (GAM8678) oligonucleotides modulates expression of respective target genes
CACCCATTGC whose function and utility is known in the art.

TCAGAGTTTA GAM8678 is a novel bioinformatically detectable regulatory, non protein coding,
TATTGGACTT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8678 was detected is

GCTTTCTAGC described with additional reference to Figs. 9-15.

ACATACCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM8678 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8678

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8678 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8678 precursor RNA is designated SEQ ID:6897, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6897 is located from position 62449343 to position 62449421 relative to chromosome 19 on the `+` strand.

GAM8678 precursor RNA folds onto itself, forming GAM8678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8678 precursor RNA, designated SEQ ID NO: 6897, and a schematic representation of a predicted secondary folding of GAM8678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8678 folded precursor RNA yielding a GAM8678 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8678 RNA, hereby incorporated herein. Expression of GAM8678 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM8678 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8678 target RNA, herein designated GAM TARGET RNA. GAM8678 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8678 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8678 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8678 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8678 RNA, herein designated GAM RNA, to target

binding sites on GAM8678 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8678 target RNA into GAM8678 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8678 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8678 target genes. The mRNA of each one of this plurality of GAM8678 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8678 RNA, herein designated GAM RNA, and which when bound by GAM8678 RNA causes inhibition of translation of the GAM8678 target mRNA into a corresponding GAM8678 target protein.

The mechanism of the translational inhibition exerted by GAM8678 RNA, herein designated GAM RNA, on one or more GAM8678 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8678 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8678 RNA, herein designated GAM RNA, of GAM8678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8678 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8678 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8678 RNA correlate with, and may be deduced from, the identity of the GAM8678 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM8693 5795 AGGTGGCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGCAATAT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAATCCTTCT Messenger 8693 (GAM8693) oligonucleotides modulates expression of respective target genes

GCATCACACA whose function and utility is known in the art.

GTGGGAAAAG GAM8693 is a novel bioinformatically detectable regulatory, non protein coding,

TTTGTCTCAT micro RNA (miRNA)-like oligonucleotide. The method by which GAM8693 was detected is

TGCAGTTCT described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM8693 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM8693 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM8693 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM8693 precursor RNA is designated SEQ ID:5795, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5795 is located from position 105533389 to position 105533457 relative to chromosome 10 on the `-` strand.

GAM8693 precursor RNA folds onto itself, forming GAM8693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM8693 precursor RNA, designated SEQ ID NO: 5795, and a schematic representation of a predicted secondary folding of GAM8693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM8693 folded precursor RNA yielding a GAM8693 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM8693 RNA, hereby incorporated herein.

GAM8693 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM8693 target RNA, herein designated GAM TARGET RNA. GAM8693 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM8693 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM8693 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM8693 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM8693 RNA, herein designated GAM RNA, to target binding sites on GAM8693 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM8693 target RNA into GAM8693 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM8693 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM8693 target genes. The mRNA of each one of this plurality of GAM8693 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM8693 RNA, herein designated GAM RNA, and which when bound by GAM8693 RNA causes inhibition of translation of the GAM8693 target mRNA into a corresponding GAM8693 target protein.

The mechanism of the translational inhibition exerted by GAM8693 RNA, herein designated GAM RNA, on one or more GAM8693 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM8693 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM8693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM8693 RNA, herein designated GAM RNA, of GAM8693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in

Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM8693 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM8693 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM8693 RNA correlate with, and may be deduced from, the identity of the GAM8693 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336121 5682 ACACACGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GATGTGTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGAAGTCGT Messenger 336121 (GAM336121) oligonucleotides modulates expression of respective target

CTTGAGCACC genes whose function and utility is known in the art.

CATTGCTCAG GAM336121 is a novel bioinformatically detectable regulatory, non protein
AGTTTATATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336121 was detected
GGACTTGCTT is described with additional reference to Figs. 9-15.

TCTAGCACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACCACAATTG encoded by the human genome.

T GAM336121 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336121 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336121 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336121 precursor RNA is designated SEQ ID:5682, and is provided hereinbelow with reference to the sequence listing part.

GAM336121 precursor RNA folds onto itself, forming GAM336121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336121 precursor RNA, designated SEQ ID NO: 5682, and a schematic representation of a predicted secondary folding of GAM336121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336121 folded precursor RNA yielding a GAM336121 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336121 RNA, hereby incorporated herein. Expression of GAM336121 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336121 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336121 target RNA, herein designated GAM TARGET RNA.

GAM336121 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336121 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336121 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336121 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336121 RNA, herein designated GAM RNA, to target binding sites on GAM336121 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336121 target RNA into GAM336121 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336121 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336121 target genes. The mRNA of each one of this plurality of GAM336121 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336121 RNA, herein designated GAM RNA, and which when bound by GAM336121 RNA causes inhibition of translation of the GAM336121 target mRNA into a corresponding GAM336121 target protein.

The mechanism of the translational inhibition exerted by GAM336121 RNA, herein designated GAM RNA, on one or more GAM336121 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336121 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336121 RNA, herein designated GAM RNA, of GAM336121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336121 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336121 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336121 RNA correlate with, and may be deduced from, the identity of the GAM336121 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336122 5768 AGGCAGGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGCTTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCAGGAGGT Messenger 336122 (GAM336122) oligonucleotides modulates expression of respective target

GGAGGTTGCA genes whose function and utility is known in the art.

GGGAGTCGAG GAM336122 is a novel bioinformatically detectable regulatory, non protein

ATCGTGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336122 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGAGCAAAA encoded by the human genome.

CTCCATCT GAM336122 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336122 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336122 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336122 precursor RNA is designated SEQ ID:5768, and is provided hereinbelow with reference to the sequence listing part.

GAM336122 precursor RNA folds onto itself, forming GAM336122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336122 precursor RNA, designated SEQ ID NO: 5768, and a schematic representation of a predicted secondary folding of GAM336122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336122 folded precursor RNA yielding a GAM336122 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336122 RNA, hereby incorporated herein. Expression of GAM336122 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336122 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336122 target RNA, herein designated GAM TARGET RNA.

GAM336122 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336122 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336122 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336122 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336122 RNA, herein designated GAM RNA, to target binding sites on GAM336122 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336122 target RNA into GAM336122 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336122 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336122 target genes. The mRNA of each one of this plurality of GAM336122 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336122 RNA, herein designated GAM RNA, and which when bound by GAM336122 RNA causes inhibition of translation of the GAM336122 target mRNA into a corresponding GAM336122 target protein.

The mechanism of the translational inhibition exerted by GAM336122 RNA, herein designated GAM RNA, on one or more GAM336122 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336122 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336122 RNA, herein designated GAM RNA, of GAM336122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336122 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336122 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336122 RNA correlate with, and may be deduced from, the identity of the GAM336122 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336123 5769 AGGCAGGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTGCTTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTGGAAGGC Messenger 336123 (GAM336123) oligonucleotides modulates expression of respective target
GGAGGTTGCA genes whose function and utility is known in the art.

GTGAGCCAAG GAM336123 is a novel bioinformatically detectable regulatory, non protein
ATTGTGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336123 was detected
TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGCGAGAC encoded by the human genome.

TCTGTCT GAM336123 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336123 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336123 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336123 precursor RNA is designated SEQ ID:5769, and is provided hereinbelow with reference to the sequence listing part.

GAM336123 precursor RNA folds onto itself, forming GAM336123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336123 precursor RNA, designated SEQ ID NO: 5769, and a schematic representation of a predicted secondary folding of GAM336123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336123 folded precursor RNA yielding a GAM336123 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336123 RNA, hereby incorporated herein. Expression of GAM336123 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336123 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336123 target RNA, herein designated GAM TARGET RNA.

GAM336123 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336123 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336123 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336123 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336123 RNA, herein designated GAM RNA, to target binding sites on GAM336123 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336123 target RNA into GAM336123 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336123 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336123 target genes. The mRNA of each one of this plurality of GAM336123 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336123 RNA, herein designated GAM RNA, and which when bound by GAM336123 RNA causes inhibition of translation of the GAM336123 target mRNA into a corresponding GAM336123 target protein.

The mechanism of the translational inhibition exerted by GAM336123 RNA, herein designated GAM RNA, on one or more GAM336123 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336123 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336123 RNA, herein designated GAM RNA, of

GAM336123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336123 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336123 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336123 RNA correlate with, and may be deduced from, the identity of the GAM336123 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336124 5771 AGGCAGGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCGCTGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTGAGAGGC Messenger 336124 (GAM336124) oligonucleotides modulates expression of respective target

GGAGCTTGCA genes whose function and utility is known in the art.

GTGAGCCGAG GAM336124 is a novel bioinformatically detectable regulatory, non protein

ATCGCGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336124 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGCGAGAC encoded by the human genome.

TCCGTCT GAM336124 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336124 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336124 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336124 precursor RNA is designated SEQ ID:5771, and is provided hereinbelow with reference to the sequence listing part.

GAM336124 precursor RNA folds onto itself, forming GAM336124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336124 precursor RNA, designated SEQ ID NO: 5771, and a schematic representation of a predicted secondary folding of GAM336124 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336124 folded precursor RNA yielding a GAM336124 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336124 RNA, hereby incorporated herein. Expression of GAM336124 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336124 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336124 target RNA, herein designated GAM TARGET RNA.

GAM336124 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336124 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336124 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336124 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336124 RNA, herein designated GAM RNA, to target binding sites on GAM336124 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336124 target RNA into GAM336124 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336124 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336124 target genes. The mRNA of each one of this plurality of GAM336124 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336124 RNA, herein designated GAM RNA, and which when bound by GAM336124 RNA causes inhibition of translation of the GAM336124 target mRNA into a corresponding GAM336124 target protein.

The mechanism of the translational inhibition exerted by GAM336124 RNA, herein designated GAM RNA, on one or more GAM336124 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336124 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336124 RNA, herein designated GAM RNA, of GAM336124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336124 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336124 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336124 RNA correlate with, and may be deduced from, the identity of the GAM336124 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336125 5973 ATGGCGTGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCGGGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGCTTGCA Messenger 336125 (GAM336125) oligonucleotides modulates expression of respective target

GTGAGCCGAG genes whose function and utility is known in the art.

ATCGAGCCAC GAM336125 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336125 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

AGAGCGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336125 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336125 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336125 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336125 precursor RNA is designated SEQ ID:5973, and is provided hereinbelow with reference to the sequence listing part.

GAM336125 precursor RNA folds onto itself, forming GAM336125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336125 precursor RNA, designated SEQ ID NO: 5973, and a schematic representation of a predicted secondary folding of GAM336125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336125 folded precursor RNA yielding a GAM336125 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336125 RNA, hereby incorporated herein. Expression of GAM336125 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336125 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336125 target RNA, herein designated GAM TARGET RNA.

GAM336125 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336125 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336125 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336125 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336125 RNA, herein designated GAM RNA, to target binding sites on GAM336125 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336125 target RNA into GAM336125 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336125 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336125 target genes. The mRNA of each one of this plurality of GAM336125 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336125 RNA,

herein designated GAM RNA, and which when bound by GAM336125 RNA causes inhibition of translation of the GAM336125 target mRNA into a corresponding GAM336125 target protein.

The mechanism of the translational inhibition exerted by GAM336125 RNA, herein designated GAM RNA, on one or more GAM336125 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336125 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336125 RNA, herein designated GAM RNA, of GAM336125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336125 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336125 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336125 RNA correlate with, and may be deduced from, the identity of the GAM336125 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336126 6150 CTACTCTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGAATCGC Messenger 336126 (GAM336126) oligonucleotides modulates expression of respective target
TTTAACCCGG genes whose function and utility is known in the art.

GAGGCAGAGG GAM336126 is a novel bioinformatically detectable regulatory, non protein
TTGTGGTGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336126 was detected
CCGAGATCGC is described with additional reference to Figs. 9-15.

GCCATTGCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCAGCCTGG encoded by the human genome.

GCAACAAGAG GAM336126 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CGGAATTCTG GAM336126 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TCTCAAAAAA GAM336126 precursor RNA does not encode a protein. A nucleotide sequence identical or

AAAAAAGAGA highly similar to the nucleotide sequence of GAM336126 precursor RNA is designated SEQ

G ID:6150, and is provided hereinbelow with reference to the sequence listing part.

GAM336126 precursor RNA folds onto itself, forming GAM336126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336126 precursor RNA, designated SEQ ID NO: 6150, and a schematic representation of a predicted secondary folding of GAM336126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336126 folded precursor RNA yielding a GAM336126 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336126 RNA, hereby incorporated herein. Expression of GAM336126 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336126 target RNA, herein designated GAM TARGET RNA.

GAM336126 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336126 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336126 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336126 RNA, herein designated GAM RNA, to target binding sites on GAM336126 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336126 target RNA into GAM336126 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336126 target genes. The mRNA of each one of this plurality of GAM336126 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336126 RNA, herein designated GAM RNA, and which when bound by GAM336126 RNA causes inhibition of translation of the GAM336126 target mRNA into a corresponding GAM336126 target protein.

The mechanism of the translational inhibition exerted by GAM336126 RNA, herein designated GAM RNA, on one or more GAM336126 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336126 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336126 RNA, herein designated GAM RNA, of GAM336126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336126 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336126 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336126 RNA correlate with, and may be deduced from, the identity of the GAM336126 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336127 6160 CTCAGGAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAGGCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGATCACTTG Messenger 336127 (GAM336127) oligonucleotides modulates expression of respective target
AGCCTGGGAG genes whose function and utility is known in the art.

GTCTAGGCTG GAM336127 is a novel bioinformatically detectable regulatory, non protein
CAGTGAGCCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336127 was detected
GGACGATGCC is described with additional reference to Figs. 9-15.

ACTGCACTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCCTGGGCA encoded by the human genome.

ACAGAGTGAG GAM336127 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

ACCCTGTCCC GAM336127 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AGCACTCTGG GAM336127 precursor RNA does not encode a protein. A nucleotide sequence identical or

G highly similar to the nucleotide sequence of GAM336127 precursor RNA is designated SEQ ID:6160, and is provided hereinbelow with reference to the sequence listing part.

GAM336127 precursor RNA folds onto itself, forming GAM336127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336127 precursor RNA, designated SEQ ID NO: 6160, and a schematic representation of a predicted secondary folding of GAM336127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336127 folded precursor RNA yielding a GAM336127 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336127 RNA, hereby incorporated herein. Expression of GAM336127 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336127 target RNA, herein designated GAM TARGET RNA.

GAM336127 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336127 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336127 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336127 RNA, herein designated GAM RNA, to target binding sites on GAM336127 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336127 target RNA into GAM336127 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336127 target genes. The mRNA of each one of this plurality of GAM336127 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336127 RNA, herein designated GAM RNA, and which when bound by GAM336127 RNA causes inhibition of translation of the GAM336127 target mRNA into a corresponding GAM336127 target protein.

The mechanism of the translational inhibition exerted by GAM336127 RNA, herein designated GAM RNA, on one or more GAM336127 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336127 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336127 RNA, herein designated GAM RNA, of GAM336127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336127 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336127 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336127 RNA correlate with, and may be deduced from, the identity of the GAM336127 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336128 6202 CTGAGGCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCTCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGGGAG Messenger 336128 (GAM336128) oligonucleotides modulates expression of respective target
GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336128 is a novel bioinformatically detectable regulatory, non protein
AGATTGTCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336128 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTAAGA encoded by the human genome.

CTCTGTCTCA GAM336128 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
G GAM336128 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336128 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336128 precursor RNA is designated SEQ ID:6202, and is provided hereinbelow with reference to the sequence listing part.

GAM336128 precursor RNA folds onto itself, forming GAM336128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336128 precursor RNA, designated SEQ ID NO: 6202, and a schematic representation of a predicted secondary folding of GAM336128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336128 folded precursor RNA yielding a GAM336128 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336128 RNA, hereby incorporated herein. Expression of GAM336128 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336128 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336128 target RNA, herein designated GAM TARGET RNA.

GAM336128 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336128 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336128 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336128 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336128 RNA, herein designated GAM RNA, to target binding sites on GAM336128 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336128 target RNA into GAM336128 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336128 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336128 target genes. The mRNA of each one of this plurality of GAM336128 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336128 RNA, herein designated GAM RNA, and which when bound by GAM336128 RNA causes inhibition of translation of the GAM336128 target mRNA into a corresponding GAM336128 target protein.

The mechanism of the translational inhibition exerted by GAM336128 RNA, herein designated GAM RNA, on one or more GAM336128 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336128 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336128 RNA, herein designated GAM RNA, of GAM336128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336128 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336128 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336128 RNA correlate with, and may be deduced from, the identity of the GAM336128 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336129 6204 CTGAGGCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAATCACTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAACCTGGGA Messenger 336129 (GAM336129) oligonucleotides modulates expression of respective target
AATGGAGGTT genes whose function and utility is known in the art.

GCAGTGAGCC GAM336129 is a novel bioinformatically detectable regulatory, non protein
AAGATTGAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336129 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAGAGTG encoded by the human genome.

AAACTCTGTC GAM336129 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCAG GAM336129 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336129 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336129 precursor RNA is designated SEQ ID:6204, and is provided hereinbelow with reference to the sequence listing part.

GAM336129 precursor RNA folds onto itself, forming GAM336129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336129 precursor RNA, designated SEQ ID NO: 6204, and a schematic representation of a predicted secondary folding of GAM336129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336129 folded precursor RNA yielding a GAM336129 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336129 RNA, hereby incorporated herein.

Expression of GAM336129 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336129 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336129 target RNA, herein designated GAM TARGET RNA.

GAM336129 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336129 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336129 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336129 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336129 RNA, herein designated GAM RNA, to target binding sites on GAM336129 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336129 target RNA into GAM336129 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336129 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336129 target genes. The mRNA of each one of this plurality of GAM336129 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336129 RNA, herein designated GAM RNA, and which when bound by GAM336129 RNA causes inhibition of translation of the GAM336129 target mRNA into a corresponding GAM336129 target protein.

The mechanism of the translational inhibition exerted by GAM336129 RNA, herein designated GAM RNA, on one or more GAM336129 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336129 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336129 RNA, herein designated GAM RNA, of GAM336129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336129 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336129 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336129 RNA correlate with, and may be deduced from, the identity of the GAM336129 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336130 6222 CTGGAACCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAGGAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTGTGGTGA Messenger 336130 (GAM336130) oligonucleotides modulates expression of respective target
GCCAAGATCG genes whose function and utility is known in the art.

TGCCACTGCA GAM336130 is a novel bioinformatically detectable regulatory, non protein
CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336130 was detected
GGCAACAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336130 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336130 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336130 precursor RNA is designated SEQ ID:6222, and is provided hereinbelow with reference to the sequence listing part.

GAM336130 precursor RNA folds onto itself, forming GAM336130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336130 precursor RNA, designated SEQ ID NO: 6222, and a schematic representation of a predicted secondary folding of GAM336130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336130 folded precursor RNA yielding a GAM336130 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336130 RNA, hereby incorporated herein. Expression of GAM336130 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336130 target RNA, herein designated GAM TARGET RNA.

GAM336130 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336130 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336130 RNA, herein designated GAM RNA, to target binding sites on GAM336130 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336130 target RNA into GAM336130 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336130 target genes. The mRNA of each one of this plurality of GAM336130 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336130 RNA, herein designated GAM RNA, and which when bound by GAM336130 RNA causes inhibition of translation of the GAM336130 target mRNA into a corresponding GAM336130 target protein.

The mechanism of the translational inhibition exerted by GAM336130 RNA, herein designated GAM RNA, on one or more GAM336130 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336130 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336130 RNA, herein designated GAM RNA, of GAM336130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336130 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336130 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336130 RNA correlate with, and may be deduced from, the identity of the GAM336130 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336131 6258 CTTGAACCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGCAGTGA Messenger 336131 (GAM336131) oligonucleotides modulates expression of respective target

GCCGAGACCA genes whose function and utility is known in the art.

CGCCACTGCA GAM336131 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336131 was detected

GGCAACAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336131 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336131 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336131 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336131 precursor RNA is designated SEQ ID:6258, and is provided hereinbelow with reference to the sequence listing part.

GAM336131 precursor RNA folds onto itself, forming GAM336131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336131 precursor RNA, designated SEQ ID NO: 6258, and a schematic representation of a predicted secondary folding of GAM336131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336131 folded precursor RNA yielding a GAM336131 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336131 RNA, hereby incorporated herein. Expression of GAM336131 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336131 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336131 target RNA, herein designated GAM TARGET RNA.

GAM336131 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336131 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336131 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336131 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336131 RNA, herein designated GAM RNA, to target binding sites on GAM336131 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336131 target RNA into GAM336131 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336131 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336131 target genes. The mRNA of each one of this plurality of GAM336131 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336131 RNA, herein designated GAM RNA, and which when bound by GAM336131 RNA causes inhibition of translation of the GAM336131 target mRNA into a corresponding GAM336131 target protein.

The mechanism of the translational inhibition exerted by GAM336131 RNA, herein designated GAM RNA, on one or more GAM336131 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336131 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336131 RNA, herein designated GAM RNA, of GAM336131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336131 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336131 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336131 RNA correlate with, and may be deduced from, the identity of the GAM336131 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336132 6261 CTTGAACCCG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGCAGTGA Messenger 336132 (GAM336132) oligonucleotides modulates expression of respective target

ACCCAGACCC genes whose function and utility is known in the art.

TGCCACTGCA GAM336132 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336132 was detected

GGCAACAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336132 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336132 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336132 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336132 precursor RNA is designated SEQ ID:6261, and is provided hereinbelow with reference to the sequence listing part.

GAM336132 precursor RNA folds onto itself, forming GAM336132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336132 precursor RNA, designated SEQ ID NO: 6261, and a schematic representation of a predicted secondary folding of GAM336132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336132 folded precursor RNA yielding a GAM336132 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336132 RNA, hereby incorporated herein. Expression of GAM336132 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336132 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336132 target RNA, herein designated GAM TARGET RNA.

GAM336132 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336132 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336132 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336132 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336132 RNA, herein designated GAM RNA, to target binding sites on GAM336132 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336132 target RNA into GAM336132 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336132 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336132 target genes. The mRNA of each one of this plurality of GAM336132 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336132 RNA, herein designated GAM RNA, and which when bound by GAM336132 RNA causes inhibition of translation of the GAM336132 target mRNA into a corresponding GAM336132 target protein.

The mechanism of the translational inhibition exerted by GAM336132 RNA, herein designated GAM RNA, on one or more GAM336132 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336132 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336132 RNA, herein designated GAM RNA, of GAM336132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336132 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336132 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336132 RNA correlate with, and may be deduced from, the identity of the GAM336132 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336133 6263 CTTGAACCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTACAGTGA Messenger 336133 (GAM336133) oligonucleotides modulates expression of respective target

GCTGAGATCA genes whose function and utility is known in the art.

TGCCACTGCA GAM336133 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336133 was detected

GGCAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336133 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336133 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336133 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336133 precursor RNA is designated SEQ ID:6263, and is provided hereinbelow with reference to the sequence listing part.

GAM336133 precursor RNA folds onto itself, forming GAM336133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336133 precursor RNA, designated SEQ ID NO: 6263, and a schematic representation of a predicted secondary folding of GAM336133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336133 folded precursor RNA yielding a GAM336133 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336133 RNA, hereby incorporated herein. Expression of GAM336133 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336133 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336133 target RNA, herein designated GAM TARGET RNA.

GAM336133 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336133 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336133 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336133 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336133 RNA, herein designated GAM RNA, to target binding sites on GAM336133 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336133 target RNA into GAM336133 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336133 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336133 target genes. The mRNA of each one of this plurality of GAM336133 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336133 RNA, herein designated GAM RNA, and which when bound by GAM336133 RNA causes inhibition of translation of the GAM336133 target mRNA into a corresponding GAM336133 target protein.

The mechanism of the translational inhibition exerted by GAM336133 RNA, herein designated GAM RNA, on one or more GAM336133 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336133 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336133 RNA, herein designated GAM RNA, of GAM336133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336133 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336133 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336133 RNA correlate with, and may be deduced from, the identity of the GAM336133 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336134 6304 GAATCGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AACCTGGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGAGGTTG Messenger 336134 (GAM336134) oligonucleotides modulates expression of respective target

CAGTGAGCCG genes whose function and utility is known in the art.

AGATGGCACC GAM336134 is a novel bioinformatically detectable regulatory, non protein

ACTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336134 was detected

AGCCTGGGCA is described with additional reference to Figs. 9-15.

ACAGAGCAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATTC encoded by the human genome.

GAM336134 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336134 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336134 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336134 precursor RNA is designated SEQ ID:6304, and is provided hereinbelow with reference to the sequence listing part.

GAM336134 precursor RNA folds onto itself, forming GAM336134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336134 precursor RNA, designated SEQ ID NO: 6304, and a schematic representation of a predicted secondary folding of GAM336134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336134 folded precursor RNA yielding a GAM336134 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336134 RNA, hereby incorporated herein. Expression of GAM336134 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336134 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336134 target RNA, herein designated GAM TARGET RNA.

GAM336134 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336134 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336134 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336134 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336134 RNA, herein designated GAM RNA, to target binding sites on GAM336134 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336134 target RNA into GAM336134 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336134 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336134 target genes. The mRNA of each one of this plurality of GAM336134 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336134 RNA, herein designated GAM RNA, and which when bound by GAM336134 RNA causes inhibition of translation of the GAM336134 target mRNA into a corresponding GAM336134 target protein.

The mechanism of the translational inhibition exerted by GAM336134 RNA, herein designated GAM RNA, on one or more GAM336134 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336134 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336134 RNA, herein designated GAM RNA, of GAM336134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336134 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336134 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336134 RNA correlate with, and may be deduced from, the identity of the GAM336134 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336135 6309 GACAGCTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTTCTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAACTGGGTG Messenger 336135 (GAM336135) oligonucleotides modulates expression of respective target
ATCTTGTGAA genes whose function and utility is known in the art.

ATCTGTGGAC GAM336135 is a novel bioinformatically detectable regulatory, non protein
CCTACATTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336135 was detected
CACTTAGTGT is described with additional reference to Figs. 9-15.

GTACCTAAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTAACGTCC encoded by the human genome.

CAAATAAAGT GAM336135 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CATTCAGTGC GAM336135 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TTTGCAGAAA GAM336135 precursor RNA does not encode a protein. A nucleotide sequence identical or

CAGGTCAAGT highly similar to the nucleotide sequence of GAM336135 precursor RNA is designated SEQ
C ID:6309, and is provided hereinbelow with reference to the sequence listing part.

GAM336135 precursor RNA folds onto itself, forming GAM336135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336135 precursor RNA, designated SEQ ID NO: 6309, and a schematic representation of a predicted secondary folding of GAM336135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336135 folded precursor RNA yielding a GAM336135 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336135 RNA, hereby incorporated herein. Expression of GAM336135 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336135 target RNA, herein designated GAM TARGET RNA.

GAM336135 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336135 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336135 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336135 RNA, herein designated GAM RNA, to target binding sites on GAM336135 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336135 target RNA into GAM336135 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336135 target genes. The mRNA of each one of this plurality of GAM336135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336135 RNA, herein designated GAM RNA, and which when bound by GAM336135 RNA causes inhibition of translation of the GAM336135 target mRNA into a corresponding GAM336135 target protein.

The mechanism of the translational inhibition exerted by GAM336135 RNA, herein designated GAM RNA, on one or more GAM336135 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336135 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336135 RNA, herein designated GAM RNA, of GAM336135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336135 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336135 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336135 RNA correlate with, and may be deduced from, the identity of the GAM336135 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336136 6321 GAGAATCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGAGGAGGT Messenger 336136 (GAM336136) oligonucleotides modulates expression of respective target
TGTGGTGAGC genes whose function and utility is known in the art.

CAAGATCGTG GAM336136 is a novel bioinformatically detectable regulatory, non protein
CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336136 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTC encoded by the human genome.

GAM336136 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336136 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336136 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336136 precursor RNA is designated SEQ ID:6321, and is provided hereinbelow with reference to the sequence listing part.

GAM336136 precursor RNA folds onto itself, forming GAM336136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336136 precursor RNA, designated SEQ ID NO: 6321, and a schematic representation of a predicted secondary folding of GAM336136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336136 folded precursor RNA yielding a GAM336136 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336136 RNA, hereby incorporated herein. Expression of GAM336136 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336136 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336136 target RNA, herein designated GAM TARGET RNA.

GAM336136 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336136 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336136 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336136 RNA, herein designated GAM RNA, to target binding sites on GAM336136 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336136 target RNA into GAM336136 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336136 target genes. The mRNA of each one of this plurality of GAM336136 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336136 RNA, herein designated GAM RNA, and which when bound by GAM336136 RNA causes inhibition of translation of the GAM336136 target mRNA into a corresponding GAM336136 target protein.

The mechanism of the translational inhibition exerted by GAM336136 RNA, herein designated GAM RNA, on one or more GAM336136 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336136 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336136 RNA, herein designated GAM RNA, of GAM336136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336136 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336136 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336136 RNA correlate with, and may be deduced from, the identity of the GAM336136 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336137 6322 GAGAATCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGAGGAGGT Messenger 336137 (GAM336137) oligonucleotides modulates expression of respective target
TGTGGTGAGC genes whose function and utility is known in the art.

CAAGATCGTG GAM336137 is a novel bioinformatically detectable regulatory, non protein
CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336137 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTCCGTC encoded by the human genome.

TC GAM336137 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336137 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336137 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336137 precursor RNA is designated SEQ ID:6322, and is provided hereinbelow with reference to the sequence listing part.

GAM336137 precursor RNA folds onto itself, forming GAM336137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336137 precursor RNA, designated SEQ ID NO: 6322, and a schematic representation of a predicted secondary folding of GAM336137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336137 folded precursor RNA yielding a GAM336137 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336137 RNA, hereby incorporated herein. Expression of GAM336137 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336137 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336137 target RNA, herein designated GAM TARGET RNA.

GAM336137 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336137 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336137 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336137 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336137 RNA, herein designated GAM RNA, to target binding sites on GAM336137 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336137 target RNA into GAM336137 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336137 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336137 target genes. The mRNA of each one of this plurality of GAM336137 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336137 RNA, herein designated GAM RNA, and which when bound by GAM336137 RNA causes inhibition of translation of the GAM336137 target mRNA into a corresponding GAM336137 target protein.

The mechanism of the translational inhibition exerted by GAM336137 RNA, herein designated GAM RNA, on one or more GAM336137 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336137 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336137 RNA, herein designated GAM RNA, of GAM336137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336137 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336137 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336137 RNA correlate with, and may be deduced from, the identity of the GAM336137 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336138 6325 GAGAATCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCAGAGAT Messenger 336138 (GAM336138) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CGAGATCATG GAM336138 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336138 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAACTC encoded by the human genome.

GAM336138 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336138 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336138 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336138 precursor RNA is designated SEQ ID:6325, and is provided hereinbelow with reference to the sequence listing part.

GAM336138 precursor RNA folds onto itself, forming GAM336138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336138 precursor RNA, designated SEQ ID NO: 6325, and a schematic representation of a predicted secondary folding of GAM336138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336138 folded precursor RNA yielding a GAM336138 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336138 RNA, hereby incorporated herein. Expression of GAM336138 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336138 target RNA, herein designated GAM TARGET RNA.

GAM336138 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336138 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336138 RNA, herein designated GAM RNA, to target binding sites on GAM336138 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336138 target RNA into GAM336138 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336138 target genes. The mRNA of each one of this plurality of GAM336138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336138 RNA, herein designated GAM RNA, and which when bound by GAM336138 RNA causes inhibition of translation of the GAM336138 target mRNA into a corresponding GAM336138 target protein.

The mechanism of the translational inhibition exerted by GAM336138 RNA, herein designated GAM RNA, on one or more GAM336138 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336138 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336138 RNA, herein designated GAM RNA, of GAM336138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336138 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336138 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336138 RNA correlate with, and may be deduced from, the identity of the GAM336138 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336139 6331 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGGAGGT Messenger 336139 (GAM336139) oligonucleotides modulates expression of respective target

TGTAGTGAGC genes whose function and utility is known in the art.

CGAGATCGCG GAM336139 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336139 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTC encoded by the human genome.

GAM336139 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336139 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336139 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336139 precursor RNA is designated SEQ ID:6331, and is provided hereinbelow with reference to the sequence listing part.

GAM336139 precursor RNA folds onto itself, forming GAM336139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336139 precursor RNA, designated SEQ ID NO: 6331, and a schematic representation of a predicted secondary folding of GAM336139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336139 folded precursor RNA yielding a GAM336139 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336139 RNA, hereby incorporated herein. Expression of GAM336139 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336139 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336139 target RNA, herein designated GAM TARGET RNA.

GAM336139 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336139 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336139 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336139 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336139 RNA, herein designated GAM RNA, to target binding sites on GAM336139 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336139 target RNA into GAM336139 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336139 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336139 target genes. The mRNA of each one of this plurality of GAM336139 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336139 RNA, herein designated GAM RNA, and which when bound by GAM336139 RNA causes inhibition of translation of the GAM336139 target mRNA into a corresponding GAM336139 target protein.

The mechanism of the translational inhibition exerted by GAM336139 RNA, herein designated GAM RNA, on one or more GAM336139 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336139 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336139 RNA, herein designated GAM RNA, of GAM336139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336139 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336139 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336139 RNA correlate with, and may be deduced from, the identity of the GAM336139 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336140 6340 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCTAGAGG Messenger 336140 (GAM336140) oligonucleotides modulates expression of respective target
CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCAGA GAM336140 is a novel bioinformatically detectable regulatory, non protein
GAGAGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336140 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGTGAA encoded by the human genome.

ATTCCGTCTC GAM336140 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336140 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336140 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336140 precursor RNA is designated SEQ ID:6340, and is provided hereinbelow with reference to the sequence listing part.

GAM336140 precursor RNA folds onto itself, forming GAM336140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336140 precursor RNA, designated SEQ ID NO: 6340, and a schematic representation of a predicted secondary folding of GAM336140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336140 folded precursor RNA yielding a GAM336140 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336140 RNA, hereby incorporated herein. Expression of GAM336140 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336140 target RNA, herein designated GAM TARGET RNA.

GAM336140 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336140 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336140 RNA, herein designated GAM RNA, to target binding sites on GAM336140 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336140 target RNA into GAM336140 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336140 target genes. The mRNA of each one of this plurality of GAM336140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336140 RNA, herein designated GAM RNA, and which when bound by GAM336140 RNA causes inhibition of translation of the GAM336140 target mRNA into a corresponding GAM336140 target protein.

The mechanism of the translational inhibition exerted by GAM336140 RNA, herein designated GAM RNA, on one or more GAM336140 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336140 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336140 RNA, herein designated GAM RNA, of GAM336140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336140 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336140 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336140 RNA correlate with, and may be deduced from, the identity of the GAM336140 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336141 6345 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCATGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336141 (GAM336141) oligonucleotides modulates expression of respective target

CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336141 is a novel bioinformatically detectable regulatory, non protein
GCTCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336141 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAAGCGAGA encoded by the human genome.

CTCCGTCTC GAM336141 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336141 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336141 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336141 precursor RNA is designated SEQ ID:6345, and is provided hereinbelow with reference to the sequence listing part.

GAM336141 precursor RNA folds onto itself, forming GAM336141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336141 precursor RNA, designated SEQ ID NO: 6345, and a schematic representation of a predicted secondary folding of GAM336141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336141 folded precursor RNA yielding a GAM336141 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336141 RNA, hereby incorporated herein. Expression of GAM336141 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336141 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336141 target RNA, herein designated GAM TARGET RNA.

GAM336141 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336141 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336141 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336141 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336141 RNA, herein designated GAM RNA, to target binding sites on GAM336141 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336141 target RNA into GAM336141 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336141 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336141 target genes. The mRNA of each one of this plurality of GAM336141 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336141 RNA, herein designated GAM RNA, and which when bound by GAM336141 RNA causes inhibition of translation of the GAM336141 target mRNA into a corresponding GAM336141 target protein.

The mechanism of the translational inhibition exerted by GAM336141 RNA, herein designated GAM RNA, on one or more GAM336141 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336141 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336141 RNA, herein designated GAM RNA, of GAM336141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336141 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336141 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336141 RNA correlate with, and may be deduced from, the identity of the GAM336141 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336142 6346 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGCAGG Messenger 336142 (GAM336142) oligonucleotides modulates expression of respective target

CGGAGGTTAC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336142 is a novel bioinformatically detectable regulatory, non protein

GATGGTACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336142 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CATAGCAACA encoded by the human genome.

CTCTGTCTC GAM336142 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336142 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336142 precursor RNA is designated SEQ ID:6346, and is provided hereinbelow with reference to the sequence listing part.

GAM336142 precursor RNA folds onto itself, forming GAM336142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336142 precursor RNA, designated SEQ ID NO: 6346, and a schematic representation of a predicted secondary folding of GAM336142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336142 folded precursor RNA yielding a GAM336142 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336142 RNA, hereby incorporated herein. Expression of GAM336142 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336142 target RNA, herein designated GAM TARGET RNA.

GAM336142 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336142 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336142 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336142 RNA, herein designated GAM RNA, to target binding sites on GAM336142 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336142 target RNA into GAM336142 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336142 target genes. The mRNA of each one of this plurality of GAM336142 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336142 RNA, herein designated GAM RNA, and which when bound by GAM336142 RNA causes inhibition of translation of the GAM336142 target mRNA into a corresponding GAM336142 target protein.

The mechanism of the translational inhibition exerted by GAM336142 RNA, herein designated GAM RNA, on one or more GAM336142 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336142 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336142 RNA, herein designated GAM RNA, of GAM336142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336142 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336142 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336142 RNA correlate with, and may be deduced from, the identity of the GAM336142 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336143 6357 GAGATGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 336143 (GAM336143) oligonucleotides modulates expression of respective target
TGGAGGCTGT genes whose function and utility is known in the art.

GGTGAGCCAA GAM336143 is a novel bioinformatically detectable regulatory, non protein
CATCCTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336143 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCCAAA encoded by the human genome.

CTCTGACTC GAM336143 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336143 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336143 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336143 precursor RNA is designated SEQ ID:6357, and is provided hereinbelow with reference to the sequence listing part.

GAM336143 precursor RNA folds onto itself, forming GAM336143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336143 precursor RNA, designated SEQ ID NO: 6357, and a schematic representation of a predicted secondary folding of GAM336143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336143 folded precursor RNA yielding a GAM336143 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336143 RNA, hereby incorporated herein. Expression of GAM336143 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336143 target RNA, herein designated GAM TARGET RNA.

GAM336143 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336143 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336143 RNA, herein designated GAM RNA, to target binding sites on GAM336143 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336143 target RNA into GAM336143 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336143 target genes. The mRNA of each one of this plurality of GAM336143 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336143 RNA, herein designated GAM RNA, and which when bound by GAM336143 RNA causes inhibition of translation of the GAM336143 target mRNA into a corresponding GAM336143 target protein.

The mechanism of the translational inhibition exerted by GAM336143 RNA, herein designated GAM RNA, on one or more GAM336143 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336143 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336143 RNA, herein designated GAM RNA, of

GAM336143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336143 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336143 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336143 RNA correlate with, and may be deduced from, the identity of the GAM336143 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336144 6367 GAGGATCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGTGGGGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGGCTGCA Messenger 336144 (GAM336144) oligonucleotides modulates expression of respective target

GTGAGCCATG genes whose function and utility is known in the art.

ATCAAGCCAC GAM336144 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336144 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

ACTGAGACAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TC encoded by the human genome.

GAM336144 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336144 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336144 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336144 precursor RNA is designated SEQ ID:6367, and is provided hereinbelow with reference to the sequence listing part.

GAM336144 precursor RNA folds onto itself, forming GAM336144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336144 precursor RNA, designated SEQ ID NO: 6367, and a schematic representation of a predicted secondary folding of GAM336144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336144 folded precursor RNA yielding a GAM336144 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336144 RNA, hereby incorporated herein. Expression of GAM336144 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336144 target RNA, herein designated GAM TARGET RNA.

GAM336144 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336144 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336144 RNA, herein designated GAM RNA, to target binding sites on GAM336144 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336144 target RNA into GAM336144 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336144 target genes. The mRNA of each one of this plurality of GAM336144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336144 RNA, herein designated GAM RNA, and which when bound by GAM336144 RNA causes inhibition of translation of the GAM336144 target mRNA into a corresponding GAM336144 target protein.

The mechanism of the translational inhibition exerted by GAM336144 RNA, herein designated GAM RNA, on one or more GAM336144 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336144 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336144 RNA, herein designated GAM RNA, of GAM336144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336144 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336144 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336144 RNA correlate with, and may be deduced from, the identity of the GAM336144 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336145 6368 GAGGATCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGTGGGGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGGCTGCA Messenger 336145 (GAM336145) oligonucleotides modulates expression of respective target

GTGAGCCATG genes whose function and utility is known in the art.

ATCAAGCCAC GAM336145 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336145 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

ACTGAGACAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTCTC encoded by the human genome.

GAM336145 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336145 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336145 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336145 precursor RNA is designated SEQ ID:6368, and is provided hereinbelow with reference to the sequence listing part.

GAM336145 precursor RNA folds onto itself, forming GAM336145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336145 precursor RNA, designated SEQ ID NO: 6368, and a schematic representation of a predicted secondary folding of GAM336145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336145 folded precursor RNA yielding a GAM336145 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336145 RNA, hereby incorporated herein. Expression of GAM336145 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336145 target RNA, herein designated GAM TARGET RNA.

GAM336145 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336145 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336145 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336145 RNA, herein designated GAM RNA, to target binding sites on GAM336145 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336145 target RNA into GAM336145 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336145 target genes. The mRNA of each one of this plurality of GAM336145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336145 RNA, herein designated GAM RNA, and which when bound by GAM336145 RNA causes inhibition of

translation of the GAM336145 target mRNA into a corresponding GAM336145 target protein.

The mechanism of the translational inhibition exerted by GAM336145 RNA, herein designated GAM RNA, on one or more GAM336145 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336145 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336145 RNA, herein designated GAM RNA, of GAM336145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336145 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336145 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336145 RNA correlate with, and may be deduced from, the identity of the GAM336145 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336146 6373 GAGGCAGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCACTTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 336146 (GAM336146) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336146 is a novel bioinformatically detectable regulatory, non protein

CATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336146 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGGGACA encoded by the human genome.

CTCTGTCTC GAM336146 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336146 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336146 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336146 precursor RNA is designated SEQ ID:6373, and is provided hereinbelow with reference to the sequence listing part.

GAM336146 precursor RNA folds onto itself, forming GAM336146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336146 precursor RNA, designated SEQ ID NO: 6373, and a schematic representation of a predicted secondary folding of GAM336146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336146 folded precursor RNA yielding a GAM336146 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336146 RNA, hereby incorporated herein. Expression of GAM336146 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336146 target RNA, herein designated GAM TARGET RNA.

GAM336146 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336146 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336146 RNA, herein designated GAM RNA, to target binding sites on GAM336146 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336146 target RNA

into GAM336146 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336146 target genes. The mRNA of each one of this plurality of GAM336146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336146 RNA, herein designated GAM RNA, and which when bound by GAM336146 RNA causes inhibition of translation of the GAM336146 target mRNA into a corresponding GAM336146 target protein.

The mechanism of the translational inhibition exerted by GAM336146 RNA, herein designated GAM RNA, on one or more GAM336146 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336146 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336146 RNA, herein designated GAM RNA, of GAM336146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336146 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336146 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336146 RNA correlate with, and may be deduced from, the identity of the GAM336146 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336147 6374 GAGGCAGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGGCCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336147 (GAM336147) oligonucleotides modulates expression of respective target

CGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336147 is a novel bioinformatically detectable regulatory, non protein

GATCACGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336147 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAGA encoded by the human genome.

CTCTGTCTC GAM336147 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336147 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336147 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336147 precursor RNA is designated SEQ ID:6374, and is provided hereinbelow with reference to the sequence listing part.

GAM336147 precursor RNA folds onto itself, forming GAM336147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336147 precursor RNA, designated SEQ ID NO: 6374, and a schematic representation of a predicted secondary folding of GAM336147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336147 folded precursor RNA yielding a GAM336147 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336147 RNA, hereby incorporated herein. Expression of GAM336147 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336147 target RNA, herein designated GAM TARGET RNA.

GAM336147 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336147 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336147 RNA, herein designated GAM RNA, to target binding sites on GAM336147 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336147 target RNA into GAM336147 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336147 target genes. The mRNA of each one of this plurality of GAM336147 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336147 RNA, herein designated GAM RNA, and which when bound by GAM336147 RNA causes inhibition of translation of the GAM336147 target mRNA into a corresponding GAM336147 target protein.

The mechanism of the translational inhibition exerted by GAM336147 RNA, herein designated GAM RNA, on one or more GAM336147 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336147 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336147 RNA, herein designated GAM RNA, of GAM336147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336147 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336147 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336147 RNA correlate with, and may be deduced from, the identity of the GAM336147 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336148 6375 GAGGCAGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGCTCGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCGGGAGAC Messenger 336148 (GAM336148) oligonucleotides modulates expression of respective target

AGAGGTTGCA genes whose function and utility is known in the art.

GTGAGCCGAG GAM336148 is a novel bioinformatically detectable regulatory, non protein
ATTGTGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336148 was
detected
TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is
a humen gene
AGAGCGAGAC encoded by the human genome.

TGCGTC GAM336148 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336148 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA
genes

GAM336148 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336148 precursor RNA is designated SEQ ID:6375, and is provided hereinbelow with reference to the sequence listing part.

GAM336148 precursor RNA folds onto itself, forming GAM336148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336148 precursor RNA, designated SEQ ID NO: 6375, and a schematic representation of a predicted secondary folding of GAM336148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336148 folded precursor RNA yielding a GAM336148 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336148 RNA, hereby incorporated herein. Expression of GAM336148 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336148 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336148 target RNA, herein designated GAM TARGET RNA.

GAM336148 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336148 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336148 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336148 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336148 RNA, herein designated GAM RNA, to target binding sites on GAM336148 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336148 target RNA into GAM336148 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336148 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336148 target genes. The mRNA of each one of this plurality of GAM336148 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336148 RNA, herein designated GAM RNA, and which when bound by GAM336148 RNA causes inhibition of translation of the GAM336148 target mRNA into a corresponding GAM336148 target protein.

The mechanism of the translational inhibition exerted by GAM336148 RNA, herein designated GAM RNA, on one or more GAM336148 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336148 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336148 RNA, herein designated GAM RNA, of GAM336148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336148 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336148 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336148 RNA correlate with, and may be deduced from, the identity of the GAM336148 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336149 6381 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AACAGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGTGG Messenger 336149 (GAM336149) oligonucleotides modulates expression of respective target
CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336149 is a novel bioinformatically detectable regulatory, non protein
GATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336149 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCGAG encoded by the human genome.

ACTCCGTCTC GAM336149 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336149 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336149 precursor RNA is designated SEQ ID:6381, and is provided hereinbelow with reference to the sequence listing part.

GAM336149 precursor RNA folds onto itself, forming GAM336149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336149 precursor RNA, designated SEQ ID NO: 6381, and a schematic representation of a predicted secondary folding of GAM336149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336149 folded precursor RNA yielding a GAM336149 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336149 RNA, hereby incorporated herein. Expression of GAM336149 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336149 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336149 target RNA, herein designated GAM TARGET RNA.

GAM336149 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336149 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336149 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336149 RNA, herein designated GAM RNA, to target binding sites on GAM336149 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336149 target RNA into GAM336149 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336149 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336149 target genes. The mRNA of each one of this plurality of GAM336149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336149 RNA, herein designated GAM RNA, and which when bound by GAM336149 RNA causes inhibition of translation of the GAM336149 target mRNA into a corresponding GAM336149 target protein.

The mechanism of the translational inhibition exerted by GAM336149 RNA, herein designated GAM RNA, on one or more GAM336149 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336149 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336149 RNA, herein designated GAM RNA, of GAM336149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336149 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336149 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336149 RNA correlate with, and may be deduced from, the identity of the GAM336149 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336150 6386 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAAA Messenger 336150 (GAM336150) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336150 is a novel bioinformatically detectable regulatory, non protein
GATTGAGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336150 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGTGAA encoded by the human genome.

ACTCTGTCTC GAM336150 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336150 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336150 precursor RNA is designated SEQ ID:6386, and is provided hereinbelow with reference to the sequence listing part.

GAM336150 precursor RNA folds onto itself, forming GAM336150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336150 precursor RNA, designated SEQ ID NO: 6386, and a schematic representation of a predicted secondary folding of GAM336150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336150 folded precursor RNA yielding a GAM336150 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336150 RNA, hereby incorporated herein. Expression of GAM336150 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336150 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336150 target RNA, herein designated GAM TARGET RNA.

GAM336150 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336150 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336150 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336150 RNA, herein designated GAM RNA, to target binding sites on GAM336150 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336150 target RNA into GAM336150 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336150 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336150 target genes. The mRNA of each one of this plurality of GAM336150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336150 RNA, herein designated GAM RNA, and which when bound by GAM336150 RNA causes inhibition of translation of the GAM336150 target mRNA into a corresponding GAM336150 target protein.

The mechanism of the translational inhibition exerted by GAM336150 RNA, herein designated GAM RNA, on one or more GAM336150 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336150 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336150 RNA, herein designated GAM RNA, of GAM336150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336150 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336150 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336150 RNA correlate with, and may be deduced from, the identity of the GAM336150 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336151 6387 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAGA Messenger 336151 (GAM336151) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

GGTGAGCCGA GAM336151 is a novel bioinformatically detectable regulatory, non protein
GATCGCATCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336151 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCGAA encoded by the human genome.

ACTCTGTCTC GAM336151 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336151 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336151 precursor RNA is designated SEQ ID:6387, and is provided hereinbelow with reference to the sequence listing part.

GAM336151 precursor RNA folds onto itself, forming GAM336151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336151 precursor RNA, designated SEQ ID NO: 6387, and a schematic representation of a predicted secondary folding of GAM336151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336151 folded precursor RNA yielding a GAM336151 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336151 RNA, hereby incorporated herein. Expression of GAM336151 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336151 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336151 target RNA, herein designated GAM TARGET RNA.

GAM336151 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336151 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336151 RNA, herein designated GAM RNA, to target binding sites on GAM336151 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336151 target RNA into GAM336151 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336151 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336151 target genes. The mRNA of each one of this plurality of GAM336151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336151 RNA, herein designated GAM RNA, and which when bound by GAM336151 RNA causes inhibition of translation of the GAM336151 target mRNA into a corresponding GAM336151 target protein.

The mechanism of the translational inhibition exerted by GAM336151 RNA, herein

designated GAM RNA, on one or more GAM336151 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336151 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336151 RNA, herein designated GAM RNA, of GAM336151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336151 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336151 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336151 RNA correlate with, and may be deduced from, the identity of the GAM336151 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336152 6388 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAGG Messenger 336152 (GAM336152) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGTCGA GAM336152 is a novel bioinformatically detectable regulatory, non protein
GATGGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336152 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGTGAA encoded by the human genome.

ACTCCGTCTC GAM336152 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336152 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336152 precursor RNA is designated SEQ ID:6388, and is provided hereinbelow with reference to the sequence listing part.

GAM336152 precursor RNA folds onto itself, forming GAM336152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336152 precursor RNA, designated SEQ ID NO: 6388, and a schematic representation of a predicted secondary folding of GAM336152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336152 folded precursor RNA yielding a GAM336152 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336152 RNA, hereby incorporated herein. Expression of GAM336152 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336152 target RNA, herein designated GAM TARGET RNA.

GAM336152 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336152 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336152 RNA, herein designated GAM RNA, to target binding sites on GAM336152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336152 target RNA into GAM336152 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336152 target genes. The mRNA of each one of this plurality of GAM336152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336152 RNA, herein designated GAM RNA, and which when bound by GAM336152 RNA causes inhibition of translation of the GAM336152 target mRNA into a corresponding GAM336152 target protein.

The mechanism of the translational inhibition exerted by GAM336152 RNA, herein designated GAM RNA, on one or more GAM336152 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336152 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336152 RNA, herein designated GAM RNA, of GAM336152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336152 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336152 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336152 RNA correlate with, and may be deduced from, the identity of the GAM336152 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336153 6391 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGA Messenger 336153 (GAM336153) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336153 is a novel bioinformatically detectable regulatory, non protein

GATCACGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336153 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGTGAGA encoded by the human genome.

CTCCGTCTC GAM336153 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336153 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336153 precursor RNA is designated SEQ ID:6391, and is provided hereinbelow with reference to the sequence listing part.

GAM336153 precursor RNA folds onto itself, forming GAM336153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336153 precursor RNA, designated SEQ ID NO: 6391, and a schematic representation of a predicted secondary folding of GAM336153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336153 folded precursor RNA yielding a GAM336153 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336153 RNA, hereby incorporated herein. Expression of GAM336153 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336153 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336153 target RNA, herein designated GAM TARGET RNA.

GAM336153 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336153 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336153 RNA, herein designated GAM RNA, to target binding sites on GAM336153 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336153 target RNA into GAM336153 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336153 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336153 target genes. The mRNA of each one of this plurality of GAM336153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336153 RNA, herein designated GAM RNA, and which when bound by GAM336153 RNA causes inhibition of translation of the GAM336153 target mRNA into a corresponding GAM336153 target protein.

The mechanism of the translational inhibition exerted by GAM336153 RNA, herein designated GAM RNA, on one or more GAM336153 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336153 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336153 RNA, herein designated GAM RNA, of GAM336153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336153 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336153 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336153 RNA correlate with, and may be deduced from, the identity of the GAM336153 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336154 6392 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336154 (GAM336154) oligonucleotides modulates expression of respective target

CGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336154 is a novel bioinformatically detectable regulatory, non protein
GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336154 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAAAGCAAA encoded by the human genome.

ACTTCGTCTC GAM336154 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336154 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336154 precursor RNA is designated SEQ ID:6392, and is provided hereinbelow with reference to the sequence listing part.

GAM336154 precursor RNA folds onto itself, forming GAM336154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336154 precursor RNA, designated SEQ ID NO: 6392, and a schematic representation of a predicted secondary folding of GAM336154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336154 folded precursor RNA yielding a GAM336154 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336154 RNA, hereby incorporated herein. Expression of GAM336154 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336154 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336154 target RNA, herein designated GAM TARGET RNA.

GAM336154 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336154 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336154 RNA, herein designated GAM RNA, to target binding sites on GAM336154 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336154 target RNA into GAM336154 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336154 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336154 target genes. The mRNA of each one of this plurality of GAM336154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336154 RNA, herein designated GAM RNA, and which when bound by GAM336154 RNA causes inhibition of translation of the GAM336154 target mRNA into a corresponding GAM336154 target protein.

The mechanism of the translational inhibition exerted by GAM336154 RNA, herein designated GAM RNA, on one or more GAM336154 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336154 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336154 RNA, herein designated GAM RNA, of GAM336154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336154 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336154 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336154 RNA correlate with, and may be deduced from, the identity of the GAM336154 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336155 6394 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336155 (GAM336155) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGTGCCGA GAM336155 is a novel bioinformatically detectable regulatory, non protein

GATCGCGACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336155 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGGAGTGAAA encoded by the human genome.

TTCTGTCTC GAM336155 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336155 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336155 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336155 precursor RNA is designated SEQ ID:6394, and is provided hereinbelow with reference to the sequence listing part.

GAM336155 precursor RNA folds onto itself, forming GAM336155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336155 precursor RNA, designated SEQ ID NO: 6394, and a schematic representation of a predicted secondary folding of GAM336155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336155 folded precursor RNA yielding a GAM336155 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336155 RNA, hereby incorporated herein. Expression of GAM336155 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336155 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336155 target RNA, herein designated GAM TARGET RNA.

GAM336155 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336155 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336155 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336155 RNA, herein designated GAM RNA, to target binding sites on GAM336155 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336155 target RNA into GAM336155 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336155 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336155 target genes. The mRNA of each one of this plurality of GAM336155 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336155 RNA, herein designated GAM RNA, and which when bound by GAM336155 RNA causes inhibition of translation of the GAM336155 target mRNA into a corresponding GAM336155 target protein.

The mechanism of the translational inhibition exerted by GAM336155 RNA, herein designated GAM RNA, on one or more GAM336155 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336155 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336155 RNA, herein designated GAM RNA, of GAM336155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336155 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336155 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336155 RNA correlate with, and may be deduced from, the identity of the GAM336155 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336156 6398 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGGGG Messenger 336156 (GAM336156) oligonucleotides modulates expression of respective target
AGGAGGTTAC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336156 is a novel bioinformatically detectable regulatory, non protein
GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336156 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGTGAA encoded by the human genome.

ACTGTCTC GAM336156 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336156 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336156 precursor RNA is designated SEQ ID:6398, and is provided hereinbelow with reference to the sequence listing part.

GAM336156 precursor RNA folds onto itself, forming GAM336156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336156 precursor RNA, designated SEQ ID NO: 6398, and a schematic representation of a predicted secondary folding of GAM336156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336156 folded precursor RNA yielding a GAM336156 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336156 RNA, hereby incorporated herein. Expression of GAM336156 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336156 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336156 target RNA, herein designated GAM TARGET RNA.

GAM336156 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336156 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336156 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336156 RNA, herein designated GAM RNA, to target binding sites on GAM336156 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336156 target RNA into GAM336156 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336156 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336156 target genes. The mRNA of each one of this plurality of GAM336156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336156 RNA, herein designated GAM RNA, and which when bound by GAM336156 RNA causes inhibition of translation of the GAM336156 target mRNA into a corresponding GAM336156 target protein.

The mechanism of the translational inhibition exerted by GAM336156 RNA, herein designated GAM RNA, on one or more GAM336156 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336156 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336156 RNA, herein designated GAM RNA, of

GAM336156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336156 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336156 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336156 RNA correlate with, and may be deduced from, the identity of the GAM336156 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336157 6401 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 336157 (GAM336157) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336157 is a novel bioinformatically detectable regulatory, non protein

GATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336157 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCGAGA encoded by the human genome.

CTTCGTCTC GAM336157 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336157 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336157 precursor RNA is designated SEQ ID:6401, and is provided hereinbelow with reference to the sequence listing part.

GAM336157 precursor RNA folds onto itself, forming GAM336157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336157 precursor RNA, designated SEQ ID NO: 6401, and a schematic representation of a predicted secondary folding of GAM336157 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336157 folded precursor RNA yielding a GAM336157 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336157 RNA, hereby incorporated herein. Expression of GAM336157 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336157 target RNA, herein designated GAM TARGET RNA.

GAM336157 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336157 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336157 RNA, herein designated GAM RNA, to target binding sites on GAM336157 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336157 target RNA into GAM336157 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336157 target genes. The mRNA of each one of this plurality of GAM336157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336157 RNA, herein designated GAM RNA, and which when bound by GAM336157 RNA causes inhibition of translation of the GAM336157 target mRNA into a corresponding GAM336157 target protein.

The mechanism of the translational inhibition exerted by GAM336157 RNA, herein designated GAM RNA, on one or more GAM336157 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336157 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336157 RNA, herein designated GAM RNA, of GAM336157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336157 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336157 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336157 RNA correlate with, and may be deduced from, the identity of the GAM336157 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336158 6408 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGGCATGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336158 (GAM336158) oligonucleotides modulates expression of respective target

CGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336158 is a novel bioinformatically detectable regulatory, non protein

GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336158 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGGAGCAAGA encoded by the human genome.

CTCCATCTC GAM336158 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336158 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336158 precursor RNA is designated SEQ ID:6408, and is provided hereinbelow with reference to the sequence listing part.

GAM336158 precursor RNA folds onto itself, forming GAM336158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336158 precursor RNA, designated SEQ ID NO: 6408, and a schematic representation of a predicted secondary folding of GAM336158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336158 folded precursor RNA yielding a GAM336158 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336158 RNA, hereby incorporated herein. Expression of GAM336158 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336158 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336158 target RNA, herein designated GAM TARGET RNA.

GAM336158 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336158 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336158 RNA, herein designated GAM RNA, to target binding sites on GAM336158 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336158 target RNA into GAM336158 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336158 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336158 target genes. The mRNA of each one of this plurality of GAM336158 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336158 RNA,

herein designated GAM RNA, and which when bound by GAM336158 RNA causes inhibition of translation of the GAM336158 target mRNA into a corresponding GAM336158 target protein.

The mechanism of the translational inhibition exerted by GAM336158 RNA, herein designated GAM RNA, on one or more GAM336158 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336158 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336158 RNA, herein designated GAM RNA, of GAM336158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336158 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336158 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336158 RNA correlate with, and may be deduced from, the identity of the GAM336158 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336159 6409 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGGCCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTAGGAGG Messenger 336159 (GAM336159) oligonucleotides modulates expression of respective target

TGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336159 is a novel bioinformatically detectable regulatory, non protein

GATAGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336159 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCGAGA encoded by the human genome.

CTCTGTCTC GAM336159 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336159 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336159 precursor RNA is designated SEQ ID:6409, and is provided hereinbelow with reference to the sequence listing part.

GAM336159 precursor RNA folds onto itself, forming GAM336159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336159 precursor RNA, designated SEQ ID NO: 6409, and a schematic representation of a predicted secondary folding of GAM336159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336159 folded precursor RNA yielding a GAM336159 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336159 RNA, hereby incorporated herein. Expression of GAM336159 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336159 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336159 target RNA, herein designated GAM TARGET RNA.

GAM336159 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336159 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336159 RNA, herein designated GAM RNA, to target binding sites on GAM336159 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336159 target RNA

into GAM336159 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336159 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336159 target genes. The mRNA of each one of this plurality of GAM336159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336159 RNA, herein designated GAM RNA, and which when bound by GAM336159 RNA causes inhibition of translation of the GAM336159 target mRNA into a corresponding GAM336159 target protein.

The mechanism of the translational inhibition exerted by GAM336159 RNA, herein designated GAM RNA, on one or more GAM336159 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336159 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336159 RNA, herein designated GAM RNA, of GAM336159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336159 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336159 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336159 RNA correlate with, and may be deduced from, the identity of the GAM336159 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336160 6413 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCAGGAGG Messenger 336160 (GAM336160) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

GGTGAGTCGA GAM336160 is a novel bioinformatically detectable regulatory, non protein

GATCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336160 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCAAA encoded by the human genome.

ACTCCGTCTC GAM336160 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336160 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336160 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336160 precursor RNA is designated SEQ ID:6413, and is provided hereinbelow with reference to the sequence listing part.

GAM336160 precursor RNA folds onto itself, forming GAM336160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336160 precursor RNA, designated SEQ ID NO: 6413, and a schematic representation of a predicted secondary folding of GAM336160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336160 folded precursor RNA yielding a GAM336160 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336160 RNA, hereby incorporated herein. Expression of GAM336160 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336160 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336160 target RNA, herein designated GAM TARGET RNA.

GAM336160 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336160 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336160 RNA, herein designated GAM RNA, to target binding sites on GAM336160 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336160 target RNA into GAM336160 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336160 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336160 target genes. The mRNA of each one of this plurality of GAM336160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336160 RNA, herein designated GAM RNA, and which when bound by GAM336160 RNA causes inhibition of translation of the GAM336160 target mRNA into a corresponding GAM336160 target protein.

The mechanism of the translational inhibition exerted by GAM336160 RNA, herein designated GAM RNA, on one or more GAM336160 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336160 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336160 RNA, herein designated GAM RNA, of GAM336160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336160 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336160 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336160 RNA correlate with, and may be deduced from, the identity of the GAM336160 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336161 6417 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336161 (GAM336161) oligonucleotides modulates expression of respective target

CAGAAGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336161 is a novel bioinformatically detectable regulatory, non protein
GATAGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336161 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCCGTCTC GAM336161 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336161 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336161 precursor RNA is designated SEQ ID:6417, and is provided hereinbelow with reference to the sequence listing part.

GAM336161 precursor RNA folds onto itself, forming GAM336161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336161 precursor RNA, designated SEQ ID NO: 6417, and a schematic representation of a predicted secondary folding of GAM336161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336161 folded precursor RNA yielding a GAM336161 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336161 RNA, hereby incorporated herein. Expression of GAM336161 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336161 target RNA, herein designated GAM TARGET RNA.

GAM336161 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336161 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336161 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336161 RNA, herein designated GAM RNA, to target binding sites on GAM336161 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336161 target RNA into GAM336161 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336161 target genes. The mRNA of each one of this plurality of GAM336161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336161 RNA, herein designated GAM RNA, and which when bound by GAM336161 RNA causes inhibition of translation of the GAM336161 target mRNA into a corresponding GAM336161 target protein.

The mechanism of the translational inhibition exerted by GAM336161 RNA, herein designated GAM RNA, on one or more GAM336161 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336161 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336161 RNA, herein designated GAM RNA, of GAM336161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336161 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336161 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336161 RNA correlate with, and may be deduced from, the identity of the GAM336161 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336162 6419 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 336162 (GAM336162) oligonucleotides modulates expression of respective target
CGGAGGTTGT genes whose function and utility is known in the art.

AGTGAGCTGA GAM336162 is a novel bioinformatically detectable regulatory, non protein
GATCACGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336162 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCAAGA encoded by the human genome.

CTGTCTC GAM336162 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336162 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336162 precursor RNA is designated SEQ ID:6419, and is provided hereinbelow with reference to the sequence listing part.

GAM336162 precursor RNA folds onto itself, forming GAM336162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336162 precursor RNA, designated SEQ ID NO: 6419, and a schematic representation of a predicted secondary folding of GAM336162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336162 folded precursor RNA yielding a GAM336162 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336162 RNA, hereby incorporated herein. Expression of GAM336162 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336162 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336162 target RNA, herein designated GAM TARGET RNA.

GAM336162 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336162 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336162 RNA, herein designated GAM RNA, to target binding sites on GAM336162 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336162 target RNA into GAM336162 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336162 target genes. The mRNA of each one of this plurality of GAM336162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336162 RNA, herein designated GAM RNA, and which when bound by GAM336162 RNA causes inhibition of translation of the GAM336162 target mRNA into a corresponding GAM336162 target protein.

The mechanism of the translational inhibition exerted by GAM336162 RNA, herein designated GAM RNA, on one or more GAM336162 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336162 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336162 RNA, herein designated GAM RNA, of GAM336162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336162 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336162 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336162 RNA correlate with, and may be deduced from, the identity of the GAM336162 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336163 6422 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAGG Messenger 336163 (GAM336163) oligonucleotides modulates expression of respective target
CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336163 is a novel bioinformatically detectable regulatory, non protein
AATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336163 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGGGCAAGA encoded by the human genome.

CTCCGTCTC GAM336163 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336163 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336163 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336163 precursor RNA is designated SEQ ID:6422, and is provided hereinbelow with reference to the sequence listing part.

GAM336163 precursor RNA folds onto itself, forming GAM336163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336163 precursor RNA, designated SEQ ID NO: 6422, and a schematic representation of a predicted secondary folding of GAM336163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336163 folded precursor RNA yielding a GAM336163 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336163 RNA, hereby incorporated herein. Expression of GAM336163 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336163 target RNA, herein designated GAM TARGET RNA.

GAM336163 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336163 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336163 RNA, herein designated GAM RNA, to target binding sites on GAM336163 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336163 target RNA into GAM336163 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336163 target genes. The mRNA of each one of this plurality of GAM336163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336163 RNA, herein designated GAM RNA, and which when bound by GAM336163 RNA causes inhibition of translation of the GAM336163 target mRNA into a corresponding GAM336163 target protein.

The mechanism of the translational inhibition exerted by GAM336163 RNA, herein designated GAM RNA, on one or more GAM336163 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336163 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336163 RNA, herein designated GAM RNA, of GAM336163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336163 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336163 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336163 RNA correlate with, and may be deduced from, the identity of the GAM336163 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336164 6424 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 336164 (GAM336164) oligonucleotides modulates expression of respective target

TGAAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336164 is a novel bioinformatically detectable regulatory, non protein

GACCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336164 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAAA encoded by the human genome.

CTCCGTCTC GAM336164 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336164 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336164 precursor RNA is designated SEQ ID:6424, and is provided hereinbelow with reference to the sequence listing part.

GAM336164 precursor RNA folds onto itself, forming GAM336164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336164 precursor RNA, designated SEQ ID NO: 6424, and a schematic representation of a predicted secondary folding of GAM336164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336164 folded precursor RNA yielding a GAM336164 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336164 RNA, hereby incorporated herein. Expression of GAM336164 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336164 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336164 target RNA, herein designated GAM TARGET RNA.

GAM336164 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336164 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336164 RNA, herein designated GAM RNA, to target binding sites on GAM336164 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336164 target RNA into GAM336164 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336164 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336164 target genes. The mRNA of each one of this plurality of GAM336164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336164 RNA, herein designated GAM RNA, and which when bound by GAM336164 RNA causes inhibition of translation of the GAM336164 target mRNA into a corresponding GAM336164 target protein.

The mechanism of the translational inhibition exerted by GAM336164 RNA, herein

designated GAM RNA, on one or more GAM336164 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336164 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336164 RNA, herein designated GAM RNA, of GAM336164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336164 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336164 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336164 RNA correlate with, and may be deduced from, the identity of the GAM336164 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336165 6426 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTCAGGGTC Messenger 336165 (GAM336165) oligonucleotides modulates expression of respective target

AGAGGTCGCA genes whose function and utility is known in the art.

GTGAGCCGAG GAM336165 is a novel bioinformatically detectable regulatory, non protein

ATCCCTCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336165 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGTGAGTC encoded by the human genome.

TCTGTCTC GAM336165 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336165 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336165 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336165 precursor RNA is designated SEQ ID:6426, and is provided hereinbelow with reference to the sequence listing part.

GAM336165 precursor RNA folds onto itself, forming GAM336165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336165 precursor RNA, designated SEQ ID NO: 6426, and a schematic representation of a predicted secondary folding of GAM336165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336165 folded precursor RNA yielding a GAM336165 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336165 RNA, hereby incorporated herein. Expression of GAM336165 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336165 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336165 target RNA, herein designated GAM TARGET RNA.

GAM336165 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336165 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336165 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336165 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336165 RNA, herein designated GAM RNA, to target binding sites on GAM336165 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336165 target RNA into GAM336165 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336165 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336165 target genes. The mRNA of each one of this plurality of GAM336165 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336165 RNA, herein designated GAM RNA, and which when bound by GAM336165 RNA causes inhibition of translation of the GAM336165 target mRNA into a corresponding GAM336165 target protein.

The mechanism of the translational inhibition exerted by GAM336165 RNA, herein designated GAM RNA, on one or more GAM336165 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336165 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336165 RNA, herein designated GAM RNA, of GAM336165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336165 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336165 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336165 RNA correlate with, and may be deduced from, the identity of the GAM336165 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336166 6431 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTGGAAGG Messenger 336166 (GAM336166) oligonucleotides modulates expression of respective target

TTGAGGCTGT genes whose function and utility is known in the art.

AGTGAGCCAT GAM336166 is a novel bioinformatically detectable regulatory, non protein

GATTGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336166 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGAGACA encoded by the human genome.

TCCTTTCTC GAM336166 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336166 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336166 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336166 precursor RNA is designated SEQ ID:6431, and is provided hereinbelow with reference to the sequence listing part.

GAM336166 precursor RNA folds onto itself, forming GAM336166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336166 precursor RNA, designated SEQ ID NO: 6431, and a schematic representation of a predicted secondary folding of GAM336166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336166 folded precursor RNA yielding a GAM336166 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336166 RNA, hereby incorporated herein. Expression of GAM336166 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336166 target RNA, herein designated GAM TARGET RNA.

GAM336166 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336166 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336166 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336166 RNA, herein designated GAM RNA, to target binding sites on GAM336166 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336166 target RNA into GAM336166 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336166 target genes. The mRNA of each one of this plurality of GAM336166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336166 RNA, herein designated GAM RNA, and which when bound by GAM336166 RNA causes inhibition of translation of the GAM336166 target mRNA into a corresponding GAM336166 target protein.

The mechanism of the translational inhibition exerted by GAM336166 RNA, herein designated GAM RNA, on one or more GAM336166 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336166 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336166 RNA, herein designated GAM RNA, of GAM336166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336166 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336166 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336166 RNA correlate with, and may be deduced from, the identity of the GAM336166 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336167 6433 GAGGCAGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGA Messenger 336167 (GAM336167) oligonucleotides modulates expression of respective target

CAGAGGTTTC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336167 is a novel bioinformatically detectable regulatory, non protein
GATCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336167 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGA encoded by the human genome.

CTCTGTCTC GAM336167 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336167 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336167 precursor RNA is designated SEQ ID:6433, and is provided hereinbelow with reference to the sequence listing part.

GAM336167 precursor RNA folds onto itself, forming GAM336167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336167 precursor RNA, designated SEQ ID NO: 6433, and a schematic representation of a predicted secondary folding of GAM336167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336167 folded precursor RNA yielding a GAM336167 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336167 RNA, hereby incorporated herein. Expression of GAM336167 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336167 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336167 target RNA, herein designated GAM TARGET RNA.

GAM336167 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336167 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336167 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336167 RNA, herein designated GAM RNA, to target binding sites on GAM336167 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336167 target RNA into GAM336167 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336167 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336167 target genes. The mRNA of each one of this plurality of GAM336167 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336167 RNA, herein designated GAM RNA, and which when bound by GAM336167 RNA causes inhibition of translation of the GAM336167 target mRNA into a corresponding GAM336167 target protein.

The mechanism of the translational inhibition exerted by GAM336167 RNA, herein designated GAM RNA, on one or more GAM336167 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336167 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336167 RNA, herein designated GAM RNA, of GAM336167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336167 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336167 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336167 RNA correlate with, and may be deduced from, the identity of the GAM336167 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336168 6438 GAGGCTGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGAGAATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAACCC Messenger 336168 (GAM336168) oligonucleotides modulates expression of respective target
AGGAGGTGGA genes whose function and utility is known in the art.

GGTTTCAGTG GAM336168 is a novel bioinformatically detectable regulatory, non protein
AGCCAAGATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336168 was detected
GTACCACTGC is described with additional reference to Figs. 9-15.

ACTCCAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGCAACAGA encoded by the human genome.

GCGAGACTCC GAM336168 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCCTC GAM336168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336168 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336168 precursor RNA is designated SEQ ID:6438, and is provided hereinbelow with reference to the sequence listing part.

GAM336168 precursor RNA folds onto itself, forming GAM336168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336168 precursor RNA, designated SEQ ID NO: 6438, and a schematic representation of a predicted secondary folding of GAM336168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336168 folded precursor RNA yielding a GAM336168 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336168 RNA, hereby incorporated herein. Expression of GAM336168 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336168 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336168 target RNA, herein designated GAM TARGET RNA.

GAM336168 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336168 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336168 RNA, herein designated GAM RNA, to target binding sites on GAM336168 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336168 target RNA into GAM336168 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336168 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336168 target genes. The mRNA of each one of this plurality of GAM336168 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336168 RNA, herein designated GAM RNA, and which when bound by GAM336168 RNA causes inhibition of translation of the GAM336168 target mRNA into a corresponding GAM336168 target protein.

The mechanism of the translational inhibition exerted by GAM336168 RNA, herein designated GAM RNA, on one or more GAM336168 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336168 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336168 RNA, herein designated GAM RNA, of GAM336168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336168 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336168 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336168 RNA correlate with, and may be deduced from, the identity of the GAM336168 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336169 6499 GCAGTCTGCG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGACCAGACT detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTGTGACAT Messenger 336169 (GAM336169) oligonucleotides modulates expression of respective target
GGAGAATGTA genes whose function and utility is known in the art.

GAGAAATTAT GAM336169 is a novel bioinformatically detectable regulatory, non protein
TCAATGTTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336169 was detected
GGATCAACAT is described with additional reference to Figs. 9-15.

GATCTCCTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCTAGGATG encoded by the human genome.

GATCCATACA GAM336169 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CATCCCACTC GAM336169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
AAACTGC GAM336169 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336169 precursor RNA is designated SEQ ID:6499, and is provided hereinbelow with reference to the sequence listing part.

GAM336169 precursor RNA folds onto itself, forming GAM336169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336169 precursor RNA, designated SEQ ID NO: 6499, and a schematic representation of a predicted secondary folding of GAM336169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336169 folded precursor RNA yielding a GAM336169 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336169 RNA, hereby incorporated herein. Expression of GAM336169 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336169 target RNA, herein designated GAM TARGET RNA.

GAM336169 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336169 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336169 RNA, herein designated GAM RNA, to target binding sites on GAM336169 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336169 target RNA into GAM336169 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336169 target genes. The mRNA of each one of this plurality of GAM336169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336169 RNA, herein designated GAM RNA, and which when bound by GAM336169 RNA causes inhibition of translation of the GAM336169 target mRNA into a corresponding GAM336169 target protein.

The mechanism of the translational inhibition exerted by GAM336169 RNA, herein designated GAM RNA, on one or more GAM336169 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336169 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336169 RNA, herein designated GAM RNA, of

GAM336169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336169 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336169 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336169 RNA correlate with, and may be deduced from, the identity of the GAM336169 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336170 6519 GCGTGAACCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGAGGCGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTTGCAGTG Messenger 336170 (GAM336170) oligonucleotides modulates expression of respective target

AGCCGAGATC genes whose function and utility is known in the art.

GTGCCACTGC GAM336170 is a novel bioinformatically detectable regulatory, non protein

ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336170 was detected

GGGCAACAGA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336170 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336170 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336170 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336170 precursor RNA is designated SEQ ID:6519, and is provided hereinbelow with reference to the sequence listing part.

GAM336170 precursor RNA folds onto itself, forming GAM336170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336170 precursor RNA, designated SEQ ID NO: 6519, and a schematic representation of a predicted secondary folding of GAM336170 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336170 folded precursor RNA yielding a GAM336170 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336170 RNA, hereby incorporated herein. Expression of GAM336170 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336170 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336170 target RNA, herein designated GAM TARGET RNA.

GAM336170 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336170 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336170 RNA, herein designated GAM RNA, to target binding sites on GAM336170 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336170 target RNA into GAM336170 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336170 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336170 target genes. The mRNA of each one of this plurality of GAM336170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336170 RNA, herein designated GAM RNA, and which when bound by GAM336170 RNA causes inhibition of translation of the GAM336170 target mRNA into a corresponding GAM336170 target protein.

The mechanism of the translational inhibition exerted by GAM336170 RNA, herein designated GAM RNA, on one or more GAM336170 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336170 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336170 RNA, herein designated GAM RNA, of GAM336170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336170 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336170 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336170 RNA correlate with, and may be deduced from, the identity of the GAM336170 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336171 6521 GCTACTCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGCTGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGAGGATCA Messenger 336171 (GAM336171) oligonucleotides modulates expression of respective target
CTTGAGCCTG genes whose function and utility is known in the art.

GGAGGTCTAG GAM336171 is a novel bioinformatically detectable regulatory, non protein
GCTGCAGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336171 was detected
GCCGGGACGA is described with additional reference to Figs. 9-15.

TGCCACTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCCAGCCTG encoded by the human genome.

GGCAACAGAG GAM336171 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGAGACCCTG GAM336171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TCCCAGCACT GAM336171 precursor RNA does not encode a protein. A nucleotide sequence identical or

CTGGGAGGC highly similar to the nucleotide sequence of GAM336171 precursor RNA is designated SEQ
ID:6521, and is provided hereinbelow with reference to the sequence listing part.

GAM336171 precursor RNA folds onto itself, forming GAM336171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336171 precursor RNA, designated SEQ ID NO: 6521, and a schematic representation of a predicted secondary folding of GAM336171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336171 folded precursor RNA yielding a GAM336171 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336171 RNA, hereby incorporated herein. Expression of GAM336171 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336171 target RNA, herein designated GAM TARGET RNA.

GAM336171 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336171 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336171 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336171 RNA, herein designated GAM RNA, to target binding sites on GAM336171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336171 target RNA into GAM336171 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336171 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336171 target genes. The mRNA of each one of this plurality of GAM336171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336171 RNA, herein designated GAM RNA, and which when bound by GAM336171 RNA causes inhibition of translation of the GAM336171 target mRNA into a corresponding GAM336171 target protein.

The mechanism of the translational inhibition exerted by GAM336171 RNA, herein designated GAM RNA, on one or more GAM336171 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336171 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336171 RNA, herein designated GAM RNA, of GAM336171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336171 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336171 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336171 RNA correlate with, and may be deduced from, the identity of the GAM336171 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336172 6534 GCTCGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAAGGTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTTGCAGTG Messenger 336172 (GAM336172) oligonucleotides modulates expression of respective target

AGCCGAGATC genes whose function and utility is known in the art.

GTGCCACTGC GAM336172 is a novel bioinformatically detectable regulatory, non protein

ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336172 was detected

GGGCAACACA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336172 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336172 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336172 precursor RNA is designated SEQ ID:6534, and is provided hereinbelow with reference to the sequence listing part.

GAM336172 precursor RNA folds onto itself, forming GAM336172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336172 precursor RNA, designated SEQ ID NO: 6534, and a schematic representation of a predicted secondary folding of GAM336172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336172 folded precursor RNA yielding a GAM336172 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336172 RNA, hereby incorporated herein. Expression of GAM336172 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336172 target RNA, herein designated GAM TARGET RNA.

GAM336172 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336172 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336172 RNA, herein designated GAM RNA, to target

binding sites on GAM336172 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336172 target RNA into GAM336172 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336172 target genes. The mRNA of each one of this plurality of GAM336172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336172 RNA, herein designated GAM RNA, and which when bound by GAM336172 RNA causes inhibition of translation of the GAM336172 target mRNA into a corresponding GAM336172 target protein.

The mechanism of the translational inhibition exerted by GAM336172 RNA, herein designated GAM RNA, on one or more GAM336172 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336172 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336172 RNA, herein designated GAM RNA, of GAM336172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336172 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336172 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336172 RNA correlate with, and may be deduced from, the identity of the GAM336172 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336173 6558 GCTTGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGAAGTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTGCAGGG Messenger 336173 (GAM336173) oligonucleotides modulates expression of respective target

AGCCATGATC genes whose function and utility is known in the art.

GCACCACTGC GAM336173 is a novel bioinformatically detectable regulatory, non protein

ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336173 was detected

GGGCAACAGA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336173 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336173 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336173 precursor RNA is designated SEQ ID:6558, and is provided hereinbelow with reference to the sequence listing part.

GAM336173 precursor RNA folds onto itself, forming GAM336173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336173 precursor RNA, designated SEQ ID NO: 6558, and a schematic representation of a predicted secondary folding of GAM336173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336173 folded precursor RNA yielding a GAM336173 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336173 RNA, hereby incorporated herein. Expression of GAM336173 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336173 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336173 target RNA, herein designated GAM TARGET RNA.

GAM336173 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336173 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336173 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336173 RNA, herein designated GAM RNA, to target binding sites on GAM336173 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336173 target RNA into GAM336173 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336173 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336173 target genes. The mRNA of each one of this plurality of GAM336173 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336173 RNA, herein designated GAM RNA, and which when bound by GAM336173 RNA causes inhibition of translation of the GAM336173 target mRNA into a corresponding GAM336173 target protein.

The mechanism of the translational inhibition exerted by GAM336173 RNA, herein designated GAM RNA, on one or more GAM336173 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336173 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336173 RNA, herein designated GAM RNA, of GAM336173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336173 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336173 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336173 RNA correlate with, and may be deduced from, the identity of the GAM336173 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336174 6560 GCTTGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGAGGCGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTGCAGTG Messenger 336174 (GAM336174) oligonucleotides modulates expression of respective target
AGCCAAGATT genes whose function and utility is known in the art.

GCGCCACTGC GAM336174 is a novel bioinformatically detectable regulatory, non protein
ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336174 was detected
GGGCAACAAA is described with additional reference to Figs. 9-15.

AGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336174 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336174 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336174 precursor RNA is designated SEQ ID:6560, and is provided hereinbelow with reference to the sequence listing part.

GAM336174 precursor RNA folds onto itself, forming GAM336174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336174 precursor RNA, designated SEQ ID NO: 6560, and a schematic representation of a predicted secondary folding of GAM336174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336174 folded precursor RNA yielding a GAM336174 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336174 RNA, hereby incorporated herein. Expression of GAM336174 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336174 target RNA, herein designated GAM TARGET RNA.

GAM336174 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336174 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336174 RNA, herein designated GAM RNA, to target binding sites on GAM336174 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336174 target RNA into GAM336174 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336174 target genes. The mRNA of each one of this plurality of GAM336174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336174 RNA, herein designated GAM RNA, and which when bound by GAM336174 RNA causes inhibition of translation of the GAM336174 target mRNA into a corresponding GAM336174 target protein.

The mechanism of the translational inhibition exerted by GAM336174 RNA, herein designated GAM RNA, on one or more GAM336174 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336174 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336174 RNA, herein designated GAM RNA, of GAM336174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336174 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336174 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336174 RNA correlate with, and may be deduced from, the identity of the GAM336174 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336175 6563 GCTTGAACTC Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGGTGGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCAGTGAG Messenger 336175 (GAM336175) oligonucleotides modulates expression of respective target
CCAAGATCGC genes whose function and utility is known in the art.

CCCACTGCAC GAM336175 is a novel bioinformatically detectable regulatory, non protein
TCCAGCCTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336175 was detected
GCAACAATGC is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336175 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336175 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336175 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336175 precursor RNA is designated SEQ ID:6563, and is provided hereinbelow with reference to the sequence listing part.

GAM336175 precursor RNA folds onto itself, forming GAM336175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336175 precursor RNA, designated SEQ ID NO: 6563, and a schematic representation of a predicted secondary folding of GAM336175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336175 folded precursor RNA yielding a GAM336175 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336175 RNA, hereby incorporated herein. Expression of GAM336175 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336175 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336175 target RNA, herein designated GAM TARGET RNA.

GAM336175 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336175 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336175 RNA, herein designated GAM RNA, to target binding sites on GAM336175 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336175 target RNA into GAM336175 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336175 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336175 target genes. The mRNA of each one of this plurality of GAM336175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336175 RNA, herein designated GAM RNA, and which when bound by GAM336175 RNA causes inhibition of translation of the GAM336175 target mRNA into a corresponding GAM336175 target protein.

The mechanism of the translational inhibition exerted by GAM336175 RNA, herein designated GAM RNA, on one or more GAM336175 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336175 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336175 RNA, herein designated GAM RNA, of GAM336175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336175 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336175 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336175 RNA correlate with, and may be deduced from, the identity of the GAM336175 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336176 6585 GGAATGTTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAAGAACTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGATCTTGT Messenger 336176 (GAM336176) oligonucleotides modulates expression of respective target
GAAATCTGTG genes whose function and utility is known in the art.

GACCCTACAT GAM336176 is a novel bioinformatically detectable regulatory, non protein
TGGCACTTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336176 was detected
TGTGTACCTA is described with additional reference to Figs. 9-15.

AGGGCTAACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCCAAATAA encoded by the human genome.

AGTCATTCAG GAM336176 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGCTTTGCAG GAM336176 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
AAACAGGTC GAM336176 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336176 precursor RNA is designated SEQ ID:6585, and is provided hereinbelow with reference to the sequence listing part.

GAM336176 precursor RNA folds onto itself, forming GAM336176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336176 precursor RNA, designated SEQ ID NO: 6585, and a schematic representation of a predicted secondary folding of GAM336176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336176 folded precursor RNA yielding a GAM336176 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336176 RNA, hereby incorporated herein. Expression of GAM336176 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336176 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336176 target RNA, herein designated GAM TARGET RNA.

GAM336176 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336176 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336176 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336176 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336176 RNA, herein designated GAM RNA, to target binding sites on GAM336176 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336176 target RNA into GAM336176 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336176 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336176 target genes. The mRNA of each one of this plurality of GAM336176 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336176 RNA, herein designated GAM RNA, and which when bound by GAM336176 RNA causes inhibition of translation of the GAM336176 target mRNA into a corresponding GAM336176 target protein.

The mechanism of the translational inhibition exerted by GAM336176 RNA, herein designated GAM RNA, on one or more GAM336176 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336176 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336176 RNA, herein designated GAM RNA, of GAM336176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336176 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336176 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336176 RNA correlate with, and may be deduced from, the identity of the GAM336176 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336177 6588 GGACCAGACT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGTGACAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGAATGTA Messenger 336177 (GAM336177) oligonucleotides modulates expression of respective target

GAGAAATTAT genes whose function and utility is known in the art.

TCAATGTTCA GAM336177 is a novel bioinformatically detectable regulatory, non protein

GGATCAACAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336177 was detected

GATCTCCTCA is described with additional reference to Figs. 9-15.

CTCTAGGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATCC encoded by the human genome.

GAM336177 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336177 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336177 precursor RNA is designated SEQ ID:6588, and is provided hereinbelow with reference to the sequence listing part.

GAM336177 precursor RNA folds onto itself, forming GAM336177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336177 precursor RNA, designated SEQ ID NO: 6588, and a schematic representation of a predicted secondary folding of GAM336177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336177 folded precursor RNA yielding a GAM336177 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336177 RNA, hereby incorporated herein. Expression of GAM336177 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336177 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336177 target RNA, herein designated GAM TARGET RNA.

GAM336177 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336177 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336177 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336177 RNA, herein designated GAM RNA, to target binding sites on GAM336177 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336177 target RNA into GAM336177 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336177 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336177 target genes. The mRNA of each one of this plurality of GAM336177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336177 RNA, herein designated GAM RNA, and which when bound by GAM336177 RNA causes inhibition of translation of the GAM336177 target mRNA into a corresponding GAM336177 target protein.

The mechanism of the translational inhibition exerted by GAM336177 RNA, herein designated GAM RNA, on one or more GAM336177 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336177 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336177 RNA, herein designated GAM RNA, of GAM336177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336177 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336177 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336177 RNA correlate with, and may be deduced from, the identity of the GAM336177 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336178 6602 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGCGAAGG Messenger 336178 (GAM336178) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CGGAGATCGT GAM336178 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336178 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATACTCC encoded by the human genome.

GAM336178 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336178 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336178 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336178 precursor RNA is designated SEQ ID:6602, and is provided hereinbelow with reference to the sequence listing part.

GAM336178 precursor RNA folds onto itself, forming GAM336178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336178 precursor RNA, designated SEQ ID NO: 6602, and a schematic representation of a predicted secondary folding of GAM336178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336178 folded precursor RNA yielding a GAM336178 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336178 RNA, hereby incorporated herein. Expression of GAM336178 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336178 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336178 target RNA, herein designated GAM TARGET RNA.

GAM336178 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336178 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336178 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336178 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336178 RNA, herein designated GAM RNA, to target binding sites on GAM336178 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336178 target RNA into GAM336178 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336178 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336178 target genes. The mRNA of each one of this plurality of GAM336178 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336178 RNA, herein designated GAM RNA, and which when bound by GAM336178 RNA causes inhibition of translation of the GAM336178 target mRNA into a corresponding GAM336178 target protein.

The mechanism of the translational inhibition exerted by GAM336178 RNA, herein designated GAM RNA, on one or more GAM336178 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336178 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336178 RNA, herein designated GAM RNA, of GAM336178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336178 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336178 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336178 RNA correlate with, and may be deduced from, the identity of the GAM336178 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336179 6612 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 336179 (GAM336179) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCAC GAM336179 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336179 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGACTCC encoded by the human genome.

GAM336179 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336179 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336179 precursor RNA is designated SEQ ID:6612, and is provided hereinbelow with reference to the sequence listing part.

GAM336179 precursor RNA folds onto itself, forming GAM336179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336179 precursor RNA, designated SEQ ID NO: 6612, and a schematic representation of a predicted secondary folding of GAM336179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336179 folded precursor RNA yielding a GAM336179 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336179 RNA, hereby incorporated herein. Expression of GAM336179 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336179 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336179 target RNA, herein designated GAM TARGET RNA.

GAM336179 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336179 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336179 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336179 RNA, herein designated GAM RNA, to target binding sites on GAM336179 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336179 target RNA into GAM336179 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336179 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336179 target genes. The mRNA of each one of this plurality of GAM336179 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336179 RNA, herein designated GAM RNA, and which when bound by GAM336179 RNA causes inhibition of translation of the GAM336179 target mRNA into a corresponding GAM336179 target protein.

The mechanism of the translational inhibition exerted by GAM336179 RNA, herein designated GAM RNA, on one or more GAM336179 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336179 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336179 RNA, herein designated GAM RNA, of GAM336179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336179 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336179 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336179 RNA correlate with, and may be deduced from, the identity of the GAM336179 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336180 6625 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGCAGAGG Messenger 336180 (GAM336180) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATGGT GAM336180 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336180 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCT encoded by the human genome.

GAM336180 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336180 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336180 precursor RNA is designated SEQ ID:6625, and is provided hereinbelow with reference to the sequence listing part.

GAM336180 precursor RNA folds onto itself, forming GAM336180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336180 precursor RNA, designated SEQ ID NO: 6625, and a schematic representation of a predicted secondary folding of GAM336180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336180 folded precursor RNA yielding a GAM336180 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336180 RNA, hereby incorporated herein. Expression of GAM336180 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336180 target RNA, herein designated GAM TARGET RNA.

GAM336180 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336180 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336180 RNA, herein designated GAM RNA, to target binding sites on GAM336180 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336180 target RNA into GAM336180 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336180 target genes. The mRNA of each one of this plurality of GAM336180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336180 RNA, herein designated GAM RNA, and which when bound by GAM336180 RNA causes inhibition of translation of the GAM336180 target mRNA into a corresponding GAM336180 target protein.

The mechanism of the translational inhibition exerted by GAM336180 RNA, herein designated GAM RNA, on one or more GAM336180 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336180 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336180 RNA, herein designated GAM RNA, of GAM336180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336180 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336180 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336180 RNA correlate with, and may be deduced from, the identity of the GAM336180 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336181 6626 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGTGGAGG Messenger 336181 (GAM336181) oligonucleotides modulates expression of respective target
TTGCAGGGAG genes whose function and utility is known in the art.

CCATGATCGC GAM336181 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336181 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM336181 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336181 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336181 precursor RNA is designated SEQ ID:6626, and is provided hereinbelow with reference to the sequence listing part.

GAM336181 precursor RNA folds onto itself, forming GAM336181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336181 precursor RNA, designated SEQ ID NO: 6626, and a schematic representation of a predicted secondary folding of GAM336181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336181 folded precursor RNA yielding a GAM336181 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336181 RNA, hereby incorporated herein. Expression of GAM336181 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336181 target RNA, herein designated GAM TARGET RNA.

GAM336181 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336181 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336181 RNA, herein designated GAM RNA, to target binding sites on GAM336181 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336181 target RNA into GAM336181 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336181 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336181 target genes. The mRNA of each one of this plurality of GAM336181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336181 RNA, herein designated GAM RNA, and which when bound by GAM336181 RNA causes inhibition of translation of the GAM336181 target mRNA into a corresponding GAM336181 target protein.

The mechanism of the translational inhibition exerted by GAM336181 RNA, herein designated GAM RNA, on one or more GAM336181 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336181 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336181 RNA, herein designated GAM RNA, of GAM336181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336181 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336181 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336181

RNA correlate with, and may be deduced from, the identity of the GAM336181 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336182 6628 GGAGAATCGC TTGAACCCAG GAGATGGAGG TTGCAGTGAG CTGAGATCAC GCCACTGCAC TCCAGCCTGG GCAACAGAGT GAGACTCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336182 (GAM336182) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336182 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336182 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336182 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336182 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336182 precursor RNA is designated SEQ ID:6628, and is provided hereinbelow with reference to the sequence listing part.

GAM336182 precursor RNA folds onto itself, forming GAM336182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336182 precursor RNA, designated SEQ ID NO: 6628, and a schematic representation of a predicted secondary folding of GAM336182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336182 folded precursor RNA yielding a GAM336182 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336182 RNA, hereby incorporated herein. Expression of GAM336182 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336182 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336182 target RNA, herein designated GAM TARGET RNA.

GAM336182 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336182 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336182 RNA, herein designated GAM RNA, to target binding sites on GAM336182 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336182 target RNA into GAM336182 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336182 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336182 target genes. The mRNA of each one of this plurality of GAM336182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336182 RNA, herein designated GAM RNA, and which when bound by GAM336182 RNA causes inhibition of translation of the GAM336182 target mRNA into a corresponding GAM336182 target protein.

The mechanism of the translational inhibition exerted by GAM336182 RNA, herein designated GAM RNA, on one or more GAM336182 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336182 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336182 RNA, herein designated GAM RNA, of GAM336182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336182 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336182 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336182 RNA correlate with, and may be deduced from, the identity of the GAM336182 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336183 6631 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGA Messenger 336183 (GAM336183) oligonucleotides modulates expression of respective target
GGTTGCAGGG genes whose function and utility is known in the art.

AGCCGAGATC GAM336183 is a novel bioinformatically detectable regulatory, non protein
ACACACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336183 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCAAA encoded by the human genome.

ACTCC GAM336183 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336183 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336183 precursor RNA is designated SEQ ID:6631, and is provided hereinbelow with reference to the sequence listing part.

GAM336183 precursor RNA folds onto itself, forming GAM336183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336183 precursor RNA, designated SEQ ID NO: 6631, and a schematic representation of a predicted secondary folding of GAM336183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336183 folded precursor

RNA yielding a GAM336183 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336183 RNA, hereby incorporated herein. Expression of GAM336183 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336183 target RNA, herein designated GAM TARGET RNA.

GAM336183 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336183 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336183 RNA, herein designated GAM RNA, to target binding sites on GAM336183 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336183 target RNA into GAM336183 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336183 target genes. The mRNA of each one of this plurality of GAM336183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336183 RNA, herein designated GAM RNA, and which when bound by GAM336183 RNA causes inhibition of translation of the GAM336183 target mRNA into a corresponding GAM336183 target protein.

The mechanism of the translational inhibition exerted by GAM336183 RNA, herein designated GAM RNA, on one or more GAM336183 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336183 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336183 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336183 RNA, herein designated GAM RNA, of GAM336183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336183 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336183 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336183 RNA correlate with, and may be deduced from, the identity of the GAM336183 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336184 6639 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 336184 (GAM336184) oligonucleotides modulates expression of respective target

TTGTGGCGAG genes whose function and utility is known in the art.

CTGAGATCAT GAM336184 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336184 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336184 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336184 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336184 precursor RNA is designated SEQ ID:6639, and is provided hereinbelow with reference to the sequence listing part.

GAM336184 precursor RNA folds onto itself, forming GAM336184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336184 precursor RNA, designated SEQ ID NO: 6639, and a schematic representation of a predicted secondary folding of GAM336184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336184 folded precursor RNA yielding a GAM336184 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336184 RNA, hereby incorporated herein. Expression of GAM336184 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336184 target RNA, herein designated GAM TARGET RNA.

GAM336184 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336184 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336184 RNA, herein designated GAM RNA, to target binding sites on GAM336184 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336184 target RNA into GAM336184 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336184 target genes. The mRNA of each one of this plurality of GAM336184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336184 RNA, herein designated GAM RNA, and which when bound by GAM336184 RNA causes inhibition of translation of the GAM336184 target mRNA into a corresponding GAM336184 target protein.

The mechanism of the translational inhibition exerted by GAM336184 RNA, herein

designated GAM RNA, on one or more GAM336184 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336184 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336184 RNA, herein designated GAM RNA, of GAM336184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336184 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336184 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336184 RNA correlate with, and may be deduced from, the identity of the GAM336184 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336185 6656 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336185 (GAM336185) oligonucleotides modulates expression of respective target
TTGTGGTGAG genes whose function and utility is known in the art.

CTGAGATTGT GAM336185 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336185 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336185 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336185 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336185 precursor RNA is designated SEQ ID:6656, and is provided hereinbelow with reference to the sequence listing part.

GAM336185 precursor RNA folds onto itself, forming GAM336185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336185 precursor RNA, designated SEQ ID NO: 6656, and a schematic representation of a predicted secondary folding of GAM336185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336185 folded precursor RNA yielding a GAM336185 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336185 RNA, hereby incorporated herein. Expression of GAM336185 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336185 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336185 target RNA, herein designated GAM TARGET RNA.

GAM336185 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336185 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336185 RNA, herein designated GAM RNA, to target binding sites on GAM336185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336185 target RNA into GAM336185 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336185 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336185 target genes. The mRNA of each one of this plurality of GAM336185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336185 RNA, herein designated GAM RNA, and which when bound by GAM336185 RNA causes inhibition of translation of the GAM336185 target mRNA into a corresponding GAM336185 target protein.

The mechanism of the translational inhibition exerted by GAM336185 RNA, herein designated GAM RNA, on one or more GAM336185 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336185 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336185 RNA, herein designated GAM RNA, of GAM336185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336185 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336185 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336185 RNA correlate with, and may be deduced from, the identity of the GAM336185 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336186 6663 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGGGAGGC Messenger 336186 (GAM336186) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM336186 is a novel bioinformatically detectable regulatory, non protein

CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336186 was detected

CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACCC encoded by the human genome.

GAM336186 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336186 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336186 precursor RNA is designated SEQ ID:6663, and is provided hereinbelow with reference to the sequence listing part.

GAM336186 precursor RNA folds onto itself, forming GAM336186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336186 precursor RNA, designated SEQ ID NO: 6663, and a schematic representation of a predicted secondary folding of GAM336186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336186 folded precursor RNA yielding a GAM336186 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336186 RNA, hereby incorporated herein. Expression of GAM336186 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336186 target RNA, herein designated GAM TARGET RNA.

GAM336186 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336186 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336186 RNA, herein designated GAM RNA, to target

binding sites on GAM336186 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336186 target RNA into GAM336186 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336186 target genes. The mRNA of each one of this plurality of GAM336186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336186 RNA, herein designated GAM RNA, and which when bound by GAM336186 RNA causes inhibition of translation of the GAM336186 target mRNA into a corresponding GAM336186 target protein.

The mechanism of the translational inhibition exerted by GAM336186 RNA, herein designated GAM RNA, on one or more GAM336186 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336186 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336186 RNA, herein designated GAM RNA, of GAM336186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336186 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336186 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336186 RNA correlate with, and may be deduced from, the identity of the GAM336186 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336187 6670 GGAGAATGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 336187 (GAM336187) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCCAGATTGC GAM336187 is a novel bioinformatically detectable regulatory, non protein

AACACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336187 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGACTCT encoded by the human genome.

GAM336187 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336187 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336187 precursor RNA is designated SEQ ID:6670, and is provided hereinbelow with reference to the sequence listing part.

GAM336187 precursor RNA folds onto itself, forming GAM336187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336187 precursor RNA, designated SEQ ID NO: 6670, and a schematic representation of a predicted secondary folding of GAM336187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336187 folded precursor RNA yielding a GAM336187 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336187 RNA, hereby incorporated herein. Expression of GAM336187 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336187 target RNA, herein designated GAM TARGET RNA.

GAM336187 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336187 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336187 RNA, herein designated GAM RNA, to target binding sites on GAM336187 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336187 target RNA into GAM336187 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336187 target genes. The mRNA of each one of this plurality of GAM336187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336187 RNA, herein designated GAM RNA, and which when bound by GAM336187 RNA causes inhibition of translation of the GAM336187 target mRNA into a corresponding GAM336187 target protein.

The mechanism of the translational inhibition exerted by GAM336187 RNA, herein designated GAM RNA, on one or more GAM336187 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336187 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336187 RNA, herein designated GAM RNA, of GAM336187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336187 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336187 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336187 RNA correlate with, and may be deduced from, the identity of the GAM336187 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336188 6671 GGAGAATGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 336188 (GAM336188) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336188 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336188 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM336188 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336188 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336188 precursor RNA is designated SEQ ID:6671, and is provided hereinbelow with reference to the sequence listing part.

GAM336188 precursor RNA folds onto itself, forming GAM336188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336188 precursor RNA, designated SEQ ID NO: 6671, and a schematic representation of a predicted secondary folding of GAM336188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336188 folded precursor RNA yielding a GAM336188 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336188 RNA, hereby incorporated herein. Expression of GAM336188 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336188 target RNA, herein designated GAM TARGET RNA.

GAM336188 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336188 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336188 RNA, herein designated GAM RNA, to target binding sites on GAM336188 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336188 target RNA into GAM336188 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336188 target genes. The mRNA of each one of this plurality of GAM336188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336188 RNA, herein designated GAM RNA, and which when bound by GAM336188 RNA causes inhibition of translation of the GAM336188 target mRNA into a corresponding GAM336188 target protein.

The mechanism of the translational inhibition exerted by GAM336188 RNA, herein designated GAM RNA, on one or more GAM336188 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336188 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336188 RNA, herein designated GAM RNA, of GAM336188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336188 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336188 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336188 RNA correlate with, and may be deduced from, the identity of the GAM336188 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336189 6674 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGCAGAGG Messenger 336189 (GAM336189) oligonucleotides modulates expression of respective target
TTGCACCACT genes whose function and utility is known in the art.

GCACTCCAGC GAM336189 is a novel bioinformatically detectable regulatory, non protein
CTGGGCAACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336189 was detected
GAGCAAGACT is described with additional reference to Figs. 9-15.

CC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336189 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336189 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336189 precursor RNA is designated SEQ ID:6674, and is provided hereinbelow with reference to the sequence listing part.

GAM336189 precursor RNA folds onto itself, forming GAM336189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336189 precursor RNA, designated SEQ ID NO: 6674, and a schematic representation of a predicted secondary folding of GAM336189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336189 folded precursor RNA yielding a GAM336189 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336189 RNA, hereby incorporated herein. Expression of GAM336189 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336189 target RNA, herein designated GAM TARGET RNA.

GAM336189 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336189 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336189 RNA, herein designated GAM RNA, to target binding sites on GAM336189 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336189 target RNA into GAM336189 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336189 target genes. The mRNA of each one of this plurality of GAM336189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336189 RNA, herein designated GAM RNA, and which when bound by GAM336189 RNA causes inhibition of translation of the GAM336189 target mRNA into a corresponding GAM336189 target protein.

The mechanism of the translational inhibition exerted by GAM336189 RNA, herein designated GAM RNA, on one or more GAM336189 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336189 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336189 RNA, herein designated GAM RNA, of GAM336189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336189 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336189 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336189 RNA correlate with, and may be deduced from, the identity of the GAM336189 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336190 6676 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336190 (GAM336190) oligonucleotides modulates expression of respective target
CTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCAT GAM336190 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336190 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM336190 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336190 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336190 precursor RNA is designated SEQ ID:6676, and is provided hereinbelow with reference to the sequence listing part.

GAM336190 precursor RNA folds onto itself, forming GAM336190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336190 precursor RNA, designated SEQ ID NO: 6676, and a schematic representation of a predicted secondary folding of GAM336190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336190 folded precursor RNA yielding a GAM336190 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336190 RNA, hereby incorporated herein. Expression of GAM336190 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336190 target RNA, herein designated GAM TARGET RNA.

GAM336190 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336190 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336190 RNA, herein designated GAM RNA, to target binding sites on GAM336190 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336190 target RNA into GAM336190 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336190 target genes. The mRNA of each one of this plurality of GAM336190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336190 RNA, herein designated GAM RNA, and which when bound by GAM336190 RNA causes inhibition of translation of the GAM336190 target mRNA into a corresponding GAM336190 target protein.

The mechanism of the translational inhibition exerted by GAM336190 RNA, herein designated GAM RNA, on one or more GAM336190 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336190 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336190 RNA, herein designated GAM RNA, of GAM336190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336190 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336190 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336190 RNA correlate with, and may be deduced from, the identity of the GAM336190 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336191 6683 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAAG Messenger 336191 (GAM336191) oligonucleotides modulates expression of respective target

CTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATAGT GAM336191 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336191 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336191 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336191 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336191 precursor RNA is designated SEQ ID:6683, and is provided hereinbelow with reference to the sequence listing part.

GAM336191 precursor RNA folds onto itself, forming GAM336191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336191 precursor RNA, designated SEQ ID NO: 6683, and

a schematic representation of a predicted secondary folding of GAM336191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336191 folded precursor RNA yielding a GAM336191 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336191 RNA, hereby incorporated herein. Expression of GAM336191 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336191 target RNA, herein designated GAM TARGET RNA.

GAM336191 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336191 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336191 RNA, herein designated GAM RNA, to target binding sites on GAM336191 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336191 target RNA into GAM336191 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336191 target genes. The mRNA of each one of this plurality of GAM336191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336191 RNA, herein designated GAM RNA, and which when bound by GAM336191 RNA causes inhibition of translation of the GAM336191 target mRNA into a corresponding GAM336191 target protein.

The mechanism of the translational inhibition exerted by GAM336191 RNA, herein designated GAM RNA, on one or more GAM336191 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336191 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336191 RNA, herein designated GAM RNA, of GAM336191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336191 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336191 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336191 RNA correlate with, and may be deduced from, the identity of the GAM336191 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336192 6685 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 336192 (GAM336192) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATTGA GAM336192 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336192 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAACTCC encoded by the human genome.

GAM336192 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336192 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336192 precursor RNA is designated SEQ ID:6685, and is provided hereinbelow with reference to the sequence listing part.

GAM336192 precursor RNA folds onto itself, forming GAM336192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336192 precursor RNA, designated SEQ ID NO: 6685, and a schematic representation of a predicted secondary folding of GAM336192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336192 folded precursor RNA yielding a GAM336192 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336192 RNA, hereby incorporated herein. Expression of GAM336192 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336192 target RNA, herein designated GAM TARGET RNA.

GAM336192 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336192 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336192 RNA, herein designated GAM RNA, to target binding sites on GAM336192 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336192 target RNA into GAM336192 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336192 target genes. The mRNA of each one of this plurality of GAM336192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336192 RNA,

herein designated GAM RNA, and which when bound by GAM336192 RNA causes inhibition of translation of the GAM336192 target mRNA into a corresponding GAM336192 target protein.

The mechanism of the translational inhibition exerted by GAM336192 RNA, herein designated GAM RNA, on one or more GAM336192 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336192 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336192 RNA, herein designated GAM RNA, of GAM336192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336192 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336192 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336192 RNA correlate with, and may be deduced from, the identity of the GAM336192 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336193 6686 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 336193 (GAM336193) oligonucleotides modulates expression of respective target

TTTCAGTGAG genes whose function and utility is known in the art.

CCAAGATTGT GAM336193 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336193 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336193 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336193 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336193 precursor RNA is designated SEQ ID:6686, and is provided hereinbelow with reference to the sequence listing part.

GAM336193 precursor RNA folds onto itself, forming GAM336193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336193 precursor RNA, designated SEQ ID NO: 6686, and a schematic representation of a predicted secondary folding of GAM336193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336193 folded precursor RNA yielding a GAM336193 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336193 RNA, hereby incorporated herein. Expression of GAM336193 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336193 target RNA, herein designated GAM TARGET RNA.

GAM336193 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336193 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336193 RNA, herein designated GAM RNA, to target binding sites on GAM336193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336193 target RNA

into GAM336193 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336193 target genes. The mRNA of each one of this plurality of GAM336193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336193 RNA, herein designated GAM RNA, and which when bound by GAM336193 RNA causes inhibition of translation of the GAM336193 target mRNA into a corresponding GAM336193 target protein.

The mechanism of the translational inhibition exerted by GAM336193 RNA, herein designated GAM RNA, on one or more GAM336193 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336193 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336193 RNA, herein designated GAM RNA, of GAM336193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336193 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336193 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336193 RNA correlate with, and may be deduced from, the identity of the GAM336193 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336194 6691 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 336194 (GAM336194) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGT GAM336194 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336194 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336194 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336194 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336194 precursor RNA is designated SEQ ID:6691, and is provided hereinbelow with reference to the sequence listing part.

GAM336194 precursor RNA folds onto itself, forming GAM336194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336194 precursor RNA, designated SEQ ID NO: 6691, and a schematic representation of a predicted secondary folding of GAM336194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336194 folded precursor RNA yielding a GAM336194 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336194 RNA, hereby incorporated herein. Expression of GAM336194 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336194 target RNA, herein designated GAM TARGET RNA.

GAM336194 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336194 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336194 RNA, herein designated GAM RNA, to target binding sites on GAM336194 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336194 target RNA into GAM336194 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336194 target genes. The mRNA of each one of this plurality of GAM336194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336194 RNA, herein designated GAM RNA, and which when bound by GAM336194 RNA causes inhibition of translation of the GAM336194 target mRNA into a corresponding GAM336194 target protein.

The mechanism of the translational inhibition exerted by GAM336194 RNA, herein designated GAM RNA, on one or more GAM336194 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336194 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336194 RNA, herein designated GAM RNA, of GAM336194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336194 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336194 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336194 RNA correlate with, and may be deduced from, the identity of the GAM336194 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336195 6693 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGTGGAGG Messenger 336195 (GAM336195) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGACTGA GAM336195 is a novel bioinformatically detectable regulatory, non protein
GCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336195 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTCT encoded by the human genome.

GAM336195 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336195 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336195 precursor RNA is designated SEQ ID:6693, and is provided hereinbelow with reference to the sequence listing part.

GAM336195 precursor RNA folds onto itself, forming GAM336195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336195 precursor RNA, designated SEQ ID NO: 6693, and a schematic representation of a predicted secondary folding of GAM336195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336195 folded precursor RNA yielding a GAM336195 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336195 RNA, hereby incorporated herein. Expression of GAM336195 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336195 target RNA, herein designated GAM TARGET RNA.

GAM336195 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336195 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336195 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336195 RNA, herein designated GAM RNA, to target binding sites on GAM336195 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336195 target RNA into GAM336195 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336195 target genes. The mRNA of each one of this plurality of GAM336195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336195 RNA, herein designated GAM RNA, and which when bound by GAM336195 RNA causes inhibition of translation of the GAM336195 target mRNA into a corresponding GAM336195 target protein.

The mechanism of the translational inhibition exerted by GAM336195 RNA, herein designated GAM RNA, on one or more GAM336195 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336195 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336195 RNA, herein designated GAM RNA, of GAM336195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336195 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336195 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336195 RNA correlate with, and may be deduced from, the identity of the GAM336195 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336196 6696 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGAAGG Messenger 336196 (GAM336196) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGACCAT GAM336196 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336196 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAAACTCC encoded by the human genome.

GAM336196 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336196 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336196 precursor RNA is designated SEQ ID:6696, and is provided hereinbelow with reference to the sequence listing part.

GAM336196 precursor RNA folds onto itself, forming GAM336196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336196 precursor RNA, designated SEQ ID NO: 6696, and a schematic representation of a predicted secondary folding of GAM336196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336196 folded precursor RNA yielding a GAM336196 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336196 RNA, hereby incorporated herein. Expression of GAM336196 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336196 target RNA, herein designated GAM TARGET RNA.

GAM336196 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336196 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336196 RNA, herein designated GAM RNA, to target binding sites on GAM336196 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336196 target RNA into GAM336196 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336196 target genes. The mRNA of each one of this plurality of GAM336196 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336196 RNA, herein designated GAM RNA, and which when bound by GAM336196 RNA causes inhibition of translation of the GAM336196 target mRNA into a corresponding GAM336196 target protein.

The mechanism of the translational inhibition exerted by GAM336196 RNA, herein designated GAM RNA, on one or more GAM336196 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336196 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336196 RNA, herein designated GAM RNA, of GAM336196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336196 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336196 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336196 RNA correlate with, and may be deduced from, the identity of the GAM336196 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336197 6711 GGAGGATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGATGGAGG Messenger 336197 (GAM336197) oligonucleotides modulates expression of respective target
TCTCAGTGAG genes whose function and utility is known in the art.

CTGAGATTGC GAM336197 is a novel bioinformatically detectable regulatory, non protein
GTCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336197 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336197 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336197 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336197 precursor RNA is designated SEQ ID:6711, and is provided hereinbelow with reference to the sequence listing part.

GAM336197 precursor RNA folds onto itself, forming GAM336197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336197 precursor RNA, designated SEQ ID NO: 6711, and a schematic representation of a predicted secondary folding of GAM336197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336197 folded precursor RNA yielding a GAM336197 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336197 RNA, hereby incorporated herein. Expression of GAM336197 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336197 target RNA, herein designated GAM TARGET RNA.

GAM336197 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336197 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336197 RNA, herein designated GAM RNA, to target binding sites on GAM336197 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336197 target RNA into GAM336197 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336197 target genes. The mRNA of each one of this plurality of GAM336197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336197 RNA, herein designated GAM RNA, and which when bound by GAM336197 RNA causes inhibition of translation of the GAM336197 target mRNA into a corresponding GAM336197 target protein.

The mechanism of the translational inhibition exerted by GAM336197 RNA, herein designated GAM RNA, on one or more GAM336197 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336197 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336197 RNA, herein designated GAM RNA, of GAM336197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336197 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336197 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336197 RNA correlate with, and may be deduced from, the identity of the GAM336197 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336198 6712 GGAGGCTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGGGAGGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACTTGAACC Messenger 336198 (GAM336198) oligonucleotides modulates expression of respective target
CAGGAGGTGG genes whose function and utility is known in the art.

AGGCTGTGGT GAM336198 is a novel bioinformatically detectable regulatory, non protein
GAGCCAACAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336198 was detected
CCTGCCACTG is described with additional reference to Figs. 9-15.

CACTCCAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGGCAACAG encoded by the human genome.

AGCCAAACTC GAM336198 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGACTCC GAM336198 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336198 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336198 precursor RNA is designated SEQ ID:6712, and is provided hereinbelow with reference to the sequence listing part.

GAM336198 precursor RNA folds onto itself, forming GAM336198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336198 precursor RNA, designated SEQ ID NO: 6712, and a schematic representation of a predicted secondary folding of GAM336198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336198 folded precursor RNA yielding a GAM336198 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336198 RNA, hereby incorporated herein. Expression of GAM336198 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336198 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336198 target RNA, herein designated GAM TARGET RNA.

GAM336198 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336198 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336198 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336198 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336198 RNA, herein designated GAM RNA, to target binding sites on GAM336198 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336198 target RNA into GAM336198 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336198 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336198 target genes. The mRNA of each one of this plurality of GAM336198 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336198 RNA, herein designated GAM RNA, and which when bound by GAM336198 RNA causes inhibition of translation of the GAM336198 target mRNA into a corresponding GAM336198 target protein.

The mechanism of the translational inhibition exerted by GAM336198 RNA, herein designated GAM RNA, on one or more GAM336198 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336198 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336198 RNA, herein designated GAM RNA, of GAM336198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336198 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336198 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336198 RNA correlate with, and may be deduced from, the identity of the GAM336198 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336199 6718 GGATCACTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTGAGGCTG Messenger 336199 (GAM336199) oligonucleotides modulates expression of respective target

CAGTGAGCCA genes whose function and utility is known in the art.

TGTTCCTGCC GAM336199 is a novel bioinformatically detectable regulatory, non protein

ACTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336199 was detected

AGCCTGGGCA is described with additional reference to Figs. 9-15.

ACAGAGTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACC encoded by the human genome.

GAM336199 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336199 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336199 precursor RNA is designated SEQ ID:6718, and is provided hereinbelow with reference to the sequence listing part.

GAM336199 precursor RNA folds onto itself, forming GAM336199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336199 precursor RNA, designated SEQ ID NO: 6718, and a schematic representation of a predicted secondary folding of GAM336199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336199 folded precursor RNA yielding a GAM336199 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336199 RNA, hereby incorporated herein. Expression of GAM336199 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336199 target RNA, herein designated GAM TARGET RNA.

GAM336199 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336199 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336199 RNA, herein designated GAM RNA, to target binding sites on GAM336199 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336199 target RNA into GAM336199 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336199 target genes. The mRNA of each one of this plurality of GAM336199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336199 RNA, herein designated GAM RNA, and which when bound by GAM336199 RNA causes inhibition of translation of the GAM336199 target mRNA into a corresponding GAM336199 target protein.

The mechanism of the translational inhibition exerted by GAM336199 RNA, herein designated GAM RNA, on one or more GAM336199 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336199 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336199 RNA, herein designated GAM RNA, of GAM336199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336199 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336199 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336199 RNA correlate with, and may be deduced from, the identity of the GAM336199 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336200 6731 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCACCTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCGGGTGGCA Messenger 336200 (GAM336200) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

GGAGGCGAGA GAM336200 is a novel bioinformatically detectable regulatory, non protein

TCGTGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336200 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGTGAGACT encoded by the human genome.

GTC GAM336200 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336200 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336200 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336200 precursor RNA is designated SEQ

ID:6731, and is provided hereinbelow with reference to the sequence listing part.

GAM336200 precursor RNA folds onto itself, forming GAM336200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336200 precursor RNA, designated SEQ ID NO: 6731, and a schematic representation of a predicted secondary folding of GAM336200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336200 folded precursor RNA yielding a GAM336200 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336200 RNA, hereby incorporated herein. Expression of GAM336200 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336200 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336200 target RNA, herein designated GAM TARGET RNA.

GAM336200 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336200 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336200 RNA, herein designated GAM RNA, to target binding sites on GAM336200 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336200 target RNA into GAM336200 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336200 target genes. The mRNA of each one of this plurality of GAM336200 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336200 RNA, herein designated GAM RNA, and which when bound by GAM336200 RNA causes inhibition of translation of the GAM336200 target mRNA into a corresponding GAM336200 target protein.

The mechanism of the translational inhibition exerted by GAM336200 RNA, herein designated GAM RNA, on one or more GAM336200 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336200 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336200 RNA, herein designated GAM RNA, of GAM336200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336200 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336200 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336200 RNA correlate with, and may be deduced from, the identity of the GAM336200 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336201 6734 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGGAGACA Messenger 336201 (GAM336201) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TGAGCCAAGA GAM336201 is a novel bioinformatically detectable regulatory, non protein

TCGTGTCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336201 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGTGAGACT encoded by the human genome.

CTGTC GAM336201 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336201 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336201 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336201 precursor RNA is designated SEQ ID:6734, and is provided hereinbelow with reference to the sequence listing part.

GAM336201 precursor RNA folds onto itself, forming GAM336201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336201 precursor RNA, designated SEQ ID NO: 6734, and a schematic representation of a predicted secondary folding of GAM336201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336201 folded precursor RNA yielding a GAM336201 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336201 RNA, hereby incorporated herein. Expression of GAM336201 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336201 target RNA, herein designated GAM TARGET RNA.

GAM336201 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336201 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336201 RNA, herein designated GAM RNA, to target binding sites on GAM336201 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336201 target RNA into GAM336201 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336201 target genes. The mRNA of each one of this plurality of GAM336201 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336201 RNA, herein designated GAM RNA, and which when bound by GAM336201 RNA causes inhibition of translation of the GAM336201 target mRNA into a corresponding GAM336201 target protein.

The mechanism of the translational inhibition exerted by GAM336201 RNA, herein designated GAM RNA, on one or more GAM336201 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336201 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336201 RNA, herein designated GAM RNA, of GAM336201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336201 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336201 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336201 RNA correlate with, and may be deduced from, the identity of the GAM336201 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336202 6736 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGGAGGTG Messenger 336202 (GAM336202) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TGAGCCGAGA GAM336202 is a novel bioinformatically detectable regulatory, non protein
TCGCACCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336202 was detected
GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGTGAGGCT encoded by the human genome.

CTGTC GAM336202 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336202 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336202 precursor RNA is designated SEQ ID:6736, and is provided hereinbelow with reference to the sequence listing part.

GAM336202 precursor RNA folds onto itself, forming GAM336202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336202 precursor RNA, designated SEQ ID NO: 6736, and a schematic representation of a predicted secondary folding of GAM336202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336202 folded precursor RNA yielding a GAM336202 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336202 RNA, hereby incorporated herein. Expression of GAM336202 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336202 target RNA, herein designated GAM TARGET RNA.

GAM336202 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336202 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336202 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336202 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336202 RNA, herein designated GAM RNA, to target binding sites on GAM336202 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336202 target RNA into GAM336202 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336202 target genes. The mRNA of each one of this plurality of GAM336202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336202 RNA, herein designated GAM RNA, and which when bound by GAM336202 RNA causes inhibition of translation of the GAM336202 target mRNA into a corresponding GAM336202 target protein.

The mechanism of the translational inhibition exerted by GAM336202 RNA, herein designated GAM RNA, on one or more GAM336202 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336202 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336202 RNA, herein designated GAM RNA, of GAM336202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336202 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336202 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336202 RNA correlate with, and may be deduced from, the identity of the GAM336202 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336203 6810 GGGGATGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCCTGATAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAATCCATT Messenger 336203 (GAM336203) oligonucleotides modulates expression of respective target
GCCAAGGCTG genes whose function and utility is known in the art.

ACCTTATCGT GAM336203 is a novel bioinformatically detectable regulatory, non protein
CACTACGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336203 was detected
GAGAAGTGGG is described with additional reference to Figs. 9-15.

ATGGAGTCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAAGCTGG encoded by the human genome.

CAAAATAGGA GAM336203 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ACTATGTTCA GAM336203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GCAAGTCACT GAM336203 precursor RNA does not encode a protein. A nucleotide sequence identical or

ATTCTC highly similar to the nucleotide sequence of GAM336203 precursor RNA is designated SEQ ID:6810, and is provided hereinbelow with reference to the sequence listing part.

GAM336203 precursor RNA folds onto itself, forming GAM336203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336203 precursor RNA, designated SEQ ID NO: 6810, and a schematic representation of a predicted secondary folding of GAM336203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336203 folded precursor RNA yielding a GAM336203 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336203 RNA, hereby incorporated herein. Expression of GAM336203 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336203 target RNA, herein designated GAM TARGET RNA.

GAM336203 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336203 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336203 RNA, herein designated GAM RNA, to target binding sites on GAM336203 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336203 target RNA into GAM336203 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336203 target genes. The mRNA of each one of this plurality of GAM336203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336203 RNA, herein designated GAM RNA, and which when bound by GAM336203 RNA causes inhibition of translation of the GAM336203 target mRNA into a corresponding GAM336203 target protein.

The mechanism of the translational inhibition exerted by GAM336203 RNA, herein designated GAM RNA, on one or more GAM336203 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336203 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336203 RNA, herein designated GAM RNA, of GAM336203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336203 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336203 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336203 RNA correlate with, and may be deduced from, the identity of the GAM336203 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336204 6893 GTGAACCCGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGACGGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCAGTGAG Messenger 336204 (GAM336204) oligonucleotides modulates expression of respective target
CTGAGATCGT genes whose function and utility is known in the art.

GCCACTGCAC GAM336204 is a novel bioinformatically detectable regulatory, non protein
TCCAGCCTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336204 was detected
GCAAC is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336204 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336204 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336204 precursor RNA is designated SEQ ID:6893, and is provided hereinbelow with reference to the sequence listing part.

GAM336204 precursor RNA folds onto itself, forming GAM336204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336204 precursor RNA, designated SEQ ID NO: 6893, and a schematic representation of a predicted secondary folding of GAM336204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336204 folded precursor RNA yielding a GAM336204 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336204 RNA, hereby incorporated herein. Expression of GAM336204 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336204 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336204 target RNA, herein designated GAM TARGET RNA.

GAM336204 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336204 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336204 RNA, herein designated GAM RNA, to target binding sites on GAM336204 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336204 target RNA into GAM336204 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336204 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336204 target genes. The mRNA of each one of this plurality of GAM336204 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336204 RNA, herein designated GAM RNA, and which when bound by GAM336204 RNA causes inhibition of translation of the GAM336204 target mRNA into a corresponding GAM336204 target protein.

The mechanism of the translational inhibition exerted by GAM336204 RNA, herein designated GAM RNA, on one or more GAM336204 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336204 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336204 RNA, herein designated GAM RNA, of GAM336204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336204 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336204 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336204 RNA correlate with, and may be deduced from, the identity of the GAM336204 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336205 6997 TCACTGGAAC CCAGGAGGTG GAGGTTGCAG TGAGTCAAGA TAGTGCCACT GCACTCCAGC CTGGGCAACA GAGTGA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336205 (GAM336205) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336205 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336205 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336205 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336205 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336205 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336205 precursor RNA is designated SEQ ID:6997, and is provided hereinbelow with reference to the sequence listing part.

GAM336205 precursor RNA folds onto itself, forming GAM336205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336205 precursor RNA, designated SEQ ID NO: 6997, and

a schematic representation of a predicted secondary folding of GAM336205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336205 folded precursor RNA yielding a GAM336205 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336205 RNA, hereby incorporated herein. Expression of GAM336205 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336205 target RNA, herein designated GAM TARGET RNA.

GAM336205 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336205 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336205 RNA, herein designated GAM RNA, to target binding sites on GAM336205 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336205 target RNA into GAM336205 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336205 target genes. The mRNA of each one of this plurality of GAM336205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336205 RNA, herein designated GAM RNA, and which when bound by GAM336205 RNA causes inhibition of translation of the GAM336205 target mRNA into a corresponding GAM336205 target protein.

The mechanism of the translational inhibition exerted by GAM336205 RNA, herein designated GAM RNA, on one or more GAM336205 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336205 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336205 RNA, herein designated GAM RNA, of GAM336205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336205 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336205 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336205 RNA correlate with, and may be deduced from, the identity of the GAM336205 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336206 6998 TCACTGGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336206 (GAM336206) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

CTGTGCCACT GAM336206 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336206 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGCAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336206 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336206 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336206 precursor RNA is designated SEQ ID:6998, and is provided hereinbelow with reference to the sequence listing part.

GAM336206 precursor RNA folds onto itself, forming GAM336206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336206 precursor RNA, designated SEQ ID NO: 6998, and a schematic representation of a predicted secondary folding of GAM336206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336206 folded precursor RNA yielding a GAM336206 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336206 RNA, hereby incorporated herein. Expression of GAM336206 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336206 target RNA, herein designated GAM TARGET RNA.

GAM336206 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336206 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336206 RNA, herein designated GAM RNA, to target binding sites on GAM336206 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336206 target RNA into GAM336206 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336206 target genes. The mRNA of each one of this plurality of GAM336206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336206 RNA,

herein designated GAM RNA, and which when bound by GAM336206 RNA causes inhibition of translation of the GAM336206 target mRNA into a corresponding GAM336206 target protein.

The mechanism of the translational inhibition exerted by GAM336206 RNA, herein designated GAM RNA, on one or more GAM336206 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336206 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336206 RNA, herein designated GAM RNA, of GAM336206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336206 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336206 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336206 RNA correlate with, and may be deduced from, the identity of the GAM336206 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336207 7003 TCACTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336207 (GAM336207) oligonucleotides modulates expression of respective target

TGAGCCGATA genes whose function and utility is known in the art.

TCATGCCACT GAM336207 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336207 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

CAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336207 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336207 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336207 precursor RNA is designated SEQ ID:7003, and is provided hereinbelow with reference to the sequence listing part.

GAM336207 precursor RNA folds onto itself, forming GAM336207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336207 precursor RNA, designated SEQ ID NO: 7003, and a schematic representation of a predicted secondary folding of GAM336207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336207 folded precursor RNA yielding a GAM336207 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336207 RNA, hereby incorporated herein. Expression of GAM336207 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336207 target RNA, herein designated GAM TARGET RNA.

GAM336207 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336207 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336207 RNA, herein designated GAM RNA, to target binding sites on GAM336207 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336207 target RNA

into GAM336207 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336207 target genes. The mRNA of each one of this plurality of GAM336207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336207 RNA, herein designated GAM RNA, and which when bound by GAM336207 RNA causes inhibition of translation of the GAM336207 target mRNA into a corresponding GAM336207 target protein.

The mechanism of the translational inhibition exerted by GAM336207 RNA, herein designated GAM RNA, on one or more GAM336207 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336207 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336207 RNA, herein designated GAM RNA, of GAM336207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336207 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336207 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336207 RNA correlate with, and may be deduced from, the identity of the GAM336207 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336208 7023 TCCATTGCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGCTGACCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TATCGTCACT Messenger 336208 (GAM336208) oligonucleotides modulates expression of respective target

ACGCCAGAGA genes whose function and utility is known in the art.

AGTGGGATGG GAM336208 is a novel bioinformatically detectable regulatory, non protein

AGTCAGCAGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336208 was detected

AGCTGGCAAA is described with additional reference to Figs. 9-15.

ATAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336208 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336208 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336208 precursor RNA is designated SEQ ID:7023, and is provided hereinbelow with reference to the sequence listing part.

GAM336208 precursor RNA folds onto itself, forming GAM336208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336208 precursor RNA, designated SEQ ID NO: 7023, and a schematic representation of a predicted secondary folding of GAM336208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336208 folded precursor RNA yielding a GAM336208 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336208 RNA, hereby incorporated herein. Expression of GAM336208 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336208 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336208 target RNA, herein designated GAM TARGET RNA.

GAM336208 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336208 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336208 RNA, herein designated GAM RNA, to target binding sites on GAM336208 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336208 target RNA into GAM336208 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336208 target genes. The mRNA of each one of this plurality of GAM336208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336208 RNA, herein designated GAM RNA, and which when bound by GAM336208 RNA causes inhibition of translation of the GAM336208 target mRNA into a corresponding GAM336208 target protein.

The mechanism of the translational inhibition exerted by GAM336208 RNA, herein designated GAM RNA, on one or more GAM336208 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336208 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336208 RNA, herein designated GAM RNA, of GAM336208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336208 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336208 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336208 RNA correlate with, and may be deduced from, the identity of the GAM336208 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336209 7051 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGATTGCAG Messenger 336209 (GAM336209) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TCATGCCACT GAM336209 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336209 was detected
CTGGGCAACA is described with additional reference to Figs. 9-15.

AGAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336209 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336209 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336209 precursor RNA is designated SEQ ID:7051, and is provided hereinbelow with reference to the sequence listing part.

GAM336209 precursor RNA folds onto itself, forming GAM336209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336209 precursor RNA, designated SEQ ID NO: 7051, and a schematic representation of a predicted secondary folding of GAM336209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336209 folded precursor RNA yielding a GAM336209 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336209 RNA, hereby incorporated herein. Expression of GAM336209 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336209 target RNA, herein designated GAM TARGET RNA.

GAM336209 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336209 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336209 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336209 RNA, herein designated GAM RNA, to target binding sites on GAM336209 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336209 target RNA into GAM336209 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336209 target genes. The mRNA of each one of this plurality of GAM336209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336209 RNA, herein designated GAM RNA, and which when bound by GAM336209 RNA causes inhibition of translation of the GAM336209 target mRNA into a corresponding GAM336209 target protein.

The mechanism of the translational inhibition exerted by GAM336209 RNA, herein designated GAM RNA, on one or more GAM336209 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336209 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336209 RNA, herein designated GAM RNA, of GAM336209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336209 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336209 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336209 RNA correlate with, and may be deduced from, the identity of the GAM336209 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336210 7095 TGAGACAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGGGAG Messenger 336210 (GAM336210) oligonucleotides modulates expression of respective target
GTGGAAGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336210 is a novel bioinformatically detectable regulatory, non protein
AGATTGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336210 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAAGGCAAG encoded by the human genome.

ACTCCGTCTC GAM336210 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336210 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336210 precursor RNA is designated SEQ ID:7095, and is provided hereinbelow with reference to the sequence listing part.

GAM336210 precursor RNA folds onto itself, forming GAM336210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336210 precursor RNA, designated SEQ ID NO: 7095, and a schematic representation of a predicted secondary folding of GAM336210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336210 folded precursor RNA yielding a GAM336210 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336210 RNA, hereby incorporated herein. Expression of GAM336210 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336210 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336210 target RNA, herein designated GAM TARGET RNA.

GAM336210 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336210 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336210 RNA, herein designated GAM RNA, to target binding sites on GAM336210 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336210 target RNA into GAM336210 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336210 target genes. The mRNA of each one of this plurality of GAM336210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336210 RNA, herein designated GAM RNA, and which when bound by GAM336210 RNA causes inhibition of translation of the GAM336210 target mRNA into a corresponding GAM336210 target protein.

The mechanism of the translational inhibition exerted by GAM336210 RNA, herein designated GAM RNA, on one or more GAM336210 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336210 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336210 RNA, herein designated GAM RNA, of GAM336210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336210 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336210 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336210 RNA correlate with, and may be deduced from, the identity of the GAM336210 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336211 7100 TGAGACAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGGCAG Messenger 336211 (GAM336211) oligonucleotides modulates expression of respective target
GCGGAGGTTA genes whose function and utility is known in the art.

CAGTGAGCCA GAM336211 is a novel bioinformatically detectable regulatory, non protein
AGATGGTACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336211 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACATAGCAAC encoded by the human genome.

ACTCTGTCTC GAM336211 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336211 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336211 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336211 precursor RNA is designated SEQ ID:7100, and is provided hereinbelow with reference to the sequence listing part.

GAM336211 precursor RNA folds onto itself, forming GAM336211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336211 precursor RNA, designated SEQ ID NO: 7100, and a schematic representation of a predicted secondary folding of GAM336211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336211 folded precursor RNA yielding a GAM336211 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336211 RNA, hereby incorporated herein. Expression of GAM336211 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336211 target RNA, herein designated GAM TARGET RNA.

GAM336211 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336211 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336211 RNA, herein designated GAM RNA, to target binding sites on GAM336211 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336211 target RNA into GAM336211 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336211 target genes. The mRNA of each one of this plurality of GAM336211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336211 RNA, herein designated GAM RNA, and which when bound by GAM336211 RNA causes inhibition of translation of the GAM336211 target mRNA into a corresponding GAM336211 target protein.

The mechanism of the translational inhibition exerted by GAM336211 RNA, herein designated GAM RNA, on one or more GAM336211 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336211 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336211 RNA, herein designated GAM RNA, of GAM336211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336211 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336211 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336211 RNA correlate with, and may be deduced from, the identity of the GAM336211 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336212 7101 TGAGACAGTA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCACTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGGGGTG Messenger 336212 (GAM336212) oligonucleotides modulates expression of respective target

GAGGTTGCGG genes whose function and utility is known in the art.

TGAGCCGAGA GAM336212 is a novel bioinformatically detectable regulatory, non protein

TTGTGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336212 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGTGAGACT encoded by the human genome.

CTGTTTCA GAM336212 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336212 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336212 precursor RNA is designated SEQ ID:7101, and is provided hereinbelow with reference to the sequence listing part.

GAM336212 precursor RNA folds onto itself, forming GAM336212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336212 precursor RNA, designated SEQ ID NO: 7101, and a schematic representation of a predicted secondary folding of GAM336212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336212 folded precursor RNA yielding a GAM336212 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336212 RNA, hereby incorporated herein. Expression of GAM336212 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336212 target RNA, herein designated GAM TARGET RNA.

GAM336212 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336212 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336212 RNA, herein designated GAM RNA, to target binding sites on GAM336212 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336212 target RNA into GAM336212 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336212 target genes. The mRNA of each one of this plurality of GAM336212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336212 RNA, herein designated GAM RNA, and which when bound by GAM336212 RNA causes inhibition of translation of the GAM336212 target mRNA into a corresponding GAM336212 target protein.

The mechanism of the translational inhibition exerted by GAM336212 RNA, herein designated GAM RNA, on one or more GAM336212 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336212 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336212 RNA, herein designated GAM RNA, of GAM336212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336212 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336212 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336212 RNA correlate with, and may be deduced from, the identity of the GAM336212 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336213 7103 TGAGAGGACT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTTGAACTC detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGTGGAGG Messenger 336213 (GAM336213) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATCGC GAM336213 is a novel bioinformatically detectable regulatory, non protein

CCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336213 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGACCCCTC encoded by the human genome.

A GAM336213 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336213 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336213 precursor RNA is designated SEQ ID:7103, and is provided hereinbelow with reference to the sequence listing part.

GAM336213 precursor RNA folds onto itself, forming GAM336213 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336213 precursor RNA, designated SEQ ID NO: 7103, and a schematic representation of a predicted secondary folding of GAM336213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336213 folded precursor RNA yielding a GAM336213 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336213 RNA, hereby incorporated herein. Expression of GAM336213 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336213 target RNA, herein designated GAM TARGET RNA.

GAM336213 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336213 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336213 RNA, herein designated GAM RNA, to target binding sites on GAM336213 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336213 target RNA into GAM336213 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336213 target genes. The mRNA of each one of this

plurality of GAM336213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336213 RNA, herein designated GAM RNA, and which when bound by GAM336213 RNA causes inhibition of translation of the GAM336213 target mRNA into a corresponding GAM336213 target protein.

The mechanism of the translational inhibition exerted by GAM336213 RNA, herein designated GAM RNA, on one or more GAM336213 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336213 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336213 RNA, herein designated GAM RNA, of GAM336213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336213 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336213 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336213 RNA correlate with, and may be deduced from, the identity of the GAM336213 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336214 7110 TGAGGCACAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGGGAG Messenger 336214 (GAM336214) oligonucleotides modulates expression of respective target
GGGGAGGTTT genes whose function and utility is known in the art.

CAGTGAGCCG GAM336214 is a novel bioinformatically detectable regulatory, non protein
AGCCGAGATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336214 was detected
GTGTCACTGC is described with additional reference to Figs. 9-15.

ACTCCAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGCAACAGA encoded by the human genome.

GTGAGACTCT GAM336214 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTCTCA GAM336214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336214 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336214 precursor RNA is designated SEQ ID:7110, and is provided hereinbelow with reference to the sequence listing part.

GAM336214 precursor RNA folds onto itself, forming GAM336214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336214 precursor RNA, designated SEQ ID NO: 7110, and a schematic representation of a predicted secondary folding of GAM336214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336214 folded precursor RNA yielding a GAM336214 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336214 RNA, hereby incorporated herein. Expression of GAM336214 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336214 target RNA, herein designated GAM TARGET RNA.

GAM336214 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336214 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336214 RNA, herein designated GAM RNA, to target binding sites on GAM336214 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336214 target RNA into GAM336214 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336214 target genes. The mRNA of each one of this plurality of GAM336214 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336214 RNA, herein designated GAM RNA, and which when bound by GAM336214 RNA causes inhibition of translation of the GAM336214 target mRNA into a corresponding GAM336214 target protein.

The mechanism of the translational inhibition exerted by GAM336214 RNA, herein designated GAM RNA, on one or more GAM336214 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336214 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336214 RNA, herein designated GAM RNA, of GAM336214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336214 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336214 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336214 RNA correlate with, and may be deduced from, the identity of the GAM336214 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336215 7113 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCTGGAG Messenger 336215 (GAM336215) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336215 is a novel bioinformatically detectable regulatory, non protein
ATATCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336215 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACACAGTGAG encoded by the human genome.

ACTCTGTCTT GAM336215 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336215 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336215 precursor RNA is designated SEQ ID:7113, and is provided hereinbelow with reference to the sequence listing part.

GAM336215 precursor RNA folds onto itself, forming GAM336215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336215 precursor RNA, designated SEQ ID NO: 7113, and a schematic representation of a predicted secondary folding of GAM336215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336215 folded precursor RNA yielding a GAM336215 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336215 RNA, hereby incorporated herein. Expression of GAM336215 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336215 target RNA, herein designated GAM TARGET RNA.

GAM336215 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336215 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336215 RNA, herein designated GAM RNA, to target binding sites on GAM336215 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336215 target RNA into GAM336215 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336215 target genes. The mRNA of each one of this plurality of GAM336215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336215 RNA, herein designated GAM RNA, and which when bound by GAM336215 RNA causes inhibition of translation of the GAM336215 target mRNA into a corresponding GAM336215 target protein.

The mechanism of the translational inhibition exerted by GAM336215 RNA, herein designated GAM RNA, on one or more GAM336215 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336215 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336215 RNA, herein designated GAM RNA, of GAM336215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336215 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336215 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336215 RNA correlate with, and may be deduced from, the identity of the GAM336215 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336216 7124 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 336216 (GAM336216) oligonucleotides modulates expression of respective target

GAGGAGGAGG genes whose function and utility is known in the art.

TTGCAGTGGG GAM336216 is a novel bioinformatically detectable regulatory, non protein

CCGAGATCGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336216 was detected

GCCACTGCAC is described with additional reference to Figs. 9-15.

TCCAGCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAACAGAGT encoded by the human genome.

GAGACTCCAT GAM336216 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTCA GAM336216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336216 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336216 precursor RNA is designated SEQ ID:7124, and is provided hereinbelow with reference to the sequence listing part.

GAM336216 precursor RNA folds onto itself, forming GAM336216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336216 precursor RNA, designated SEQ ID NO: 7124, and a schematic representation of a predicted secondary folding of GAM336216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336216 folded precursor RNA yielding a GAM336216 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336216 RNA, hereby incorporated herein. Expression of GAM336216 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336216 target RNA, herein designated GAM TARGET RNA.

GAM336216 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336216 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336216 RNA, herein designated GAM RNA, to target binding sites on GAM336216 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336216 target RNA into GAM336216 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336216 target genes. The mRNA of each one of this plurality of GAM336216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336216 RNA, herein designated GAM RNA, and which when bound by GAM336216 RNA causes inhibition of translation of the GAM336216 target mRNA into a corresponding GAM336216 target protein.

The mechanism of the translational inhibition exerted by GAM336216 RNA, herein designated GAM RNA, on one or more GAM336216 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336216 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336216 RNA, herein designated GAM RNA, of GAM336216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336216 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336216 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336216

RNA correlate with, and may be deduced from, the identity of the GAM336216 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336217 7127 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATAGGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336217 (GAM336217) oligonucleotides modulates expression of respective target
GTGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336217 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336217 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCCGTCTC GAM336217 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336217 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336217 precursor RNA is designated SEQ ID:7127, and is provided hereinbelow with reference to the sequence listing part.

GAM336217 precursor RNA folds onto itself, forming GAM336217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336217 precursor RNA, designated SEQ ID NO: 7127, and a schematic representation of a predicted secondary folding of GAM336217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336217 folded precursor RNA yielding a GAM336217 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336217 RNA, hereby incorporated herein. Expression of GAM336217 RNA was experimentally validated in HeLa cells using the methods

described with reference to Figs.22 to 24.

GAM336217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336217 target RNA, herein designated GAM TARGET RNA.

GAM336217 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336217 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336217 RNA, herein designated GAM RNA, to target binding sites on GAM336217 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336217 target RNA into GAM336217 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336217 target genes. The mRNA of each one of this plurality of GAM336217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336217 RNA, herein designated GAM RNA, and which when bound by GAM336217 RNA causes inhibition of translation of the GAM336217 target mRNA into a corresponding GAM336217 target protein.

The mechanism of the translational inhibition exerted by GAM336217 RNA, herein designated GAM RNA, on one or more GAM336217 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336217 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336217 RNA, herein designated GAM RNA, of GAM336217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336217 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336217 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336217 RNA correlate with, and may be deduced from, the identity of the GAM336217 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336218 7128 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAAGAG Messenger 336218 (GAM336218) oligonucleotides modulates expression of respective target
GCGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM336218 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336218 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCAA encoded by the human genome.

AACTCCGTCT GAM336218 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336218 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336218 precursor RNA is designated SEQ ID:7128, and is provided hereinbelow with reference to the sequence listing part.

GAM336218 precursor RNA folds onto itself, forming GAM336218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336218 precursor RNA, designated SEQ ID NO: 7128, and a schematic representation of a predicted secondary folding of GAM336218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336218 folded precursor RNA yielding a GAM336218 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336218 RNA, hereby incorporated herein. Expression of GAM336218 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336218 target RNA, herein designated GAM TARGET RNA.

GAM336218 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336218 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336218 RNA, herein designated GAM RNA, to target binding sites on GAM336218 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336218 target RNA into GAM336218 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336218 target genes. The mRNA of each one of this plurality of GAM336218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336218 RNA, herein designated GAM RNA, and which when bound by GAM336218 RNA causes inhibition of translation of the GAM336218 target mRNA into a corresponding GAM336218 target protein.

The mechanism of the translational inhibition exerted by GAM336218 RNA, herein designated GAM RNA, on one or more GAM336218 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336218 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336218 RNA, herein designated GAM RNA, of GAM336218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336218 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336218 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336218 RNA correlate with, and may be deduced from, the identity of the GAM336218 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336219 7136 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGAAG Messenger 336219 (GAM336219) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336219 is a novel bioinformatically detectable regulatory, non protein

AGATGGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336219 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCGAG encoded by the human genome.

ACTCTATCTC GAM336219 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336219 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336219 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336219 precursor RNA is designated SEQ ID:7136, and is provided hereinbelow with reference to the sequence listing part.

GAM336219 precursor RNA folds onto itself, forming GAM336219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336219 precursor RNA, designated SEQ ID NO: 7136, and a schematic representation of a predicted secondary folding of GAM336219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336219 folded precursor RNA yielding a GAM336219 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336219 RNA, hereby incorporated herein. Expression of GAM336219 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336219 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336219 target RNA, herein designated GAM TARGET RNA.

GAM336219 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336219 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336219 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336219 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336219 RNA, herein designated GAM RNA, to target binding sites on GAM336219 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336219 target RNA into GAM336219 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336219 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336219 target genes. The mRNA of each one of this plurality of GAM336219 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336219 RNA, herein designated GAM RNA, and which when bound by GAM336219 RNA causes inhibition of translation of the GAM336219 target mRNA into a corresponding GAM336219 target protein.

The mechanism of the translational inhibition exerted by GAM336219 RNA, herein designated GAM RNA, on one or more GAM336219 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336219 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336219 RNA, herein designated GAM RNA, of GAM336219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336219 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336219 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336219 RNA correlate with, and may be deduced from, the identity of the GAM336219 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336220 7144 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336220 (GAM336220) oligonucleotides modulates expression of respective target

GCGGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCCG GAM336220 is a novel bioinformatically detectable regulatory, non protein

AGATCTCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336220 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACTCCGTCTC GAM336220 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336220 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336220 precursor RNA is designated SEQ ID:7144, and is provided hereinbelow with reference to the sequence listing part.

GAM336220 precursor RNA folds onto itself, forming GAM336220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336220 precursor RNA, designated SEQ ID NO: 7144, and a schematic representation of a predicted secondary folding of GAM336220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336220 folded precursor RNA yielding a GAM336220 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336220 RNA, hereby incorporated herein. Expression of GAM336220 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336220 target RNA, herein designated GAM TARGET RNA.

GAM336220 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336220 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336220 RNA, herein designated GAM RNA, to target binding sites on GAM336220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336220 target RNA into GAM336220 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336220 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336220 target genes. The mRNA of each one of this plurality of GAM336220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336220 RNA, herein designated GAM RNA, and which when bound by GAM336220 RNA causes inhibition of translation of the GAM336220 target mRNA into a corresponding GAM336220 target protein.

The mechanism of the translational inhibition exerted by GAM336220 RNA, herein designated GAM RNA, on one or more GAM336220 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336220 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336220 RNA, herein designated GAM RNA, of GAM336220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336220 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336220 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336220 RNA correlate with, and may be deduced from, the identity of the GAM336220 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336221 7145 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGGG Messenger 336221 (GAM336221) oligonucleotides modulates expression of respective target

GAGGAGGTTA genes whose function and utility is known in the art.

CAGTGAGCTG GAM336221 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336221 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGTGA encoded by the human genome.

AACTGTCTCA GAM336221 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336221 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336221 precursor RNA is designated SEQ ID:7145, and is provided hereinbelow with reference to the sequence listing part.

GAM336221 precursor RNA folds onto itself, forming GAM336221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336221 precursor RNA, designated SEQ ID NO: 7145, and a schematic representation of a predicted secondary folding of GAM336221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336221 folded precursor RNA yielding a GAM336221 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336221 RNA, hereby incorporated herein. Expression of GAM336221 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336221 target RNA, herein designated GAM TARGET RNA.

GAM336221 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336221 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336221 RNA, herein designated GAM RNA, to target binding sites on GAM336221 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336221 target RNA into GAM336221 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336221 target genes. The mRNA of each one of this plurality of GAM336221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336221 RNA, herein designated GAM RNA, and which when bound by GAM336221 RNA causes inhibition of translation of the GAM336221 target mRNA into a corresponding GAM336221 target protein.

The mechanism of the translational inhibition exerted by GAM336221 RNA, herein designated GAM RNA, on one or more GAM336221 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336221 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336221 RNA, herein designated GAM RNA, of GAM336221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336221 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336221 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336221 RNA correlate with, and may be deduced from, the identity of the GAM336221 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336222 7152 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTAGGAG Messenger 336222 (GAM336222) oligonucleotides modulates expression of respective target

GCGGAGGTTC genes whose function and utility is known in the art.

CAGTGAGCTG GAM336222 is a novel bioinformatically detectable regulatory, non protein
AGATGGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336222 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACTGTCTCA GAM336222 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336222 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336222 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336222 precursor RNA is designated SEQ ID:7152, and is provided hereinbelow with reference to the sequence listing part.

GAM336222 precursor RNA folds onto itself, forming GAM336222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336222 precursor RNA, designated SEQ ID NO: 7152, and a schematic representation of a predicted secondary folding of GAM336222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336222 folded precursor RNA yielding a GAM336222 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336222 RNA, hereby incorporated herein. Expression of GAM336222 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336222 target RNA, herein designated GAM TARGET RNA.

GAM336222 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336222 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336222 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336222 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336222 RNA, herein designated GAM RNA, to target binding sites on GAM336222 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336222 target RNA into GAM336222 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336222 target genes. The mRNA of each one of this plurality of GAM336222 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336222 RNA, herein designated GAM RNA, and which when bound by GAM336222 RNA causes inhibition of translation of the GAM336222 target mRNA into a corresponding GAM336222 target protein.

The mechanism of the translational inhibition exerted by GAM336222 RNA, herein designated GAM RNA, on one or more GAM336222 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336222 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336222 RNA, herein designated GAM RNA, of GAM336222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336222 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336222 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336222 RNA correlate with, and may be deduced from, the identity of the GAM336222 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336223 7154 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATGGCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTAGGAG Messenger 336223 (GAM336223) oligonucleotides modulates expression of respective target
GTGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336223 is a novel bioinformatically detectable regulatory, non protein
AGATAGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336223 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCTGTCTC GAM336223 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336223 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336223 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336223 precursor RNA is designated SEQ ID:7154, and is provided hereinbelow with reference to the sequence listing part.

GAM336223 precursor RNA folds onto itself, forming GAM336223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336223 precursor RNA, designated SEQ ID NO: 7154, and a schematic representation of a predicted secondary folding of GAM336223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336223 folded precursor RNA yielding a GAM336223 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336223 RNA, hereby incorporated herein. Expression of GAM336223 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336223 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336223 target RNA, herein designated GAM TARGET RNA.

GAM336223 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336223 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336223 RNA, herein designated GAM RNA, to target binding sites on GAM336223 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336223 target RNA into GAM336223 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336223 target genes. The mRNA of each one of this plurality of GAM336223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336223 RNA, herein designated GAM RNA, and which when bound by GAM336223 RNA causes inhibition of translation of the GAM336223 target mRNA into a corresponding GAM336223 target protein.

The mechanism of the translational inhibition exerted by GAM336223 RNA, herein designated GAM RNA, on one or more GAM336223 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336223 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336223 RNA, herein designated GAM RNA, of GAM336223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336223 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336223 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336223 RNA correlate with, and may be deduced from, the identity of the GAM336223 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336224 7161 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336224 (GAM336224) oligonucleotides modulates expression of respective target
GCAGAAGCTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336224 is a novel bioinformatically detectable regulatory, non protein
AGATAGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336224 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCCGTCTC GAM336224 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336224 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336224 precursor RNA is designated SEQ ID:7161, and is provided hereinbelow with reference to the sequence listing part.

GAM336224 precursor RNA folds onto itself, forming GAM336224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336224 precursor RNA, designated SEQ ID NO: 7161, and a schematic representation of a predicted secondary folding of GAM336224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336224 folded precursor RNA yielding a GAM336224 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336224 RNA, hereby incorporated herein. Expression of GAM336224 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336224 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336224 target RNA, herein designated GAM TARGET RNA.

GAM336224 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336224 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336224 RNA, herein designated GAM RNA, to target binding sites on GAM336224 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336224 target RNA into GAM336224 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336224 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336224 target genes. The mRNA of each one of this plurality of GAM336224 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336224 RNA, herein designated GAM RNA, and which when bound by GAM336224 RNA causes inhibition of translation of the GAM336224 target mRNA into a corresponding GAM336224 target protein.

The mechanism of the translational inhibition exerted by GAM336224 RNA, herein designated GAM RNA, on one or more GAM336224 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336224 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336224 RNA, herein designated GAM RNA, of GAM336224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336224 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336224 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336224 RNA correlate with, and may be deduced from, the identity of the GAM336224 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336225 7162 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336225 (GAM336225) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336225 is a novel bioinformatically detectable regulatory, non protein

AGATTGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336225 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCAA encoded by the human genome.

AACTCTGTCT GAM336225 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336225 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336225 precursor RNA is designated SEQ ID:7162, and is provided hereinbelow with reference to the sequence listing part.

GAM336225 precursor RNA folds onto itself, forming GAM336225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336225 precursor RNA, designated SEQ ID NO: 7162, and a schematic representation of a predicted secondary folding of GAM336225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336225 folded precursor RNA yielding a GAM336225 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336225 RNA, hereby incorporated herein. Expression of GAM336225 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336225 target RNA, herein designated GAM TARGET RNA.

GAM336225 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336225 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336225 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336225 RNA, herein designated GAM RNA, to target binding sites on GAM336225 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336225 target RNA into GAM336225 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336225 target genes. The mRNA of each one of this plurality of GAM336225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336225 RNA, herein designated GAM RNA, and which when bound by GAM336225 RNA causes inhibition of translation of the GAM336225 target mRNA into a corresponding GAM336225 target protein.

The mechanism of the translational inhibition exerted by GAM336225 RNA, herein designated GAM RNA, on one or more GAM336225 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336225 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336225 RNA, herein designated GAM RNA, of GAM336225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336225 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336225 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336225 RNA correlate with, and may be deduced from, the identity of the GAM336225 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336226 7164 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGGAG Messenger 336226 (GAM336226) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM336226 is a novel bioinformatically detectable regulatory, non protein

AAATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336226 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATAGGGCAAG encoded by the human genome.

ACTCCGTCTC GAM336226 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336226 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336226 precursor RNA is designated SEQ ID:7164, and is provided hereinbelow with reference to the sequence listing part.

GAM336226 precursor RNA folds onto itself, forming GAM336226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336226 precursor RNA, designated SEQ ID NO: 7164, and a schematic representation of a predicted secondary folding of GAM336226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336226 folded precursor RNA yielding a GAM336226 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336226 RNA, hereby incorporated herein. Expression of GAM336226 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336226 target RNA, herein designated GAM TARGET RNA.

GAM336226 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336226 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336226 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336226 RNA, herein designated GAM RNA, to target binding sites on GAM336226 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336226 target RNA into GAM336226 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336226 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336226 target genes. The mRNA of each one of this plurality of GAM336226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336226 RNA, herein designated GAM RNA, and which when bound by GAM336226 RNA causes inhibition of translation of the GAM336226 target mRNA into a corresponding GAM336226 target protein.

The mechanism of the translational inhibition exerted by GAM336226 RNA, herein designated GAM RNA, on one or more GAM336226 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336226 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336226 RNA, herein designated GAM RNA, of GAM336226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336226 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336226 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336226 RNA correlate with, and may be deduced from, the identity of the GAM336226 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336227 7167 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGTCGCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCTGAGAG Messenger 336227 (GAM336227) oligonucleotides modulates expression of respective target
GCGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336227 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336227 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACACAGCGAG encoded by the human genome.

ACTCCGTCTC GAM336227 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336227 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336227 precursor RNA is designated SEQ ID:7167, and is provided hereinbelow with reference to the sequence listing part.

GAM336227 precursor RNA folds onto itself, forming GAM336227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336227 precursor RNA, designated SEQ ID NO: 7167, and a schematic representation of a predicted secondary folding of GAM336227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336227 folded precursor RNA yielding a GAM336227 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336227 RNA, hereby incorporated herein. Expression of GAM336227 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336227 target RNA, herein designated GAM TARGET RNA.

GAM336227 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336227 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336227 RNA, herein designated GAM RNA, to target binding sites on GAM336227 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336227 target RNA into GAM336227 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336227 target genes. The mRNA of each one of this plurality of GAM336227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336227 RNA, herein designated GAM RNA, and which when bound by GAM336227 RNA causes inhibition of translation of the GAM336227 target mRNA into a corresponding GAM336227 target protein.

The mechanism of the translational inhibition exerted by GAM336227 RNA, herein designated GAM RNA, on one or more GAM336227 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336227 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336227 RNA, herein designated GAM RNA, of GAM336227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336227 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336227 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336227 RNA correlate with, and may be deduced from, the identity of the GAM336227 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336228 7168 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGATTGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 336228 (GAM336228) oligonucleotides modulates expression of respective target

CTGGAGGCTG genes whose function and utility is known in the art.

CAGTGAGCTA GAM336228 is a novel bioinformatically detectable regulatory, non protein

TGATCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336228 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAATAAT encoded by the human genome.

ATCCTGCCTC GAM336228 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336228 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336228 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336228 precursor RNA is designated SEQ ID:7168, and is provided hereinbelow with reference to the sequence listing part.

GAM336228 precursor RNA folds onto itself, forming GAM336228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336228 precursor RNA, designated SEQ ID NO: 7168, and a schematic representation of a predicted secondary folding of GAM336228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336228 folded precursor RNA yielding a GAM336228 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336228 RNA, hereby incorporated herein. Expression of GAM336228 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336228 target RNA, herein designated GAM TARGET RNA.

GAM336228 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336228 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336228 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336228 RNA, herein designated GAM RNA, to target binding sites on GAM336228 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336228 target RNA into GAM336228 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336228 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336228 target genes. The mRNA of each one of this plurality of GAM336228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336228 RNA, herein designated GAM RNA, and which when bound by GAM336228 RNA causes inhibition of translation of the GAM336228 target mRNA into a corresponding GAM336228 target protein.

The mechanism of the translational inhibition exerted by GAM336228 RNA, herein designated GAM RNA, on one or more GAM336228 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336228 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336228 RNA, herein designated GAM RNA, of GAM336228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336228 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336228 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336228 RNA correlate with, and may be deduced from, the identity of the GAM336228 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336229 7169 TGAGGCAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336229 (GAM336229) oligonucleotides modulates expression of respective target
ACAGAGGTTT genes whose function and utility is known in the art.

CAGTGAGCCG GAM336229 is a novel bioinformatically detectable regulatory, non protein
AGATCGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336229 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACTCTGTCTC GAM336229 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336229 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336229 precursor RNA is designated SEQ ID:7169, and is provided hereinbelow with reference to the sequence listing part.

GAM336229 precursor RNA folds onto itself, forming GAM336229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336229 precursor RNA, designated SEQ ID NO: 7169, and a schematic representation of a predicted secondary folding of GAM336229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336229 folded precursor RNA yielding a GAM336229 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336229 RNA, hereby incorporated herein. Expression of GAM336229 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336229 target RNA, herein designated GAM TARGET RNA.

GAM336229 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336229 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336229 RNA, herein designated GAM RNA, to target binding sites on GAM336229 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336229 target RNA into GAM336229 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336229 target genes. The mRNA of each one of this plurality of GAM336229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336229 RNA, herein designated GAM RNA, and which when bound by GAM336229 RNA causes inhibition of translation of the GAM336229 target mRNA into a corresponding GAM336229 target protein.

The mechanism of the translational inhibition exerted by GAM336229 RNA, herein designated GAM RNA, on one or more GAM336229 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336229 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336229 RNA, herein designated GAM RNA, of GAM336229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336229 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336229 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336229 RNA correlate with, and may be deduced from, the identity of the GAM336229 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336230 7173 TGAGGCGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336230 (GAM336230) oligonucleotides modulates expression of respective target
GTGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCGG GAM336230 is a novel bioinformatically detectable regulatory, non protein
AGATCTTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336230 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCTGTCTC GAM336230 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336230 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336230 precursor RNA is designated SEQ ID:7173, and is provided hereinbelow with reference to the sequence listing part.

GAM336230 precursor RNA folds onto itself, forming GAM336230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336230 precursor RNA, designated SEQ ID NO: 7173, and a schematic representation of a predicted secondary folding of GAM336230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336230 folded precursor RNA yielding a GAM336230 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336230 RNA, hereby incorporated herein. Expression of GAM336230 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336230 target RNA, herein designated GAM TARGET RNA.

GAM336230 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336230 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336230 RNA, herein designated GAM RNA, to target binding sites on GAM336230 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336230 target RNA into GAM336230 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336230 target genes. The mRNA of each one of this plurality of GAM336230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336230 RNA, herein designated GAM RNA, and which when bound by GAM336230 RNA causes inhibition of translation of the GAM336230 target mRNA into a corresponding GAM336230 target protein.

The mechanism of the translational inhibition exerted by GAM336230 RNA, herein designated GAM RNA, on one or more GAM336230 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336230 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336230 RNA, herein designated GAM RNA, of

GAM336230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336230 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336230 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336230 RNA correlate with, and may be deduced from, the identity of the GAM336230 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336231 7174 TGAGGGAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCATG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGGAG Messenger 336231 (GAM336231) oligonucleotides modulates expression of respective target

GTGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCC GAM336231 is a novel bioinformatically detectable regulatory, non protein

AGATTGCAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336231 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCCAG encoded by the human genome.

ACTCTGTCTC GAM336231 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336231 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336231 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336231 precursor RNA is designated SEQ ID:7174, and is provided hereinbelow with reference to the sequence listing part.

GAM336231 precursor RNA folds onto itself, forming GAM336231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336231 precursor RNA, designated SEQ ID NO: 7174, and a schematic representation of a predicted secondary folding of GAM336231 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336231 folded precursor RNA yielding a GAM336231 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336231 RNA, hereby incorporated herein. Expression of GAM336231 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336231 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336231 target RNA, herein designated GAM TARGET RNA.

GAM336231 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336231 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336231 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336231 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336231 RNA, herein designated GAM RNA, to target binding sites on GAM336231 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336231 target RNA into GAM336231 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336231 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336231 target genes. The mRNA of each one of this plurality of GAM336231 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336231 RNA, herein designated GAM RNA, and which when bound by GAM336231 RNA causes inhibition of translation of the GAM336231 target mRNA into a corresponding GAM336231 target protein.

The mechanism of the translational inhibition exerted by GAM336231 RNA, herein designated GAM RNA, on one or more GAM336231 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336231 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336231 RNA, herein designated GAM RNA, of GAM336231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336231 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336231 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336231 RNA correlate with, and may be deduced from, the identity of the GAM336231 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336232 7176 TGAGGTACGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 336232 (GAM336232) oligonucleotides modulates expression of respective target

GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGAGTGA GAM336232 is a novel bioinformatically detectable regulatory, non protein

GATCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336232 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGTGAGA encoded by the human genome.

CCCTATCTCA GAM336232 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336232 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336232 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336232 precursor RNA is designated SEQ ID:7176, and is provided hereinbelow with reference to the sequence listing part.

GAM336232 precursor RNA folds onto itself, forming GAM336232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336232 precursor RNA, designated SEQ ID NO: 7176, and a schematic representation of a predicted secondary folding of GAM336232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336232 folded precursor RNA yielding a GAM336232 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336232 RNA, hereby incorporated herein. Expression of GAM336232 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336232 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336232 target RNA, herein designated GAM TARGET RNA.

GAM336232 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336232 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336232 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336232 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336232 RNA, herein designated GAM RNA, to target binding sites on GAM336232 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336232 target RNA into GAM336232 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336232 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336232 target genes. The mRNA of each one of this plurality of GAM336232 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336232 RNA,

herein designated GAM RNA, and which when bound by GAM336232 RNA causes inhibition of translation of the GAM336232 target mRNA into a corresponding GAM336232 target protein.

The mechanism of the translational inhibition exerted by GAM336232 RNA, herein designated GAM RNA, on one or more GAM336232 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336232 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336232 RNA, herein designated GAM RNA, of GAM336232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336232 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336232 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336232 RNA correlate with, and may be deduced from, the identity of the GAM336232 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336233 7212 TGCTTGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAAAAGGCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTTGCAGT Messenger 336233 (GAM336233) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

TGTGCCACTG GAM336233 is a novel bioinformatically detectable regulatory, non protein

CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336233 was detected

TGGGCAACAG is described with additional reference to Figs. 9-15.

AGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336233 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336233 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336233 precursor RNA is designated SEQ ID:7212, and is provided hereinbelow with reference to the sequence listing part.

GAM336233 precursor RNA folds onto itself, forming GAM336233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336233 precursor RNA, designated SEQ ID NO: 7212, and a schematic representation of a predicted secondary folding of GAM336233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336233 folded precursor RNA yielding a GAM336233 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336233 RNA, hereby incorporated herein. Expression of GAM336233 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336233 target RNA, herein designated GAM TARGET RNA.

GAM336233 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336233 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336233 RNA, herein designated GAM RNA, to target binding sites on GAM336233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336233 target RNA

into GAM336233 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336233 target genes. The mRNA of each one of this plurality of GAM336233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336233 RNA, herein designated GAM RNA, and which when bound by GAM336233 RNA causes inhibition of translation of the GAM336233 target mRNA into a corresponding GAM336233 target protein.

The mechanism of the translational inhibition exerted by GAM336233 RNA, herein designated GAM RNA, on one or more GAM336233 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336233 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336233 RNA, herein designated GAM RNA, of GAM336233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336233 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336233 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336233 RNA correlate with, and may be deduced from, the identity of the GAM336233 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336234 7213 TGCTTGAACT Fig. 8 further provides a conceptual description of another novel bioinformatically

CGGGGTGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTGCAGTGA Messenger 336234 (GAM336234) oligonucleotides modulates expression of respective target

GCCAAGATCG genes whose function and utility is known in the art.

CCCCACTGCA GAM336234 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336234 was detected

GGCAACAATG is described with additional reference to Figs. 9-15.

CA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336234 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336234 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336234 precursor RNA is designated SEQ ID:7213, and is provided hereinbelow with reference to the sequence listing part.

GAM336234 precursor RNA folds onto itself, forming GAM336234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336234 precursor RNA, designated SEQ ID NO: 7213, and a schematic representation of a predicted secondary folding of GAM336234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336234 folded precursor RNA yielding a GAM336234 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336234 RNA, hereby incorporated herein. Expression of GAM336234 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336234 target RNA, herein designated GAM TARGET RNA.

GAM336234 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336234 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336234 RNA, herein designated GAM RNA, to target binding sites on GAM336234 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336234 target RNA into GAM336234 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336234 target genes. The mRNA of each one of this plurality of GAM336234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336234 RNA, herein designated GAM RNA, and which when bound by GAM336234 RNA causes inhibition of translation of the GAM336234 target mRNA into a corresponding GAM336234 target protein.

The mechanism of the translational inhibition exerted by GAM336234 RNA, herein designated GAM RNA, on one or more GAM336234 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336234 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336234 RNA, herein designated GAM RNA, of GAM336234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336234 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336234 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336234 RNA correlate with, and may be deduced from, the identity of the GAM336234 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336235 7215 TGGAATGTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAAGAACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTGATCTTG Messenger 336235 (GAM336235) oligonucleotides modulates expression of respective target

TGAAATCTGT genes whose function and utility is known in the art.

GGACCCTACA GAM336235 is a novel bioinformatically detectable regulatory, non protein
TTGGCACTTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336235 was detected
GTGTGTACCT is described with additional reference to Figs. 9-15.

AAGGGCTAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTCCCAAATA encoded by the human genome.

AAGTCATTCA GAM336235 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTGCTTTGCA GAM336235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAAACAGGTC GAM336235 precursor RNA does not encode a protein. A nucleotide sequence identical or

AAGTCCA highly similar to the nucleotide sequence of GAM336235 precursor RNA is designated SEQ ID:7215, and is provided hereinbelow with reference to the sequence listing part.

GAM336235 precursor RNA folds onto itself, forming GAM336235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336235 precursor RNA, designated SEQ ID NO: 7215, and a schematic representation of a predicted secondary folding of GAM336235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336235 folded precursor RNA yielding a GAM336235 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336235 RNA, hereby incorporated herein. Expression of GAM336235 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336235 target RNA, herein designated GAM TARGET RNA.

GAM336235 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336235 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336235 RNA, herein designated GAM RNA, to target binding sites on GAM336235 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336235 target RNA into GAM336235 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336235 target genes. The mRNA of each one of this plurality of GAM336235 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336235 RNA, herein designated GAM RNA, and which when bound by GAM336235 RNA causes inhibition of translation of the GAM336235 target mRNA into a corresponding GAM336235 target protein.

The mechanism of the translational inhibition exerted by GAM336235 RNA, herein designated GAM RNA, on one or more GAM336235 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336235 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336235 RNA, herein designated GAM RNA, of GAM336235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336235 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336235 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336235 RNA correlate with, and may be deduced from, the identity of the GAM336235 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336236 7239 TGGGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CGATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCCCAGGAG Messenger 336236 (GAM336236) oligonucleotides modulates expression of respective target
CTTAAAGCTG genes whose function and utility is known in the art.

CAGTAAGTGG GAM336236 is a novel bioinformatically detectable regulatory, non protein
TGACTTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336236 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAAGCAAGA encoded by the human genome.

CTCTGTCTCA GAM336236 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336236 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336236 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336236 precursor RNA is designated SEQ ID:7239, and is provided hereinbelow with reference to the sequence listing part.

GAM336236 precursor RNA folds onto itself, forming GAM336236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336236 precursor RNA, designated SEQ ID NO: 7239, and a schematic representation of a predicted secondary folding of GAM336236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336236 folded precursor RNA yielding a GAM336236 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336236 RNA, hereby incorporated herein. Expression of GAM336236 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336236 target RNA, herein designated GAM TARGET RNA.

GAM336236 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336236 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336236 RNA, herein designated GAM RNA, to target binding sites on GAM336236 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336236 target RNA into GAM336236 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336236 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336236 target genes. The mRNA of each one of this plurality of GAM336236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336236 RNA, herein designated GAM RNA, and which when bound by GAM336236 RNA causes inhibition of translation of the GAM336236 target mRNA into a corresponding GAM336236 target protein.

The mechanism of the translational inhibition exerted by GAM336236 RNA, herein designated GAM RNA, on one or more GAM336236 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336236 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336236 RNA, herein designated GAM RNA, of GAM336236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336236 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336236 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336236 RNA correlate with, and may be deduced from, the identity of the GAM336236 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336237 7309 TTGAACCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGCGGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCAGTGAG Messenger 336237 (GAM336237) oligonucleotides modulates expression of respective target
CCGAGATGGC genes whose function and utility is known in the art.

ACCACTGCAC GAM336237 is a novel bioinformatically detectable regulatory, non protein
TCCAGCCTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336237 was detected
GCAACAA is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336237 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336237 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336237 precursor RNA is designated SEQ ID:7309, and is provided hereinbelow with reference to the sequence listing part.

GAM336237 precursor RNA folds onto itself, forming GAM336237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336237 precursor RNA, designated SEQ ID NO: 7309, and a schematic representation of a predicted secondary folding of GAM336237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336237 folded precursor

RNA yielding a GAM336237 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336237 RNA, hereby incorporated herein. Expression of GAM336237 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336237 target RNA, herein designated GAM TARGET RNA.

GAM336237 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336237 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336237 RNA, herein designated GAM RNA, to target binding sites on GAM336237 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336237 target RNA into GAM336237 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336237 target genes. The mRNA of each one of this plurality of GAM336237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336237 RNA, herein designated GAM RNA, and which when bound by GAM336237 RNA causes inhibition of translation of the GAM336237 target mRNA into a corresponding GAM336237 target protein.

The mechanism of the translational inhibition exerted by GAM336237 RNA, herein designated GAM RNA, on one or more GAM336237 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336237 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336237 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336237 RNA, herein designated GAM RNA, of GAM336237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336237 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336237 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336237 RNA correlate with, and may be deduced from, the identity of the GAM336237 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336238 7314 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTGCAG Messenger 336238 (GAM336238) oligonucleotides modulates expression of respective target
TGAGCCAAGA genes whose function and utility is known in the art.

TTGTGCCACT GAM336238 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336238 was detected
CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336238 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336238 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336238 precursor RNA is designated SEQ ID:7314, and is provided hereinbelow with reference to the sequence listing part.

GAM336238 precursor RNA folds onto itself, forming GAM336238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336238 precursor RNA, designated SEQ ID NO: 7314, and a schematic representation of a predicted secondary folding of GAM336238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336238 folded precursor RNA yielding a GAM336238 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336238 RNA, hereby incorporated herein. Expression of GAM336238 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336238 target RNA, herein designated GAM TARGET RNA.

GAM336238 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336238 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336238 RNA, herein designated GAM RNA, to target binding sites on GAM336238 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336238 target RNA into GAM336238 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336238 target genes. The mRNA of each one of this plurality of GAM336238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336238 RNA, herein designated GAM RNA, and which when bound by GAM336238 RNA causes inhibition of translation of the GAM336238 target mRNA into a corresponding GAM336238 target protein.

The mechanism of the translational inhibition exerted by GAM336238 RNA, herein

designated GAM RNA, on one or more GAM336238 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336238 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336238 RNA, herein designated GAM RNA, of GAM336238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336238 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336238 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336238 RNA correlate with, and may be deduced from, the identity of the GAM336238 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336239 7316 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336239 (GAM336239) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

CCATGCCATT GAM336239 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336239 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336239 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336239 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336239 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336239 precursor RNA is designated SEQ ID:7316, and is provided hereinbelow with reference to the sequence listing part.

GAM336239 precursor RNA folds onto itself, forming GAM336239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336239 precursor RNA, designated SEQ ID NO: 7316, and a schematic representation of a predicted secondary folding of GAM336239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336239 folded precursor RNA yielding a GAM336239 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336239 RNA, hereby incorporated herein. Expression of GAM336239 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336239 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336239 target RNA, herein designated GAM TARGET RNA.

GAM336239 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336239 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336239 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336239 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336239 RNA, herein designated GAM RNA, to target binding sites on GAM336239 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336239 target RNA into GAM336239 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336239 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336239 target genes. The mRNA of each one of this plurality of GAM336239 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336239 RNA, herein designated GAM RNA, and which when bound by GAM336239 RNA causes inhibition of translation of the GAM336239 target mRNA into a corresponding GAM336239 target protein.

The mechanism of the translational inhibition exerted by GAM336239 RNA, herein designated GAM RNA, on one or more GAM336239 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336239 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336239 RNA, herein designated GAM RNA, of GAM336239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336239 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336239 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336239 RNA correlate with, and may be deduced from, the identity of the GAM336239 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336240 7322 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTTCAG Messenger 336240 (GAM336240) oligonucleotides modulates expression of respective target

TGAGCCGAGC genes whose function and utility is known in the art.

CGAGATTGTG GAM336240 is a novel bioinformatically detectable regulatory, non protein

TCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336240 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

A encoded by the human genome.

GAM336240 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336240 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336240 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336240 precursor RNA is designated SEQ ID:7322, and is provided hereinbelow with reference to the sequence listing part.

GAM336240 precursor RNA folds onto itself, forming GAM336240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336240 precursor RNA, designated SEQ ID NO: 7322, and a schematic representation of a predicted secondary folding of GAM336240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336240 folded precursor RNA yielding a GAM336240 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336240 RNA, hereby incorporated herein. Expression of GAM336240 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336240 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336240 target RNA, herein designated GAM TARGET RNA.

GAM336240 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336240 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336240 RNA, herein designated GAM RNA, to target

binding sites on GAM336240 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336240 target RNA into GAM336240 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336240 target genes. The mRNA of each one of this plurality of GAM336240 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336240 RNA, herein designated GAM RNA, and which when bound by GAM336240 RNA causes inhibition of translation of the GAM336240 target mRNA into a corresponding GAM336240 target protein.

The mechanism of the translational inhibition exerted by GAM336240 RNA, herein designated GAM RNA, on one or more GAM336240 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336240 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336240 RNA, herein designated GAM RNA, of GAM336240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336240 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336240 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336240 RNA correlate with, and may be deduced from, the identity of the GAM336240 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336241 7323 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGTTGCAG Messenger 336241 (GAM336241) oligonucleotides modulates expression of respective target

TGAGCCAAGA genes whose function and utility is known in the art.

TTGTGCCACT GAM336241 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336241 was detected

CTGGGCAATA is described with additional reference to Figs. 9-15.

AGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336241 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336241 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336241 precursor RNA is designated SEQ ID:7323, and is provided hereinbelow with reference to the sequence listing part.

GAM336241 precursor RNA folds onto itself, forming GAM336241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336241 precursor RNA, designated SEQ ID NO: 7323, and a schematic representation of a predicted secondary folding of GAM336241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336241 folded precursor RNA yielding a GAM336241 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336241 RNA, hereby incorporated herein. Expression of GAM336241 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336241 target RNA, herein designated GAM TARGET RNA.

GAM336241 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336241 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336241 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336241 RNA, herein designated GAM RNA, to target binding sites on GAM336241 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336241 target RNA into GAM336241 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336241 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336241 target genes. The mRNA of each one of this plurality of GAM336241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336241 RNA, herein designated GAM RNA, and which when bound by GAM336241 RNA causes inhibition of translation of the GAM336241 target mRNA into a corresponding GAM336241 target protein.

The mechanism of the translational inhibition exerted by GAM336241 RNA, herein designated GAM RNA, on one or more GAM336241 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336241 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336241 RNA, herein designated GAM RNA, of GAM336241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336241 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336241 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336241 RNA correlate with, and may be deduced from, the identity of the GAM336241 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336242 7325 TTGCTTGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAGCTGCAG Messenger 336242 (GAM336242) oligonucleotides modulates expression of respective target

TAAGTGGTGA genes whose function and utility is known in the art.

CTTGCCACTG GAM336242 is a novel bioinformatically detectable regulatory, non protein
CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336242 was detected

TGGGCAACAA is described with additional reference to Figs. 9-15.

AGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336242 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336242 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336242 precursor RNA is designated SEQ ID:7325, and is provided hereinbelow with reference to the sequence listing part.

GAM336242 precursor RNA folds onto itself, forming GAM336242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336242 precursor RNA, designated SEQ ID NO: 7325, and a schematic representation of a predicted secondary folding of GAM336242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336242 folded precursor RNA yielding a GAM336242 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336242 RNA, hereby incorporated herein. Expression of GAM336242 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336242 target RNA, herein designated GAM TARGET RNA.

GAM336242 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336242 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336242 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336242 RNA, herein designated GAM RNA, to target binding sites on GAM336242 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336242 target RNA into GAM336242 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336242 target genes. The mRNA of each one of this plurality of GAM336242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336242 RNA, herein designated GAM RNA, and which when bound by GAM336242 RNA causes inhibition of translation of the GAM336242 target mRNA into a corresponding GAM336242 target protein.

The mechanism of the translational inhibition exerted by GAM336242 RNA, herein designated GAM RNA, on one or more GAM336242 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336242 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336242 RNA, herein designated GAM RNA, of GAM336242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336242 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336242 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336242 RNA correlate with, and may be deduced from, the identity of the GAM336242 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336243 7326 TTGCTTGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCAGAGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCTGCAG Messenger 336243 (GAM336243) oligonucleotides modulates expression of respective target
TGAGCTGTGA genes whose function and utility is known in the art.

TCACACCACT GAM336243 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336243 was detected
CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336243 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336243 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336243 precursor RNA is designated SEQ ID:7326, and is provided hereinbelow with reference to the sequence listing part.

GAM336243 precursor RNA folds onto itself, forming GAM336243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336243 precursor RNA, designated SEQ ID NO: 7326, and a schematic representation of a predicted secondary folding of GAM336243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336243 folded precursor RNA yielding a GAM336243 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336243 RNA, hereby incorporated herein. Expression of GAM336243 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336243 target RNA, herein designated GAM TARGET RNA.

GAM336243 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336243 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336243 RNA, herein designated GAM RNA, to target binding sites on GAM336243 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336243 target RNA into GAM336243 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336243 target genes. The mRNA of each one of this plurality of GAM336243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336243 RNA, herein designated GAM RNA, and which when bound by GAM336243 RNA causes inhibition of translation of the GAM336243 target mRNA into a corresponding GAM336243 target protein.

The mechanism of the translational inhibition exerted by GAM336243 RNA, herein designated GAM RNA, on one or more GAM336243 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336243 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336243 RNA, herein designated GAM RNA, of GAM336243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336243 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336243 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336243 RNA correlate with, and may be deduced from, the identity of the GAM336243 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336244 7329 TTGGAGCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAAGGTTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGCAGTGA Messenger 336244 (GAM336244) oligonucleotides modulates expression of respective target
GCTGTGATCA genes whose function and utility is known in the art.

TGCCACTGCA GAM336244 is a novel bioinformatically detectable regulatory, non protein
CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336244 was detected
GGCAACAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336244 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336244 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336244 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336244 precursor RNA is designated SEQ ID:7329, and is provided hereinbelow with reference to the sequence listing part.

GAM336244 precursor RNA folds onto itself, forming GAM336244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336244 precursor RNA, designated SEQ ID NO: 7329, and a schematic representation of a predicted secondary folding of GAM336244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336244 folded precursor RNA yielding a GAM336244 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336244 RNA, hereby incorporated herein. Expression of GAM336244 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336244 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336244 target RNA, herein designated GAM TARGET RNA.

GAM336244 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336244 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336244 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336244 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336244 RNA, herein designated GAM RNA, to target binding sites on GAM336244 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336244 target RNA into GAM336244 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336244 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336244 target genes. The mRNA of each one of this plurality of GAM336244 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336244 RNA, herein designated GAM RNA, and which when bound by GAM336244 RNA causes inhibition of translation of the GAM336244 target mRNA into a corresponding GAM336244 target protein.

The mechanism of the translational inhibition exerted by GAM336244 RNA, herein designated GAM RNA, on one or more GAM336244 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336244 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336244 RNA, herein designated GAM RNA, of GAM336244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336244 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336244 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336244 RNA correlate with, and may be deduced from, the identity of the GAM336244 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336245 6836 GGTCCAGATG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCCATGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGACTGAGGG Messenger 336245 (GAM336245) oligonucleotides modulates expression of respective target

GCGGACGTGT genes whose function and utility is known in the art.

TCCTGGGTGC GAM336245 is a novel bioinformatically detectable regulatory, non protein

TTCCTTCATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336245 was detected

TCAGTCTCCT is described with additional reference to Figs. 9-15.

CACTGAGACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336245 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336245 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336245 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336245 precursor RNA is designated SEQ ID:6836, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6836 is located from position 253589 to position 253668 relative to chromosome 16 on the `+` strand.

GAM336245 precursor RNA folds onto itself, forming GAM336245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336245 precursor RNA, designated SEQ ID NO: 6836, and a schematic representation of a predicted secondary folding of GAM336245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336245 folded precursor RNA yielding a GAM336245 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336245 RNA, hereby incorporated herein.

GAM336245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336245 target RNA, herein designated GAM TARGET RNA.

GAM336245 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336245 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336245 RNA, herein designated GAM RNA, to target binding sites on GAM336245 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336245 target RNA into GAM336245 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336245 target genes. The mRNA of each one of this plurality of GAM336245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336245 RNA, herein designated GAM RNA, and which when bound by GAM336245 RNA causes inhibition of translation of the GAM336245 target mRNA into a corresponding GAM336245 target protein.

The mechanism of the translational inhibition exerted by GAM336245 RNA, herein designated GAM RNA, on one or more GAM336245 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336245 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336245 RNA, herein designated GAM RNA, of GAM336245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336245 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336245 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336245 RNA correlate with, and may be deduced from, the identity of the GAM336245 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336246 5803 AGTCACCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCCATTGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTAGTCTTAT Messenger 336246 (GAM336246) oligonucleotides modulates expression of respective target

TTTCATCACC genes whose function and utility is known in the art.

GTGGGCGTAC GAM336246 is a novel bioinformatically detectable regulatory, non protein

CCTGTGGGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336246 was detected

GATGTTAAAC is described with additional reference to Figs. 9-15.

GTACTCTAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTCTGTTGGC encoded by the human genome.

T GAM336246 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336246 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336246 precursor RNA is designated SEQ ID:5803, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5803 is located from position 265415 to position 265505 relative to chromosome 12 on the `-` strand.

GAM336246 precursor RNA folds onto itself, forming GAM336246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336246 precursor RNA, designated SEQ ID NO: 5803, and a schematic representation of a predicted secondary folding of GAM336246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336246 folded precursor RNA yielding a GAM336246 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336246 RNA, hereby incorporated herein.

GAM336246 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336246 target RNA, herein designated GAM TARGET RNA.

GAM336246 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336246 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336246 RNA, herein designated GAM RNA, to target binding sites on GAM336246 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336246 target RNA into GAM336246 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336246 target genes. The mRNA of each one of this plurality of GAM336246 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336246 RNA, herein designated GAM RNA, and which when bound by GAM336246 RNA causes inhibition of translation of the GAM336246 target mRNA into a corresponding GAM336246 target protein.

The mechanism of the translational inhibition exerted by GAM336246 RNA, herein designated GAM RNA, on one or more GAM336246 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336246 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336246 RNA, herein designated GAM RNA, of GAM336246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336246 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336246 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336246 RNA correlate with, and may be deduced from, the identity of the GAM336246 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336247 6642 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 336247 (GAM336247) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATCAC GAM336247 is a novel bioinformatically detectable regulatory, non protein

ATCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336247 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGACTCC encoded by the human genome.

GAM336247 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336247 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336247 precursor RNA is designated SEQ ID:6642, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6642 is located from position 377662 to position 377749 relative to chromosome 16 on the `+` strand.

GAM336247 precursor RNA folds onto itself, forming GAM336247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336247 precursor RNA, designated SEQ ID NO: 6642, and a schematic representation of a predicted secondary folding of GAM336247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336247 folded precursor RNA yielding a GAM336247 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336247 RNA, hereby incorporated herein.

GAM336247 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336247 target RNA, herein designated GAM TARGET RNA.

GAM336247 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336247 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336247 RNA, herein designated GAM RNA, to target binding sites on GAM336247 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336247 target RNA

into GAM336247 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336247 target genes. The mRNA of each one of this plurality of GAM336247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336247 RNA, herein designated GAM RNA, and which when bound by GAM336247 RNA causes inhibition of translation of the GAM336247 target mRNA into a corresponding GAM336247 target protein.

The mechanism of the translational inhibition exerted by GAM336247 RNA, herein designated GAM RNA, on one or more GAM336247 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336247 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336247 RNA, herein designated GAM RNA, of GAM336247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336247 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336247 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336247 RNA correlate with, and may be deduced from, the identity of the GAM336247 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336251 7050 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336251 (GAM336251) oligonucleotides modulates expression of respective target

TGAATGAAGA genes whose function and utility is known in the art.

TCGTGCCACT GAM336251 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336251 was detected

CTGGGCGATA is described with additional reference to Figs. 9-15.

GAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336251 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336251 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336251 precursor RNA is designated SEQ ID:7050, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7050 is located from position 851357 to position 851432 relative to chromosome 19 on the `+` strand.

GAM336251 precursor RNA folds onto itself, forming GAM336251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336251 precursor RNA, designated SEQ ID NO: 7050, and a schematic representation of a predicted secondary folding of GAM336251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336251 folded precursor RNA yielding a GAM336251 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336251 RNA, hereby incorporated herein.

GAM336251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336251 target RNA, herein designated GAM TARGET RNA.

GAM336251 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336251 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336251 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336251 RNA, herein designated GAM RNA, to target binding sites on GAM336251 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336251 target RNA into GAM336251 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336251 target genes. The mRNA of each one of this plurality of GAM336251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336251 RNA, herein designated GAM RNA, and which when bound by GAM336251 RNA causes inhibition of translation of the GAM336251 target mRNA into a corresponding GAM336251 target protein.

The mechanism of the translational inhibition exerted by GAM336251 RNA, herein designated GAM RNA, on one or more GAM336251 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336251 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336251 RNA, herein designated GAM RNA, of GAM336251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336251 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336251 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336251 RNA correlate with, and may be deduced from, the identity of the GAM336251 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336252 6200 CTGAGCTTAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTATCTTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTCAATTC Messenger 336252 (GAM336252) oligonucleotides modulates expression of respective target

ACCGGAGTCT genes whose function and utility is known in the art.

CAAAACCTGG GAM336252 is a novel bioinformatically detectable regulatory, non protein
CAGGTGTTAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336252 was detected
CATCTTCCTG is described with additional reference to Figs. 9-15.

AGGCACCGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTCGGGACT encoded by the human genome.

GCCAGAGGCC GAM336252 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGCACAG GAM336252 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336252 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336252 precursor RNA is designated SEQ ID:6200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6200 is located from position 960158 to position 960264 relative to chromosome 17 on the `+` strand.

GAM336252 precursor RNA folds onto itself, forming GAM336252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336252 precursor RNA, designated SEQ ID NO: 6200, and a schematic representation of a predicted secondary folding of GAM336252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336252 folded precursor RNA yielding a GAM336252 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336252 RNA, hereby incorporated herein.

GAM336252 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336252 target RNA, herein designated GAM TARGET RNA.

GAM336252 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336252 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336252 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336252 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336252 RNA, herein designated GAM RNA, to target binding sites on GAM336252 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336252 target RNA into GAM336252 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336252 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336252 target genes. The mRNA of each one of this plurality of GAM336252 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336252 RNA, herein designated GAM RNA, and which when bound by GAM336252 RNA causes inhibition of translation of the GAM336252 target mRNA into a corresponding GAM336252 target protein.

The mechanism of the translational inhibition exerted by GAM336252 RNA, herein designated GAM RNA, on one or more GAM336252 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336252 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336252 RNA, herein designated GAM RNA, of GAM336252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336252 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336252 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336252 RNA correlate with, and may be deduced from, the identity of the GAM336252 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336255 6921 GTGTAGCATG Fig. 8 further provides a conceptual description of another novel bioinformatically
CATCAGTACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCACCTACTG Messenger 336255 (GAM336255) oligonucleotides modulates expression of respective target
TATGGATATA genes whose function and utility is known in the art.

CTATGCTTTA GAM336255 is a novel bioinformatically detectable regulatory, non protein
AAAATCCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336255 was detected
CATTAGGCCA is described with additional reference to Figs. 9-15.

GGTGCGGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCAC encoded by the human genome.

GAM336255 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336255 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336255 precursor RNA is designated SEQ ID:6921, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6921 is located from position 1228075 to position 1228159 relative to chromosome 17 on the `+` strand.

GAM336255 precursor RNA folds onto itself, forming GAM336255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336255 precursor RNA, designated SEQ ID NO: 6921, and a schematic representation of a predicted secondary folding of GAM336255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336255 folded precursor RNA yielding a GAM336255 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336255 RNA, hereby incorporated herein.

GAM336255 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336255 target RNA, herein designated GAM TARGET RNA.

GAM336255 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336255 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336255 RNA, herein designated GAM RNA, to target binding sites on GAM336255 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336255 target RNA into GAM336255 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336255 target genes. The mRNA of each one of this plurality of GAM336255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336255 RNA, herein designated GAM RNA, and which when bound by GAM336255 RNA causes inhibition of translation of the GAM336255 target mRNA into a corresponding GAM336255 target protein.

The mechanism of the translational inhibition exerted by GAM336255 RNA, herein designated GAM RNA, on one or more GAM336255 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336255 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336255 RNA, herein designated GAM RNA, of GAM336255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336255 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336255 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336255 RNA correlate with, and may be deduced from, the identity of the GAM336255 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336256 6922 GTGTAGCATG Fig. 8 further provides a conceptual description of another novel bioinformatically
CATCAGTACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCACCTACTG Messenger 336256 (GAM336256) oligonucleotides modulates expression of respective target
TATGGATATA genes whose function and utility is known in the art.

CTATGCTTTA GAM336256 is a novel bioinformatically detectable regulatory, non protein
AAAATCCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336256 was detected
CATTAGGCCA is described with additional reference to Figs. 9-15.

GGTGCGGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCACGC encoded by the human genome.

GAM336256 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336256 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336256 precursor RNA is designated SEQ ID:6922, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6922 is located from position 1228075 to position 1228161 relative to chromosome 17 on the `+` strand.

GAM336256 precursor RNA folds onto itself, forming GAM336256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336256 precursor RNA, designated SEQ ID NO: 6922, and a schematic representation of a predicted secondary folding of GAM336256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336256 folded precursor RNA yielding a GAM336256 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336256 RNA, hereby incorporated herein.

GAM336256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336256 target RNA, herein designated GAM TARGET RNA.

GAM336256 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336256 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336256 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336256 RNA, herein designated GAM RNA, to target binding sites on GAM336256 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336256 target RNA into GAM336256 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336256 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336256 target genes. The mRNA of each one of this plurality of GAM336256 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336256 RNA, herein designated GAM RNA, and which when bound by GAM336256 RNA causes inhibition of translation of the GAM336256 target mRNA into a corresponding GAM336256 target protein.

The mechanism of the translational inhibition exerted by GAM336256 RNA, herein designated GAM RNA, on one or more GAM336256 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336256 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336256 RNA, herein designated GAM RNA, of GAM336256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336256 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336256 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336256 RNA correlate with, and may be deduced from, the identity of the GAM336256 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336257 6496 GCAGGGATTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGACTAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTGCACCTT Messenger 336257 (GAM336257) oligonucleotides modulates expression of respective target

CTGAACCATG genes whose function and utility is known in the art.

AGCTAGACCA GAM336257 is a novel bioinformatically detectable regulatory, non protein

TGTCTGGAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336257 was detected

CTGGAACCTG is described with additional reference to Figs. 9-15.

GTGACCCAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTCCCTGC encoded by the human genome.

GAM336257 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336257 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336257 precursor RNA is designated SEQ ID:6496, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6496 is located from position 1312908 to position 1312995 relative to chromosome 19 on the `+` strand.

GAM336257 precursor RNA folds onto itself, forming GAM336257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336257 precursor RNA, designated SEQ ID NO: 6496, and a schematic representation of a predicted secondary folding of GAM336257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336257 folded precursor RNA yielding a GAM336257 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336257 RNA, hereby incorporated herein.

GAM336257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336257 target RNA, herein designated GAM TARGET RNA.

GAM336257 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336257 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336257 RNA, herein designated GAM RNA, to target binding sites on GAM336257 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336257 target RNA into GAM336257 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336257 target genes. The mRNA of each one of this plurality of GAM336257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336257 RNA, herein designated GAM RNA, and which when bound by GAM336257 RNA causes inhibition of translation of the GAM336257 target mRNA into a corresponding GAM336257 target protein.

The mechanism of the translational inhibition exerted by GAM336257 RNA, herein designated GAM RNA, on one or more GAM336257 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336257 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336257 RNA, herein designated GAM RNA, of GAM336257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336257 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336257 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336257 RNA correlate with, and may be deduced from, the identity of the GAM336257 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336259 6548 GCTGTAACAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAGCAGGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGAATGGCT Messenger 336259 (GAM336259) oligonucleotides modulates expression of respective target
CCACCCACAG genes whose function and utility is known in the art.

GGCCACAAGA GAM336259 is a novel bioinformatically detectable regulatory, non protein
AACAAACCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336259 was detected
TGGAGAGTTC is described with additional reference to Figs. 9-15.

CAGATCTGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCAGC encoded by the human genome.

GAM336259 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336259 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336259 precursor RNA is designated SEQ ID:6548, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6548 is located from position 1889566 to position 1889651 relative to chromosome 8 on the `+` strand.

GAM336259 precursor RNA folds onto itself, forming GAM336259 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336259 precursor RNA, designated SEQ ID NO: 6548, and a schematic representation of a predicted secondary folding of GAM336259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336259 folded precursor RNA yielding a GAM336259 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336259 RNA, hereby incorporated herein.

GAM336259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336259 target RNA, herein designated GAM TARGET RNA.

GAM336259 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336259 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336259 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336259 RNA, herein designated GAM RNA, to target binding sites on GAM336259 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336259 target RNA into GAM336259 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336259 target genes. The mRNA of each one of this plurality of GAM336259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336259 RNA,

herein designated GAM RNA, and which when bound by GAM336259 RNA causes inhibition of translation of the GAM336259 target mRNA into a corresponding GAM336259 target protein.

The mechanism of the translational inhibition exerted by GAM336259 RNA, herein designated GAM RNA, on one or more GAM336259 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336259 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336259 RNA, herein designated GAM RNA, of GAM336259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336259 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336259 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336259 RNA correlate with, and may be deduced from, the identity of the GAM336259 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336260 6463 GAGTCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTCGGGAGG Messenger 336260 (GAM336260) oligonucleotides modulates expression of respective target

TGGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCTAA GAM336260 is a novel bioinformatically detectable regulatory, non protein

GATCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336260 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCGAA encoded by the human genome.

ACTCCATCTC GAM336260 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336260 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336260 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336260 precursor RNA is designated SEQ ID:6463, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6463 is located from position 1984914 to position 1985013 relative to chromosome X on the `+` strand.

GAM336260 precursor RNA folds onto itself, forming GAM336260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336260 precursor RNA, designated SEQ ID NO: 6463, and a schematic representation of a predicted secondary folding of GAM336260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336260 folded precursor RNA yielding a GAM336260 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336260 RNA, hereby incorporated herein. Expression of GAM336260 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336260 target RNA, herein designated GAM TARGET RNA.

GAM336260 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336260 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336260 RNA, herein designated GAM RNA, to target binding sites on GAM336260 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336260 target RNA into GAM336260 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336260 target genes. The mRNA of each one of this plurality of GAM336260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336260 RNA, herein designated GAM RNA, and which when bound by GAM336260 RNA causes inhibition of translation of the GAM336260 target mRNA into a corresponding GAM336260 target protein.

The mechanism of the translational inhibition exerted by GAM336260 RNA, herein designated GAM RNA, on one or more GAM336260 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336260 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336260 RNA, herein designated GAM RNA, of GAM336260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336260 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336260 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336260 RNA correlate with, and may be deduced from, the identity of the GAM336260 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336261 6760 GGCTCCGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTGCAGTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGGCAGCT Messenger 336261 (GAM336261) oligonucleotides modulates expression of respective target

GGAGGTGGAG genes whose function and utility is known in the art.

CAACCTGATG GAM336261 is a novel bioinformatically detectable regulatory, non protein

TCGTGGTTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336261 was detected

GCATCCACGA is described with additional reference to Figs. 9-15.

CAGCTTCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGACAAGTG encoded by the human genome.

ATCCTAGCC GAM336261 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336261 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336261 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336261 precursor RNA is designated SEQ ID:6760, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6760 is located from position 2004805 to position 2004903 relative to chromosome 10 on the `+` strand.

GAM336261 precursor RNA folds onto itself, forming GAM336261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336261 precursor RNA, designated SEQ ID NO: 6760, and a schematic representation of a predicted secondary folding of GAM336261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336261 folded precursor RNA yielding a GAM336261 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336261 RNA, hereby incorporated herein.

GAM336261 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336261 target RNA, herein designated GAM TARGET RNA.

GAM336261 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336261 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336261 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336261 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336261 RNA, herein designated GAM RNA, to target binding sites on GAM336261 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336261 target RNA into GAM336261 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336261 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336261 target genes. The mRNA of each one of this plurality of GAM336261 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336261 RNA, herein designated GAM RNA, and which when bound by GAM336261 RNA causes inhibition of translation of the GAM336261 target mRNA into a corresponding GAM336261 target protein.

The mechanism of the translational inhibition exerted by GAM336261 RNA, herein designated GAM RNA, on one or more GAM336261 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336261 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336261 RNA, herein designated GAM RNA, of GAM336261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336261 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336261 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336261 RNA correlate with, and may be deduced from, the identity of the GAM336261 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336264 6970 TAGGAATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGTTGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGGTAGGCT Messenger 336264 (GAM336264) oligonucleotides modulates expression of respective target
TGGGAGCCAG genes whose function and utility is known in the art.

GCTGCCCTGA GAM336264 is a novel bioinformatically detectable regulatory, non protein
ACTCTGGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336264 was detected
TCCACACTTC is described with additional reference to Figs. 9-15.

TA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336264 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336264 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336264 precursor RNA is designated SEQ ID:6970, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6970 is located from position 2764962 to position 2765033 relative to chromosome 20 on the `+` strand.

GAM336264 precursor RNA folds onto itself, forming GAM336264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336264 precursor RNA, designated SEQ ID NO: 6970, and a schematic representation of a predicted secondary folding of GAM336264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336264 folded precursor RNA yielding a GAM336264 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336264 RNA, hereby incorporated herein.

GAM336264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336264 target RNA, herein designated GAM TARGET RNA.

GAM336264 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336264 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336264 RNA, herein designated GAM RNA, to target binding sites on GAM336264 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336264 target RNA into GAM336264 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336264 target genes. The mRNA of each one of this plurality of GAM336264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336264 RNA, herein designated GAM RNA, and which when bound by GAM336264 RNA causes inhibition of translation of the GAM336264 target mRNA into a corresponding GAM336264 target protein.

The mechanism of the translational inhibition exerted by GAM336264 RNA, herein designated GAM RNA, on one or more GAM336264 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336264 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336264 RNA, herein designated GAM RNA, of GAM336264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336264 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336264 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336264 RNA correlate with, and may be deduced from, the identity of the GAM336264 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336267 6293 GAAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAATCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AAGGTGGAGG Messenger 336267 (GAM336267) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336267 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336267 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

CGACAGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTCCGTC encoded by the human genome.

GAM336267 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336267 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336267 precursor RNA is designated SEQ ID:6293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6293 is located from position 2999427 to position 2999516 relative to chromosome 19 on the `+` strand.

GAM336267 precursor RNA folds onto itself, forming GAM336267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336267 precursor RNA, designated SEQ ID NO: 6293, and a schematic representation of a predicted secondary folding of GAM336267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336267 folded precursor RNA yielding a GAM336267 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336267 RNA, hereby incorporated herein.

GAM336267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336267 target RNA, herein designated GAM TARGET RNA.

GAM336267 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336267 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336267 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336267 RNA, herein designated GAM RNA, to target binding sites on GAM336267 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336267 target RNA into GAM336267 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336267 target genes. The mRNA of each one of this plurality of GAM336267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336267 RNA, herein designated GAM RNA, and which when bound by GAM336267 RNA causes inhibition of translation of the GAM336267 target mRNA into a corresponding GAM336267 target protein.

The mechanism of the translational inhibition exerted by GAM336267 RNA, herein designated GAM RNA, on one or more GAM336267 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336267 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336267 RNA, herein designated GAM RNA, of GAM336267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336267 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336267 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336267 RNA correlate with, and may be deduced from, the identity of the GAM336267 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336270 5995 CACCCGTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGGATTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TAAGACAAAG Messenger 336270 (GAM336270) oligonucleotides modulates expression of respective target
GAGAAGTCTT genes whose function and utility is known in the art.

AAAGCCTTAC GAM336270 is a novel bioinformatically detectable regulatory, non protein
AGCGTCTTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336270 was detected
GTCTTAGATC is described with additional reference to Figs. 9-15.

ACATTTAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACCCGGTA encoded by the human genome.

CAGGTG GAM336270 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336270 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336270 precursor RNA is designated SEQ ID:5995, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5995 is located from position 3269951 to position 3270046 relative to chromosome 10 on the `+` strand.

GAM336270 precursor RNA folds onto itself, forming GAM336270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336270 precursor RNA, designated SEQ ID NO: 5995, and a schematic representation of a predicted secondary folding of GAM336270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336270 folded precursor RNA yielding a GAM336270 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336270 RNA, hereby incorporated herein.

GAM336270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336270 target RNA, herein designated GAM TARGET RNA.

GAM336270 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336270 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336270 RNA, herein designated GAM RNA, to target binding sites on GAM336270 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336270 target RNA into GAM336270 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336270 target genes. The mRNA of each one of this plurality of GAM336270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336270 RNA, herein designated GAM RNA, and which when bound by GAM336270 RNA causes inhibition of translation of the GAM336270 target mRNA into a corresponding GAM336270 target protein.

The mechanism of the translational inhibition exerted by GAM336270 RNA, herein designated GAM RNA, on one or more GAM336270 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336270 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336270 RNA, herein designated GAM RNA, of GAM336270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336270 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336270 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336270 RNA correlate with, and may be deduced from, the identity of the GAM336270 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336271 5776 AGGCGCTAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTAAGGCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCTGGGAAG Messenger 336271 (GAM336271) oligonucleotides modulates expression of respective target

AGCTGTTAAG genes whose function and utility is known in the art.

ATTAGACTGT GAM336271 is a novel bioinformatically detectable regulatory, non protein

TCTCCCAAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336271 was detected

AGCCAATAAT is described with additional reference to Figs. 9-15.

TCTGAGTGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

T encoded by the human genome.

GAM336271 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336271 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336271 precursor RNA is designated SEQ ID:5776, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5776 is located from position 3307949 to position 3308029 relative to chromosome 12 on the `+` strand.

GAM336271 precursor RNA folds onto itself, forming GAM336271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336271 precursor RNA, designated SEQ ID NO: 5776, and a schematic representation of a predicted secondary folding of GAM336271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336271 folded precursor RNA yielding a GAM336271 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336271 RNA, hereby incorporated herein.

GAM336271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336271 target RNA, herein designated GAM TARGET RNA.

GAM336271 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336271 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336271 RNA, herein designated GAM RNA, to target binding sites on GAM336271 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336271 target RNA into GAM336271 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336271 target genes. The mRNA of each one of this plurality of GAM336271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336271 RNA, herein designated GAM RNA, and which when bound by GAM336271 RNA causes inhibition of translation of the GAM336271 target mRNA into a corresponding GAM336271 target protein.

The mechanism of the translational inhibition exerted by GAM336271 RNA, herein designated GAM RNA, on one or more GAM336271 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336271 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336271 RNA, herein designated GAM RNA, of GAM336271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336271 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336271 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336271 RNA correlate with, and may be deduced from, the identity of the GAM336271 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336272 7249 TGGTAGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAGATGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCAGAATCT Messenger 336272 (GAM336272) oligonucleotides modulates expression of respective target

TTTGTCTCTG genes whose function and utility is known in the art.

AGAAGATGCC GAM336272 is a novel bioinformatically detectable regulatory, non protein

TAGAGAAAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336272 was detected

GGAATTCAAT is described with additional reference to Figs. 9-15.

AGGATAAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCATTCTCCA encoded by the human genome.

GATTCACATT GAM336272 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TATTTTCCTA GAM336272 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

CCA GAM336272 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336272 precursor RNA is designated SEQ ID:7249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7249 is located from position 3477981 to position 3478093

relative to chromosome 12 on the `+` strand.

GAM336272 precursor RNA folds onto itself, forming GAM336272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336272 precursor RNA, designated SEQ ID NO: 7249, and a schematic representation of a predicted secondary folding of GAM336272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336272 folded precursor RNA yielding a GAM336272 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336272 RNA, hereby incorporated herein.

GAM336272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336272 target RNA, herein designated GAM TARGET RNA.

GAM336272 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336272 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336272 RNA, herein designated GAM RNA, to target binding sites on GAM336272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336272 target RNA into GAM336272 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336272 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336272 target genes. The mRNA of each one of this plurality of GAM336272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336272 RNA, herein designated GAM RNA, and which when bound by GAM336272 RNA causes inhibition of translation of the GAM336272 target mRNA into a corresponding GAM336272 target protein.

The mechanism of the translational inhibition exerted by GAM336272 RNA, herein designated GAM RNA, on one or more GAM336272 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336272 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336272 RNA, herein designated GAM RNA, of GAM336272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336272 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336272 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336272 RNA correlate with, and may be deduced from, the identity of the GAM336272 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336275 7328 TTGCTTTCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTGGAGTAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGCCTTGG Messenger 336275 (GAM336275) oligonucleotides modulates expression of respective target
AACCTGTAGT genes whose function and utility is known in the art.

CAGTCATTTG GAM336275 is a novel bioinformatically detectable regulatory, non protein
CCTCAGGTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336275 was detected
ACCTGCCAGT is described with additional reference to Figs. 9-15.

CCCACCAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAAAGCAA encoded by the human genome.

GAM336275 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336275 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336275 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336275 precursor RNA is designated SEQ ID:7328, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7328 is located from position 3861125 to position 3861212 relative to chromosome 12 on the `-` strand.

GAM336275 precursor RNA folds onto itself, forming GAM336275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336275 precursor RNA, designated SEQ ID NO: 7328, and a schematic representation of a predicted secondary folding of GAM336275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336275 folded precursor RNA yielding a GAM336275 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336275 RNA, hereby incorporated herein.

GAM336275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336275 target RNA, herein designated GAM TARGET RNA.

GAM336275 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336275 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336275 RNA, herein designated GAM RNA, to target

binding sites on GAM336275 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336275 target RNA into GAM336275 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336275 target genes. The mRNA of each one of this plurality of GAM336275 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336275 RNA, herein designated GAM RNA, and which when bound by GAM336275 RNA causes inhibition of translation of the GAM336275 target mRNA into a corresponding GAM336275 target protein.

The mechanism of the translational inhibition exerted by GAM336275 RNA, herein designated GAM RNA, on one or more GAM336275 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336275 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336275 RNA, herein designated GAM RNA, of GAM336275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336275 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336275 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336275 RNA correlate with, and may be deduced from, the identity of the GAM336275 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336279 7067 TCTCTGAGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTGCTGCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCTTGTGTA Messenger 336279 (GAM336279) oligonucleotides modulates expression of respective target

ACAAAATGAA genes whose function and utility is known in the art.

TAATACCTGC GAM336279 is a novel bioinformatically detectable regulatory, non protein

CCTGAGGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336279 was detected

TATGGCAGGT is described with additional reference to Figs. 9-15.

AAAGGAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAGGCAGAG encoded by the human genome.

GTTGCAGAGG GAM336279 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336279 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336279 precursor RNA is designated SEQ ID:7067, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7067 is located from position 4367585 to position 4367684 relative to chromosome 17 on the `+` strand.

GAM336279 precursor RNA folds onto itself, forming GAM336279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336279 precursor RNA, designated SEQ ID NO: 7067, and a schematic representation of a predicted secondary folding of GAM336279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336279 folded precursor RNA yielding a GAM336279 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336279 RNA, hereby incorporated herein.

GAM336279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336279 target RNA, herein designated GAM TARGET RNA.

GAM336279 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336279 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336279 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336279 RNA, herein designated GAM RNA, to target binding sites on GAM336279 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336279 target RNA into GAM336279 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336279 target genes. The mRNA of each one of this plurality of GAM336279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336279 RNA, herein designated GAM RNA, and which when bound by GAM336279 RNA causes inhibition of translation of the GAM336279 target mRNA into a corresponding GAM336279 target protein.

The mechanism of the translational inhibition exerted by GAM336279 RNA, herein designated GAM RNA, on one or more GAM336279 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336279 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336279 RNA, herein designated GAM RNA, of GAM336279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336279 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336279 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336279 RNA correlate with, and may be deduced from, the identity of the GAM336279 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336281 5832 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336281 (GAM336281) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336281 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336281 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336281 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336281 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336281 precursor RNA is designated SEQ ID:5832, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5832 is located from position 4437001 to position 4437082 relative to chromosome 6 on the `+` strand.

GAM336281 precursor RNA folds onto itself, forming GAM336281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336281 precursor RNA, designated SEQ ID NO: 5832, and a schematic representation of a predicted secondary folding of GAM336281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336281 folded precursor RNA yielding a GAM336281 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336281 RNA, hereby incorporated herein.

GAM336281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336281 target RNA, herein designated GAM TARGET RNA.

GAM336281 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336281 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336281 RNA, herein designated GAM RNA, to target binding sites on GAM336281 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336281 target RNA into GAM336281 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336281 target genes. The mRNA of each one of this plurality of GAM336281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336281 RNA, herein designated GAM RNA, and which when bound by GAM336281 RNA causes inhibition of translation of the GAM336281 target mRNA into a corresponding GAM336281 target protein.

The mechanism of the translational inhibition exerted by GAM336281 RNA, herein designated GAM RNA, on one or more GAM336281 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336281 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336281 RNA, herein designated GAM RNA, of GAM336281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336281 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336281 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336281

RNA correlate with, and may be deduced from, the identity of the GAM336281 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336282 6012 CAGAGTCTCG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCTGTTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGCTGGAG Messenger 336282 (GAM336282) oligonucleotides modulates expression of respective target
TGCAGTGGTG genes whose function and utility is known in the art.

CAATCTTGGC GAM336282 is a novel bioinformatically detectable regulatory, non protein
TCACTGCAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336282 was detected
CTCCATCTCC is described with additional reference to Figs. 9-15.

TGGGTTTAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGATTCTCAT encoded by the human genome.

G GAM336282 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336282 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336282 precursor RNA is designated SEQ ID:6012, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6012 is located from position 4444093 to position 4444183 relative to chromosome 17 on the `+` strand.

GAM336282 precursor RNA folds onto itself, forming GAM336282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336282 precursor RNA, designated SEQ ID NO: 6012, and a schematic representation of a predicted secondary folding of GAM336282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336282 folded precursor RNA yielding a GAM336282 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336282 RNA, hereby incorporated herein.

GAM336282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336282 target RNA, herein designated GAM TARGET RNA.

GAM336282 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336282 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336282 RNA, herein designated GAM RNA, to target binding sites on GAM336282 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336282 target RNA into GAM336282 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336282 target genes. The mRNA of each one of this plurality of GAM336282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336282 RNA, herein designated GAM RNA, and which when bound by GAM336282 RNA causes inhibition of translation of the GAM336282 target mRNA into a corresponding GAM336282 target protein.

The mechanism of the translational inhibition exerted by GAM336282 RNA, herein designated GAM RNA, on one or more GAM336282 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336282 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336282 RNA, herein designated GAM RNA, of GAM336282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336282 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336282 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336282 RNA correlate with, and may be deduced from, the identity of the GAM336282 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336283 6464 GAGTCTCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGTTGCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTGGAGTG Messenger 336283 (GAM336283) oligonucleotides modulates expression of respective target
CAGTGGTGCA genes whose function and utility is known in the art.

ATCTTGGCTC GAM336283 is a novel bioinformatically detectable regulatory, non protein
ACTGCAACCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336283 was detected
CCATCTCCTG is described with additional reference to Figs. 9-15.

GGTTTAAGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTCTC encoded by the human genome.

GAM336283 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336283 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336283 precursor RNA is designated SEQ ID:6464, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6464 is located from position 4444095 to position 4444180 relative to chromosome 17 on the `+` strand.

GAM336283 precursor RNA folds onto itself, forming GAM336283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336283 precursor RNA, designated SEQ ID NO: 6464, and a schematic representation of a predicted secondary folding of GAM336283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336283 folded precursor RNA yielding a GAM336283 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336283 RNA, hereby incorporated herein.

GAM336283 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336283 target RNA, herein designated GAM TARGET RNA.

GAM336283 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336283 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336283 RNA, herein designated GAM RNA, to target binding sites on GAM336283 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336283 target RNA into GAM336283 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336283 target genes. The mRNA of each one of this plurality of GAM336283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336283 RNA, herein designated GAM RNA, and which when bound by GAM336283 RNA causes inhibition of translation of the GAM336283 target mRNA into a corresponding GAM336283 target protein.

The mechanism of the translational inhibition exerted by GAM336283 RNA, herein designated GAM RNA, on one or more GAM336283 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336283 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336283 RNA, herein designated GAM RNA, of GAM336283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336283 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336283 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336283 RNA correlate with, and may be deduced from, the identity of the GAM336283 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336284 5833 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336284 (GAM336284) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336284 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336284 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336284 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336284 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336284 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336284 precursor RNA is designated SEQ ID:5833, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5833 is located from position 4649605 to position 4649686 relative to chromosome 6 on the `+` strand.

GAM336284 precursor RNA folds onto itself, forming GAM336284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336284 precursor RNA, designated SEQ ID NO: 5833, and a schematic representation of a predicted secondary folding of GAM336284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336284 folded precursor RNA yielding a GAM336284 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336284 RNA, hereby incorporated herein.

GAM336284 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336284 target RNA, herein designated GAM TARGET RNA.

GAM336284 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336284 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336284 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336284 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336284 RNA, herein designated GAM RNA, to target binding sites on GAM336284 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336284 target RNA into GAM336284 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336284 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336284 target genes. The mRNA of each one of this plurality of GAM336284 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336284 RNA, herein designated GAM RNA, and which when bound by GAM336284 RNA causes inhibition of translation of the GAM336284 target mRNA into a corresponding GAM336284 target protein.

The mechanism of the translational inhibition exerted by GAM336284 RNA, herein designated GAM RNA, on one or more GAM336284 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336284 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336284 RNA, herein designated GAM RNA, of GAM336284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336284 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336284 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336284 RNA correlate with, and may be deduced from, the identity of the GAM336284 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336285 5834 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336285 (GAM336285) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336285 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336285 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336285 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336285 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336285 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336285 precursor RNA is designated SEQ ID:5834, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5834 is located from position 4756826 to position 4756907 relative to chromosome 18 on the `-` strand.

GAM336285 precursor RNA folds onto itself, forming GAM336285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336285 precursor RNA, designated SEQ ID NO: 5834, and a schematic representation of a predicted secondary folding of GAM336285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336285 folded precursor RNA yielding a GAM336285 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336285 RNA, hereby incorporated herein.

GAM336285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336285 target RNA, herein designated GAM TARGET RNA.

GAM336285 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336285 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336285 RNA, herein designated GAM RNA, to target binding sites on GAM336285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336285 target RNA into GAM336285 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336285 target genes. The mRNA of each one of this

plurality of GAM336285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336285 RNA, herein designated GAM RNA, and which when bound by GAM336285 RNA causes inhibition of translation of the GAM336285 target mRNA into a corresponding GAM336285 target protein.

The mechanism of the translational inhibition exerted by GAM336285 RNA, herein designated GAM RNA, on one or more GAM336285 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336285 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336285 RNA, herein designated GAM RNA, of GAM336285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336285 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336285 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336285 RNA correlate with, and may be deduced from, the identity of the GAM336285 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336289 7076 TCTGTGGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGAATGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGAAGTGTG Messenger 336289 (GAM336289) oligonucleotides modulates expression of respective target

TGAGCTAGAT genes whose function and utility is known in the art.

TGCACAGATA GAM336289 is a novel bioinformatically detectable regulatory, non protein

GCAAGCAGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336289 was detected

CATTTCTGGT is described with additional reference to Figs. 9-15.

GAACTTGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACACAGA encoded by the human genome.

GAM336289 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336289 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336289 precursor RNA is designated SEQ ID:7076, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7076 is located from position 5537268 to position 5537354 relative to chromosome 11 on the `+` strand.

GAM336289 precursor RNA folds onto itself, forming GAM336289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336289 precursor RNA, designated SEQ ID NO: 7076, and a schematic representation of a predicted secondary folding of GAM336289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336289 folded precursor RNA yielding a GAM336289 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336289 RNA, hereby incorporated herein.

GAM336289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336289 target RNA, herein designated GAM TARGET RNA.

GAM336289 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336289 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336289 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336289 RNA, herein designated GAM RNA, to target binding sites on GAM336289 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336289 target RNA into GAM336289 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336289 target genes. The mRNA of each one of this plurality of GAM336289 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336289 RNA, herein designated GAM RNA, and which when bound by GAM336289 RNA causes inhibition of translation of the GAM336289 target mRNA into a corresponding GAM336289 target protein.

The mechanism of the translational inhibition exerted by GAM336289 RNA, herein designated GAM RNA, on one or more GAM336289 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336289 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336289 RNA, herein designated GAM RNA, of GAM336289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336289 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336289 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336289 RNA correlate with, and may be deduced from, the identity of the GAM336289 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336290 6245 CTGTGGTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGAATGGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAAGTGTGT Messenger 336290 (GAM336290) oligonucleotides modulates expression of respective target
GAGCTAGATT genes whose function and utility is known in the art.

GCACAGATAG GAM336290 is a novel bioinformatically detectable regulatory, non protein
CAAGCAGAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336290 was detected
ATTTCTGGTG is described with additional reference to Figs. 9-15.

AACTTGGACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CACAG encoded by the human genome.

GAM336290 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336290 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336290 precursor RNA is designated SEQ ID:6245, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6245 is located from position 5537269 to position 5537353 relative to chromosome 11 on the `+` strand.

GAM336290 precursor RNA folds onto itself, forming GAM336290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336290 precursor RNA, designated SEQ ID NO: 6245, and a schematic representation of a predicted secondary folding of GAM336290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336290 folded precursor RNA yielding a GAM336290 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336290 RNA, hereby incorporated herein.

GAM336290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336290 target RNA, herein designated GAM TARGET RNA.

GAM336290 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336290 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336290 RNA, herein designated GAM RNA, to target binding sites on GAM336290 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336290 target RNA into GAM336290 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336290 target genes. The mRNA of each one of this plurality of GAM336290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336290 RNA, herein designated GAM RNA, and which when bound by GAM336290 RNA causes inhibition of translation of the GAM336290 target mRNA into a corresponding GAM336290 target protein.

The mechanism of the translational inhibition exerted by GAM336290 RNA, herein designated GAM RNA, on one or more GAM336290 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336290 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336290 RNA, herein designated GAM RNA, of GAM336290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336290 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336290 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336290 RNA correlate with, and may be deduced from, the identity of the GAM336290 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336291 6149 CGTCTAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATGAGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTAGTCCTT Messenger 336291 (GAM336291) oligonucleotides modulates expression of respective target

TAGAGCCTCT genes whose function and utility is known in the art.

GGACAGAAGG GAM336291 is a novel bioinformatically detectable regulatory, non protein
TAATGCTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336291 was detected
AATCCAGTGA is described with additional reference to Figs. 9-15.

TTCTCGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAATGGAG encoded by the human genome.

GATTTGCACT GAM336291 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AGATG GAM336291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336291 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336291 precursor RNA is designated SEQ ID:6149, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6149 is located from position 5605037 to position 5605141 relative to chromosome 11 on the `-` strand.

GAM336291 precursor RNA folds onto itself, forming GAM336291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336291 precursor RNA, designated SEQ ID NO: 6149, and a schematic representation of a predicted secondary folding of GAM336291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336291 folded precursor RNA yielding a GAM336291 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336291 RNA, hereby incorporated herein.

GAM336291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336291 target RNA, herein designated GAM TARGET RNA.

GAM336291 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336291 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336291 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336291 RNA, herein designated GAM RNA, to target binding sites on GAM336291 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336291 target RNA into GAM336291 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336291 target genes. The mRNA of each one of this plurality of GAM336291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336291 RNA, herein designated GAM RNA, and which when bound by GAM336291 RNA causes inhibition of translation of the GAM336291 target mRNA into a corresponding GAM336291 target protein.

The mechanism of the translational inhibition exerted by GAM336291 RNA, herein designated GAM RNA, on one or more GAM336291 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336291 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336291 RNA, herein designated GAM RNA, of GAM336291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336291 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336291 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336291 RNA correlate with, and may be deduced from, the identity of the GAM336291 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336292 5835 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336292 (GAM336292) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336292 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336292 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336292 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336292 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336292 precursor RNA is designated SEQ ID:5835, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5835 is located from position 5676458 to position 5676539 relative to chromosome 6 on the `+` strand.

GAM336292 precursor RNA folds onto itself, forming GAM336292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336292 precursor RNA, designated SEQ ID NO: 5835, and a schematic representation of a predicted secondary folding of GAM336292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336292 folded precursor RNA yielding a GAM336292 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336292 RNA, hereby incorporated herein.

GAM336292 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336292 target RNA, herein designated GAM TARGET RNA.

GAM336292 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336292 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336292 RNA, herein designated GAM RNA, to target binding sites on GAM336292 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336292 target RNA into GAM336292 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336292 target genes. The mRNA of each one of this plurality of GAM336292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336292 RNA, herein designated GAM RNA, and which when bound by GAM336292 RNA causes inhibition of translation of the GAM336292 target mRNA into a corresponding GAM336292 target protein.

The mechanism of the translational inhibition exerted by GAM336292 RNA, herein designated GAM RNA, on one or more GAM336292 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336292 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336292 RNA, herein designated GAM RNA, of GAM336292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336292 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336292 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336292 RNA correlate with, and may be deduced from, the identity of the GAM336292 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336293 6823 GGGTGCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGCTACTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCTTCTAGT Messenger 336293 (GAM336293) oligonucleotides modulates expression of respective target
CAAATGGAAA genes whose function and utility is known in the art.

TCTTTCAATG GAM336293 is a novel bioinformatically detectable regulatory, non protein
ATGCCAGGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336293 was detected
GTGCTGTTAA is described with additional reference to Figs. 9-15.

GAAGCAGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTCCCCTA encoded by the human genome.

AGCCC GAM336293 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336293 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336293 precursor RNA is designated SEQ ID:6823, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6823 is located from position 5710623 to position 5710717 relative to chromosome 17 on the `+` strand.

GAM336293 precursor RNA folds onto itself, forming GAM336293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336293 precursor RNA, designated SEQ ID NO: 6823, and a schematic representation of a predicted secondary folding of GAM336293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336293 folded precursor

RNA yielding a GAM336293 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336293 RNA, hereby incorporated herein.

GAM336293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336293 target RNA, herein designated GAM TARGET RNA.

GAM336293 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336293 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336293 RNA, herein designated GAM RNA, to target binding sites on GAM336293 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336293 target RNA into GAM336293 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336293 target genes. The mRNA of each one of this plurality of GAM336293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336293 RNA, herein designated GAM RNA, and which when bound by GAM336293 RNA causes inhibition of translation of the GAM336293 target mRNA into a corresponding GAM336293 target protein.

The mechanism of the translational inhibition exerted by GAM336293 RNA, herein designated GAM RNA, on one or more GAM336293 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336293 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336293 RNA, herein designated GAM RNA, of GAM336293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336293 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336293 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336293 RNA correlate with, and may be deduced from, the identity of the GAM336293 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336294 6861 GTAGAGATGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTTTTACTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTTGCCCAG Messenger 336294 (GAM336294) oligonucleotides modulates expression of respective target

GTTGATCTTG genes whose function and utility is known in the art.

AACTCCTGGG GAM336294 is a novel bioinformatically detectable regulatory, non protein

CTCAAGTGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336294 was detected

CCTCCCATCT is described with additional reference to Figs. 9-15.

TGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336294 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336294 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336294 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336294 precursor RNA is designated SEQ ID:6861, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6861 is located from position 5786960 to position 5787033 relative to chromosome 7 on the `-` strand.

GAM336294 precursor RNA folds onto itself, forming GAM336294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336294 precursor RNA, designated SEQ ID NO: 6861, and a schematic representation of a predicted secondary folding of GAM336294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336294 folded precursor RNA yielding a GAM336294 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336294 RNA, hereby incorporated herein.

GAM336294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336294 target RNA, herein designated GAM TARGET RNA.

GAM336294 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336294 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336294 RNA, herein designated GAM RNA, to target binding sites on GAM336294 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336294 target RNA into GAM336294 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336294 target genes. The mRNA of each one of this plurality of GAM336294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336294 RNA, herein designated GAM RNA, and which when bound by GAM336294 RNA causes inhibition of translation of the GAM336294 target mRNA into a corresponding GAM336294 target protein.

The mechanism of the translational inhibition exerted by GAM336294 RNA, herein designated GAM RNA, on one or more GAM336294 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336294 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336294 RNA, herein designated GAM RNA, of GAM336294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336294 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336294 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336294 RNA correlate with, and may be deduced from, the identity of the GAM336294 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336297 7104 TGAGATGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTTGCTCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTGCCCAGG Messenger 336297 (GAM336297) oligonucleotides modulates expression of respective target

CTGTAGTGTA genes whose function and utility is known in the art.

ATGTAGTGCA GAM336297 is a novel bioinformatically detectable regulatory, non protein

ATCTTGGCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336297 was detected

AGTACAACCT is described with additional reference to Figs. 9-15.

CTGCCTCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTTCAAGCC encoded by the human genome.

ATTCTCCTGC GAM336297 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTCA GAM336297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336297 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336297 precursor RNA is designated SEQ ID:7104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7104 is located from position 6079591 to position 6079694 relative to chromosome 10 on the `+` strand.

GAM336297 precursor RNA folds onto itself, forming GAM336297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336297 precursor RNA, designated SEQ ID NO: 7104, and a schematic representation of a predicted secondary folding of GAM336297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336297 folded precursor RNA yielding a GAM336297 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336297 RNA, hereby incorporated herein.

GAM336297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336297 target RNA, herein designated GAM TARGET RNA.

GAM336297 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336297 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336297 RNA, herein designated GAM RNA, to target binding sites on GAM336297 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336297 target RNA into GAM336297 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336297 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336297 target genes. The mRNA of each one of this

plurality of GAM336297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336297 RNA, herein designated GAM RNA, and which when bound by GAM336297 RNA causes inhibition of translation of the GAM336297 target mRNA into a corresponding GAM336297 target protein.

The mechanism of the translational inhibition exerted by GAM336297 RNA, herein designated GAM RNA, on one or more GAM336297 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336297 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336297 RNA, herein designated GAM RNA, of GAM336297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336297 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336297 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336297 RNA correlate with, and may be deduced from, the identity of the GAM336297 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336298 6354 GAGATGGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTGCTCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCCCAGGC Messenger 336298 (GAM336298) oligonucleotides modulates expression of respective target
TGTAGTGTAA genes whose function and utility is known in the art.

TGTAGTGCAA GAM336298 is a novel bioinformatically detectable regulatory, non protein
TCTTGGCTTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336298 was detected
GTACAACCTC is described with additional reference to Figs. 9-15.

TGCCTCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTCAAGCCA encoded by the human genome.

TTCTCCTGCC GAM336298 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TC GAM336298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336298 precursor RNA is designated SEQ ID:6354, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6354 is located from position 6079592 to position 6079693 relative to chromosome 10 on the `+` strand.

GAM336298 precursor RNA folds onto itself, forming GAM336298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336298 precursor RNA, designated SEQ ID NO: 6354, and a schematic representation of a predicted secondary folding of GAM336298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336298 folded precursor RNA yielding a GAM336298 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336298 RNA, hereby incorporated herein.

GAM336298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336298 target RNA, herein designated GAM TARGET RNA.

GAM336298 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336298 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336298 RNA, herein designated GAM RNA, to target binding sites on GAM336298 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336298 target RNA into GAM336298 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336298 target genes. The mRNA of each one of this plurality of GAM336298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336298 RNA, herein designated GAM RNA, and which when bound by GAM336298 RNA causes inhibition of translation of the GAM336298 target mRNA into a corresponding GAM336298 target protein.

The mechanism of the translational inhibition exerted by GAM336298 RNA, herein designated GAM RNA, on one or more GAM336298 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336298 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336298 RNA, herein designated GAM RNA, of GAM336298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336298 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336298 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336298 RNA correlate with, and may be deduced from, the identity of the GAM336298 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336299 6842 GGTGACAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCTCACTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGGTCCAGA Messenger 336299 (GAM336299) oligonucleotides modulates expression of respective target
CTGGAGTATA genes whose function and utility is known in the art.

GTGCTATCAG GAM336299 is a novel bioinformatically detectable regulatory, non protein
AGCTTACTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336299 was detected
AACTTTAAAC is described with additional reference to Figs. 9-15.

TTCTGGGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGGTGATCCT encoded by the human genome.

CCCACC GAM336299 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336299 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336299 precursor RNA is designated SEQ ID:6842, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6842 is located from position 6225060 to position 6225155 relative to chromosome 9 on the `+` strand.

GAM336299 precursor RNA folds onto itself, forming GAM336299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336299 precursor RNA, designated SEQ ID NO: 6842, and a schematic representation of a predicted secondary folding of GAM336299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336299 folded precursor RNA yielding a GAM336299 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336299 RNA, hereby incorporated herein.

GAM336299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336299 target RNA, herein designated GAM TARGET RNA.

GAM336299 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336299 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336299 RNA, herein designated GAM RNA, to target binding sites on GAM336299 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336299 target RNA into GAM336299 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336299 target genes. The mRNA of each one of this plurality of GAM336299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336299 RNA, herein designated GAM RNA, and which when bound by GAM336299 RNA causes inhibition of translation of the GAM336299 target mRNA into a corresponding GAM336299 target protein.

The mechanism of the translational inhibition exerted by GAM336299 RNA, herein designated GAM RNA, on one or more GAM336299 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336299 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336299 RNA, herein designated GAM RNA, of GAM336299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336299 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336299 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336299 RNA correlate with, and may be deduced from, the identity of the GAM336299 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336300 6995 TCACTCTGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCCAGACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTATAGTG Messenger 336300 (GAM336300) oligonucleotides modulates expression of respective target

CTATCAGAGC genes whose function and utility is known in the art.

TTACTACAAC GAM336300 is a novel bioinformatically detectable regulatory, non protein

TTTAAACTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336300 was detected

TGGGCTCAGG is described with additional reference to Figs. 9-15.

TGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336300 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336300 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336300 precursor RNA is designated SEQ ID:6995, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6995 is located from position 6225073 to position 6225145 relative to chromosome 9 on the `+` strand.

GAM336300 precursor RNA folds onto itself, forming GAM336300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336300 precursor RNA, designated SEQ ID NO: 6995, and a schematic representation of a predicted secondary folding of GAM336300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336300 folded precursor RNA yielding a GAM336300 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336300 RNA, hereby incorporated herein.

GAM336300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336300 target RNA, herein designated GAM TARGET RNA.

GAM336300 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336300 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336300 RNA, herein designated GAM RNA, to target binding sites on GAM336300 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336300 target RNA into GAM336300 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336300 target genes. The mRNA of each one of this plurality of GAM336300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336300 RNA, herein designated GAM RNA, and which when bound by GAM336300 RNA causes inhibition of translation of the GAM336300 target mRNA into a corresponding GAM336300 target protein.

The mechanism of the translational inhibition exerted by GAM336300 RNA, herein designated GAM RNA, on one or more GAM336300 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336300 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336300 RNA, herein designated GAM RNA, of GAM336300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336300 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336300 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336300 RNA correlate with, and may be deduced from, the identity of the GAM336300 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336303 5777 AGGCGTGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATCGCTTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTGGAAGGT Messenger 336303 (GAM336303) oligonucleotides modulates expression of respective target
GGTGGTTGCA genes whose function and utility is known in the art.

GTGAGCCGAG GAM336303 is a novel bioinformatically detectable regulatory, non protein
ATCCTGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336303 was detected
TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGCGAGAC encoded by the human genome.

TCTGCCT GAM336303 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336303 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336303 precursor RNA is designated SEQ ID:5777, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5777 is located from position 6623046 to position 6623142 relative to chromosome 17 on the `+` strand.

GAM336303 precursor RNA folds onto itself, forming GAM336303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336303 precursor RNA, designated SEQ ID NO: 5777, and a schematic representation of a predicted secondary folding of GAM336303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336303 folded precursor RNA yielding a GAM336303 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336303 RNA, hereby incorporated herein.

Expression of GAM336303 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336303 target RNA, herein designated GAM TARGET RNA.

GAM336303 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336303 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336303 RNA, herein designated GAM RNA, to target binding sites on GAM336303 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336303 target RNA into GAM336303 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336303 target genes. The mRNA of each one of this plurality of GAM336303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336303 RNA, herein designated GAM RNA, and which when bound by GAM336303 RNA causes inhibition of translation of the GAM336303 target mRNA into a corresponding GAM336303 target protein.

The mechanism of the translational inhibition exerted by GAM336303 RNA, herein designated GAM RNA, on one or more GAM336303 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336303 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336303 RNA, herein designated GAM RNA, of GAM336303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336303 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336303 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336303 RNA correlate with, and may be deduced from, the identity of the GAM336303 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336304 6349 GAGACGTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAGG Messenger 336304 (GAM336304) oligonucleotides modulates expression of respective target
TGGAGGTTGT genes whose function and utility is known in the art.

AGTGAGCCCA GAM336304 is a novel bioinformatically detectable regulatory, non protein
AATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336304 was detected
CATGTCACTG is described with additional reference to Figs. 9-15.

CACTCCAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGGCAACAG encoded by the human genome.

AGCAAGACTC GAM336304 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGTCTC GAM336304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336304 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336304 precursor RNA is designated SEQ ID:6349, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6349 is located from position 6644614 to position 6644719 relative to chromosome 12 on the `-` strand.

GAM336304 precursor RNA folds onto itself, forming GAM336304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336304 precursor RNA, designated SEQ ID NO: 6349, and a schematic representation of a predicted secondary folding of GAM336304 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336304 folded precursor RNA yielding a GAM336304 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336304 RNA, hereby incorporated herein.

GAM336304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336304 target RNA, herein designated GAM TARGET RNA.

GAM336304 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336304 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336304 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336304 RNA, herein designated GAM RNA, to target binding sites on GAM336304 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336304 target RNA into GAM336304 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336304 target genes. The mRNA of each one of this plurality of GAM336304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336304 RNA, herein designated GAM RNA, and which when bound by GAM336304 RNA causes inhibition of translation of the GAM336304 target mRNA into a corresponding GAM336304 target protein.

The mechanism of the translational inhibition exerted by GAM336304 RNA, herein designated GAM RNA, on one or more GAM336304 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336304 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336304 RNA, herein designated GAM RNA, of GAM336304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336304 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336304 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336304 RNA correlate with, and may be deduced from, the identity of the GAM336304 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336306 5785 AGGCTTTAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTAGCAAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCCAGGGAA Messenger 336306 (GAM336306) oligonucleotides modulates expression of respective target
TGGGCTCTGT genes whose function and utility is known in the art.

TGGGACAGCT GAM336306 is a novel bioinformatically detectable regulatory, non protein
TGTCTTTGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336306 was detected
TTCCAGTAGT is described with additional reference to Figs. 9-15.

TACTCCTCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAAGGGGTC encoded by the human genome.

AAGGTTGCTT GAM336306 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CCT GAM336306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336306 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336306 precursor RNA is designated SEQ ID:5785, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5785 is located from position 6790508 to position 6790610 relative to chromosome 19 on the `+` strand.

GAM336306 precursor RNA folds onto itself, forming GAM336306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336306 precursor RNA, designated SEQ ID NO: 5785, and a schematic representation of a predicted secondary folding of GAM336306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336306 folded precursor RNA yielding a GAM336306 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336306 RNA, hereby incorporated herein.

GAM336306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336306 target RNA, herein designated GAM TARGET RNA.

GAM336306 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336306 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336306 RNA, herein designated GAM RNA, to target binding sites on GAM336306 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336306 target RNA into GAM336306 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336306 target genes. The mRNA of each one of this plurality of GAM336306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336306 RNA, herein designated GAM RNA, and which when bound by GAM336306 RNA causes inhibition of translation of the GAM336306 target mRNA into a corresponding GAM336306 target protein.

The mechanism of the translational inhibition exerted by GAM336306 RNA, herein designated GAM RNA, on one or more GAM336306 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336306 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336306 RNA, herein designated GAM RNA, of GAM336306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336306 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336306 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336306 RNA correlate with, and may be deduced from, the identity of the GAM336306 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336307 6460 GAGTAGCAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCCCCAGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGGGCTCT Messenger 336307 (GAM336307) oligonucleotides modulates expression of respective target

GTTGGGACAG genes whose function and utility is known in the art.

CTTGTCTTTG GAM336307 is a novel bioinformatically detectable regulatory, non protein

GTTTCCAGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336307 was detected

GTTACTCCTC is described with additional reference to Figs. 9-15.

CCTGAAGGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCAAGGTTGC encoded by the human genome.

TT GAM336307 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336307 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336307 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336307 precursor RNA is designated SEQ

ID:6460, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6460 is located from position 6790516 to position 6790607 relative to chromosome 19 on the `+` strand.

GAM336307 precursor RNA folds onto itself, forming GAM336307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336307 precursor RNA, designated SEQ ID NO: 6460, and a schematic representation of a predicted secondary folding of GAM336307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336307 folded precursor RNA yielding a GAM336307 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336307 RNA, hereby incorporated herein.

GAM336307 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336307 target RNA, herein designated GAM TARGET RNA.

GAM336307 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336307 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336307 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336307 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336307 RNA, herein designated GAM RNA, to target binding sites on GAM336307 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336307 target RNA into GAM336307 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336307 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336307 target genes. The mRNA of each one of this plurality of GAM336307 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336307 RNA, herein designated GAM RNA, and which when bound by GAM336307 RNA causes inhibition of translation of the GAM336307 target mRNA into a corresponding GAM336307 target protein.

The mechanism of the translational inhibition exerted by GAM336307 RNA, herein designated GAM RNA, on one or more GAM336307 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336307 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336307 RNA, herein designated GAM RNA, of GAM336307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336307 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336307 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336307 RNA correlate with, and may be deduced from, the identity of the GAM336307 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336308 5745 AGCAGCACAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATATTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAGGGAAGC Messenger 336308 (GAM336308) oligonucleotides modulates expression of respective target

GAGTCTGCCA genes whose function and utility is known in the art.

ATATTGGCTG GAM336308 is a novel bioinformatically detectable regulatory, non protein

TGCTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336308 was detected

is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336308 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336308 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336308 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336308 precursor RNA is designated SEQ ID:5745, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5745 is located from position 6865733 to position 6865789 relative to chromosome 17 on the `-` strand.

GAM336308 precursor RNA folds onto itself, forming GAM336308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336308 precursor RNA, designated SEQ ID NO: 5745, and a schematic representation of a predicted secondary folding of GAM336308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336308 folded precursor RNA yielding a GAM336308 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336308 RNA, hereby incorporated herein.

GAM336308 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336308 target RNA, herein designated GAM TARGET RNA.

GAM336308 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336308 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336308 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336308 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336308 RNA, herein designated GAM RNA, to target binding sites on GAM336308 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336308 target RNA into GAM336308 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336308 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336308 target genes. The mRNA of each one of this plurality of GAM336308 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336308 RNA, herein designated GAM RNA, and which when bound by GAM336308 RNA causes inhibition of translation of the GAM336308 target mRNA into a corresponding GAM336308 target protein.

The mechanism of the translational inhibition exerted by GAM336308 RNA, herein designated GAM RNA, on one or more GAM336308 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336308 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336308 RNA, herein designated GAM RNA, of GAM336308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336308 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336308 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336308 RNA correlate with, and may be deduced from, the identity of the GAM336308 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336309 6881 GTCCTGGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACATGGTAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGAAGGAT Messenger 336309 (GAM336309) oligonucleotides modulates expression of respective target

CAGCCAACTT genes whose function and utility is known in the art.

TGAGACTCAG CTCTAGCTGC CTGTCTCCAG TGGC

GAM336309 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336309 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336309 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336309 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336309 precursor RNA is designated SEQ ID:6881, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6881 is located from position 6882641 to position 6882714 relative to chromosome 12 on the `+` strand.

GAM336309 precursor RNA folds onto itself, forming GAM336309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336309 precursor RNA, designated SEQ ID NO: 6881, and a schematic representation of a predicted secondary folding of GAM336309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336309 folded precursor RNA yielding a GAM336309 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336309 RNA, hereby incorporated herein.

GAM336309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336309 target RNA, herein designated GAM TARGET RNA.

GAM336309 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336309 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336309 RNA, herein designated GAM RNA, to target binding sites on GAM336309 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336309 target RNA into GAM336309 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336309 target genes. The mRNA of each one of this plurality of GAM336309 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336309 RNA, herein designated GAM RNA, and which when bound by GAM336309 RNA causes inhibition of translation of the GAM336309 target mRNA into a corresponding GAM336309 target protein.

The mechanism of the translational inhibition exerted by GAM336309 RNA, herein designated GAM RNA, on one or more GAM336309 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336309 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336309 RNA, herein designated GAM RNA, of GAM336309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336309 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336309 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336309 RNA correlate with, and may be deduced from, the identity of the GAM336309 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336311 6414 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTGGGCAG Messenger 336311 (GAM336311) oligonucleotides modulates expression of respective target
AGGTTGCAGT genes whose function and utility is known in the art.

GAGCCAAGGT GAM336311 is a novel bioinformatically detectable regulatory, non protein
TGACCCACTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336311 was detected
CACTCCAGCC is described with additional reference to Figs. 9-15.

TGGGCAACAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGCAAAACT encoded by the human genome.

CCATCTC GAM336311 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336311 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336311 precursor RNA is designated SEQ ID:6414, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6414 is located from position 7027442 to position 7027538 relative to chromosome 19 on the `+` strand.

GAM336311 precursor RNA folds onto itself, forming GAM336311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336311 precursor RNA, designated SEQ ID NO: 6414, and a schematic representation of a predicted secondary folding of GAM336311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336311 folded precursor RNA yielding a GAM336311 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336311 RNA, hereby incorporated herein. Expression of GAM336311 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336311 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336311 target RNA, herein designated GAM TARGET RNA.

GAM336311 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336311 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336311 RNA, herein designated GAM RNA, to target binding sites on GAM336311 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336311 target RNA into GAM336311 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336311 target genes. The mRNA of each one of this plurality of GAM336311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336311 RNA, herein designated GAM RNA, and which when bound by GAM336311 RNA causes inhibition of translation of the GAM336311 target mRNA into a corresponding GAM336311 target protein.

The mechanism of the translational inhibition exerted by GAM336311 RNA, herein designated GAM RNA, on one or more GAM336311 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336311 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336311 RNA, herein designated GAM RNA, of GAM336311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336311 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336311 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336311 RNA correlate with, and may be deduced from, the identity of the GAM336311 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336313 6665 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAATCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTGCAG Messenger 336313 (GAM336313) oligonucleotides modulates expression of respective target
TGAGCTGAGA genes whose function and utility is known in the art.

TCACGCCACT GAM336313 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336313 was detected
CTGGGTGACA is described with additional reference to Figs. 9-15.

GAGCAAGACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CC encoded by the human genome.

GAM336313 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336313 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336313 precursor RNA is designated SEQ ID:6665, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6665 is located from position 7192320 to position 7192401 relative to chromosome 19 on the `+` strand.

GAM336313 precursor RNA folds onto itself, forming GAM336313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336313 precursor RNA, designated SEQ ID NO: 6665, and a schematic representation of a predicted secondary folding of GAM336313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336313 folded precursor RNA yielding a GAM336313 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336313 RNA, hereby incorporated herein.

GAM336313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336313 target RNA, herein designated GAM TARGET RNA.

GAM336313 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336313 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336313 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336313 RNA, herein designated GAM RNA, to target binding sites on GAM336313 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336313 target RNA into GAM336313 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336313 target genes. The mRNA of each one of this plurality of GAM336313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336313 RNA, herein designated GAM RNA, and which when bound by GAM336313 RNA causes inhibition of translation of the GAM336313 target mRNA into a corresponding GAM336313 target protein.

The mechanism of the translational inhibition exerted by GAM336313 RNA, herein designated GAM RNA, on one or more GAM336313 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336313 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336313 RNA, herein designated GAM RNA, of GAM336313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336313 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336313 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336313 RNA correlate with, and may be deduced from, the identity of the GAM336313 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336315 7098 TGAGACAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336315 (GAM336315) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGATG GAM336315 is a novel bioinformatically detectable regulatory, non protein

AGATCACACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336315 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCGA encoded by the human genome.

AACTCCATCT GAM336315 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336315 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336315 precursor RNA is designated SEQ ID:7098, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7098 is located from position 7755711 to position 7755812 relative to chromosome 5 on the `+` strand.

GAM336315 precursor RNA folds onto itself, forming GAM336315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336315 precursor RNA, designated SEQ ID NO: 7098, and a schematic representation of a predicted secondary folding of GAM336315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336315 folded precursor RNA yielding a GAM336315 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336315 RNA, hereby incorporated herein. Expression of GAM336315 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336315 target RNA, herein designated GAM TARGET RNA.

GAM336315 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336315 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336315 RNA, herein designated GAM RNA, to target binding sites on GAM336315 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336315 target RNA into GAM336315 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336315 target genes. The mRNA of each one of this plurality of GAM336315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336315 RNA, herein designated GAM RNA, and which when bound by GAM336315 RNA causes inhibition of translation of the GAM336315 target mRNA into a corresponding GAM336315 target protein.

The mechanism of the translational inhibition exerted by GAM336315 RNA, herein

designated GAM RNA, on one or more GAM336315 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336315 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336315 RNA, herein designated GAM RNA, of GAM336315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336315 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336315 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336315 RNA correlate with, and may be deduced from, the identity of the GAM336315 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336316 6342 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 336316 (GAM336316) oligonucleotides modulates expression of respective target

CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGATGA GAM336316 is a novel bioinformatically detectable regulatory, non protein

GATCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336316 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCGAA encoded by the human genome.

ACTCCATCTC GAM336316 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336316 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336316 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336316 precursor RNA is designated SEQ ID:6342, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6342 is located from position 7755712 to position 7755811 relative to chromosome 5 on the `+` strand.

GAM336316 precursor RNA folds onto itself, forming GAM336316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336316 precursor RNA, designated SEQ ID NO: 6342, and a schematic representation of a predicted secondary folding of GAM336316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336316 folded precursor RNA yielding a GAM336316 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336316 RNA, hereby incorporated herein. Expression of GAM336316 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336316 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336316 target RNA, herein designated GAM TARGET RNA.

GAM336316 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336316 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336316 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336316 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336316 RNA, herein designated GAM RNA, to target binding sites on GAM336316 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336316 target RNA into GAM336316 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336316 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336316 target genes. The mRNA of each one of this plurality of GAM336316 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336316 RNA, herein designated GAM RNA, and which when bound by GAM336316 RNA causes inhibition of translation of the GAM336316 target mRNA into a corresponding GAM336316 target protein.

The mechanism of the translational inhibition exerted by GAM336316 RNA, herein designated GAM RNA, on one or more GAM336316 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336316 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336316 RNA, herein designated GAM RNA, of GAM336316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336316 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336316 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336316 RNA correlate with, and may be deduced from, the identity of the GAM336316 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336317 6646 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAGG Messenger 336317 (GAM336317) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

ATGAGATCAC GAM336317 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336317 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGAAACTCC encoded by the human genome.

GAM336317 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336317 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336317 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336317 precursor RNA is designated SEQ ID:6646, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6646 is located from position 7755718 to position 7755806 relative to chromosome 5 on the `+` strand.

GAM336317 precursor RNA folds onto itself, forming GAM336317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336317 precursor RNA, designated SEQ ID NO: 6646, and a schematic representation of a predicted secondary folding of GAM336317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336317 folded precursor RNA yielding a GAM336317 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336317 RNA, hereby incorporated herein. Expression of GAM336317 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336317 target RNA, herein designated GAM TARGET RNA.

GAM336317 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336317 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336317 RNA, herein designated GAM RNA, to target binding sites on GAM336317 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336317 target RNA into GAM336317 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336317 target genes. The mRNA of each one of this plurality of GAM336317 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336317 RNA, herein designated GAM RNA, and which when bound by GAM336317 RNA causes inhibition of translation of the GAM336317 target mRNA into a corresponding GAM336317 target protein.

The mechanism of the translational inhibition exerted by GAM336317 RNA, herein designated GAM RNA, on one or more GAM336317 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336317 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336317 RNA, herein designated GAM RNA, of GAM336317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336317 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336317 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336317 RNA correlate with, and may be deduced from, the identity of the GAM336317 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336318 6259 CTTGAACCCG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAGCAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTGCAGTGA Messenger 336318 (GAM336318) oligonucleotides modulates expression of respective target

GCCGACATCG genes whose function and utility is known in the art.

TGCCACTGCA GAM336318 is a novel bioinformatically detectable regulatory, non protein
CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336318 was
detected
GGCAACAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen
gene
encoded by the human genome.

GAM336318 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA
genes
GAM336318 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336318 precursor RNA is designated SEQ ID:6259, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6259 is located from position 7839733 to position 7839801 relative to chromosome 17 on the `-` strand.

GAM336318 precursor RNA folds onto itself, forming GAM336318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336318 precursor RNA, designated SEQ ID NO: 6259, and a schematic representation of a predicted secondary folding of GAM336318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336318 folded precursor RNA yielding a GAM336318 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336318 RNA, hereby incorporated herein. Expression of GAM336318 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336318 target RNA, herein designated GAM TARGET RNA.

GAM336318 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336318 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336318 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336318 RNA, herein designated GAM RNA, to target binding sites on GAM336318 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336318 target RNA into GAM336318 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336318 target genes. The mRNA of each one of this plurality of GAM336318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336318 RNA, herein designated GAM RNA, and which when bound by GAM336318 RNA causes inhibition of translation of the GAM336318 target mRNA into a corresponding GAM336318 target protein.

The mechanism of the translational inhibition exerted by GAM336318 RNA, herein designated GAM RNA, on one or more GAM336318 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336318 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336318 RNA, herein designated GAM RNA, of GAM336318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336318 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336318 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336318 RNA correlate with, and may be deduced from, the identity of the GAM336318 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336320 7160 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCAGGAA Messenger 336320 (GAM336320) oligonucleotides modulates expression of respective target
GCGGAGGTCG genes whose function and utility is known in the art.

CAGTAAGCTG GAM336320 is a novel bioinformatically detectable regulatory, non protein
AGATCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336320 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCTGTCTC GAM336320 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336320 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336320 precursor RNA is designated SEQ ID:7160, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7160 is located from position 8370724 to position 8370824 relative to chromosome 17 on the `+` strand.

GAM336320 precursor RNA folds onto itself, forming GAM336320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336320 precursor RNA, designated SEQ ID NO: 7160, and a schematic representation of a predicted secondary folding of GAM336320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336320 folded precursor RNA yielding a GAM336320 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336320 RNA, hereby incorporated herein.

Expression of GAM336320 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336320 target RNA, herein designated GAM TARGET RNA.

GAM336320 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336320 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336320 RNA, herein designated GAM RNA, to target binding sites on GAM336320 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336320 target RNA into GAM336320 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336320 target genes. The mRNA of each one of this plurality of GAM336320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336320 RNA, herein designated GAM RNA, and which when bound by GAM336320 RNA causes inhibition of translation of the GAM336320 target mRNA into a corresponding GAM336320 target protein.

The mechanism of the translational inhibition exerted by GAM336320 RNA, herein designated GAM RNA, on one or more GAM336320 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336320 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336320 RNA, herein designated GAM RNA, of GAM336320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336320 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336320 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336320 RNA correlate with, and may be deduced from, the identity of the GAM336320 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336321 6675 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGAACTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGCGGAGG Messenger 336321 (GAM336321) oligonucleotides modulates expression of respective target
TCGCAGTAAG genes whose function and utility is known in the art.

CTGAGATCAT GAM336321 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336321 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCT encoded by the human genome.

GAM336321 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336321 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336321 precursor RNA is designated SEQ ID:6675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6675 is located from position 8370731 to position 8370818 relative to chromosome 17 on the `+` strand.

GAM336321 precursor RNA folds onto itself, forming GAM336321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336321 precursor RNA, designated SEQ ID NO: 6675, and a schematic representation of a predicted secondary folding of GAM336321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336321 folded precursor RNA yielding a GAM336321 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336321 RNA, hereby incorporated herein. Expression of GAM336321 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336321 target RNA, herein designated GAM TARGET RNA.

GAM336321 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336321 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336321 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336321 RNA, herein designated GAM RNA, to target binding sites on GAM336321 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336321 target RNA into GAM336321 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336321 target genes. The mRNA of each one of this plurality of GAM336321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336321 RNA, herein designated GAM RNA, and which when bound by GAM336321 RNA causes inhibition of translation of the GAM336321 target mRNA into a corresponding GAM336321 target protein.

The mechanism of the translational inhibition exerted by GAM336321 RNA, herein designated GAM RNA, on one or more GAM336321 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336321 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336321 RNA, herein designated GAM RNA, of GAM336321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336321 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336321 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336321 RNA correlate with, and may be deduced from, the identity of the GAM336321 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336322 5836 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336322 (GAM336322) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336322 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336322 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336322 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336322 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336322 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336322 precursor RNA is designated SEQ ID:5836, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5836 is located from position 8383107 to position 8383188 relative to chromosome 11 on the `-` strand.

GAM336322 precursor RNA folds onto itself, forming GAM336322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336322 precursor RNA, designated SEQ ID NO: 5836, and a schematic representation of a predicted secondary folding of GAM336322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336322 folded precursor RNA yielding a GAM336322 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336322 RNA, hereby incorporated herein.

GAM336322 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336322 target RNA, herein designated GAM TARGET RNA.

GAM336322 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336322 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336322 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336322 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336322 RNA, herein designated GAM RNA, to target binding sites on GAM336322 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336322 target RNA into GAM336322 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336322 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336322 target genes. The mRNA of each one of this plurality of GAM336322 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336322 RNA, herein designated GAM RNA, and which when bound by GAM336322 RNA causes inhibition of translation of the GAM336322 target mRNA into a corresponding GAM336322 target protein.

The mechanism of the translational inhibition exerted by GAM336322 RNA, herein designated GAM RNA, on one or more GAM336322 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336322 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336322 RNA, herein designated GAM RNA, of GAM336322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336322 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336322 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336322 RNA correlate with, and may be deduced from, the identity of the GAM336322 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336323 5715 AGAATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACGTGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCAGAGGCT Messenger 336323 (GAM336323) oligonucleotides modulates expression of respective target

GCAGTGAGCC genes whose function and utility is known in the art.

GAGATCGTGC GAM336323 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336323 was detected

CAGCCTGGGC is described with additional reference to Figs. 9-15.

AACAGAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACT encoded by the human genome.

GAM336323 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336323 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336323 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336323 precursor RNA is designated SEQ

ID:5715, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5715 is located from position 8427810 to position 8427893 relative to chromosome 19 on the `+` strand.

GAM336323 precursor RNA folds onto itself, forming GAM336323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336323 precursor RNA, designated SEQ ID NO: 5715, and a schematic representation of a predicted secondary folding of GAM336323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336323 folded precursor RNA yielding a GAM336323 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336323 RNA, hereby incorporated herein. Expression of GAM336323 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336323 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336323 target RNA, herein designated GAM TARGET RNA.

GAM336323 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336323 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336323 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336323 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336323 RNA, herein designated GAM RNA, to target binding sites on GAM336323 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336323 target RNA

into GAM336323 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336323 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336323 target genes. The mRNA of each one of this plurality of GAM336323 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336323 RNA, herein designated GAM RNA, and which when bound by GAM336323 RNA causes inhibition of translation of the GAM336323 target mRNA into a corresponding GAM336323 target protein.

The mechanism of the translational inhibition exerted by GAM336323 RNA, herein designated GAM RNA, on one or more GAM336323 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336323 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336323 RNA, herein designated GAM RNA, of GAM336323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336323 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336323 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336323 RNA correlate with, and may be deduced from, the identity of the GAM336323 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336324 6253 CTTCACCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCACTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTTCTCCAG Messenger 336324 (GAM336324) oligonucleotides modulates expression of respective target

GGATATTAAC genes whose function and utility is known in the art.

CTGGACTTTA GAM336324 is a novel bioinformatically detectable regulatory, non protein

AGAGTCAGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336324 was detected

TGAGTCCCTG is described with additional reference to Figs. 9-15.

GGACTAGTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCCCATCCA encoded by the human genome.

GGATTCAGAC GAM336324 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGGAAG GAM336324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336324 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336324 precursor RNA is designated SEQ ID:6253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6253 is located from position 8553447 to position 8553552 relative to chromosome 19 on the `-` strand.

GAM336324 precursor RNA folds onto itself, forming GAM336324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336324 precursor RNA, designated SEQ ID NO: 6253, and a schematic representation of a predicted secondary folding of GAM336324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336324 folded precursor RNA yielding a GAM336324 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336324 RNA, hereby incorporated herein.

GAM336324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336324 target RNA, herein designated GAM TARGET RNA.

GAM336324 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336324 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336324 RNA, herein designated GAM RNA, to target binding sites on GAM336324 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336324 target RNA into GAM336324 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336324 target genes. The mRNA of each one of this plurality of GAM336324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336324 RNA, herein designated GAM RNA, and which when bound by GAM336324 RNA causes inhibition of translation of the GAM336324 target mRNA into a corresponding GAM336324 target protein.

The mechanism of the translational inhibition exerted by GAM336324 RNA, herein designated GAM RNA, on one or more GAM336324 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336324 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336324 RNA, herein designated GAM RNA, of GAM336324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336324 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336324 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336324 RNA correlate with, and may be deduced from, the identity of the GAM336324 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336325 6739 GGCATGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCGGGAGGCG Messenger 336325 (GAM336325) oligonucleotides modulates expression of respective target

GAGGCTGCAG genes whose function and utility is known in the art.

TGAGCCAAGA GAM336325 is a novel bioinformatically detectable regulatory, non protein
TCGTGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336325 was detected
GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGTGAGACT encoded by the human genome.

CTGTC GAM336325 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336325 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336325 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336325 precursor RNA is designated SEQ ID:6739, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6739 is located from position 8562574 to position 8562668 relative to chromosome 8 on the `+` strand.

GAM336325 precursor RNA folds onto itself, forming GAM336325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336325 precursor RNA, designated SEQ ID NO: 6739, and a schematic representation of a predicted secondary folding of GAM336325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336325 folded precursor RNA yielding a GAM336325 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336325 RNA, hereby incorporated herein. Expression of GAM336325 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336325 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336325 target RNA, herein designated GAM TARGET RNA.

GAM336325 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336325 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336325 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336325 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336325 RNA, herein designated GAM RNA, to target binding sites on GAM336325 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336325 target RNA into GAM336325 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336325 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336325 target genes. The mRNA of each one of this plurality of GAM336325 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336325 RNA, herein designated GAM RNA, and which when bound by GAM336325 RNA causes inhibition of translation of the GAM336325 target mRNA into a corresponding GAM336325 target protein.

The mechanism of the translational inhibition exerted by GAM336325 RNA, herein designated GAM RNA, on one or more GAM336325 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336325 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336325 RNA, herein designated GAM RNA, of GAM336325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336325 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336325 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336325

RNA correlate with, and may be deduced from, the identity of the GAM336325 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336326 5738 AGATGTATTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTCTGTCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCGGGGGTT Messenger 336326 (GAM336326) oligonucleotides modulates expression of respective target
CTGGTCCCTG genes whose function and utility is known in the art.

TGTCAGTCTT GAM336326 is a novel bioinformatically detectable regulatory, non protein
AACTCTCATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336326 was detected
AATATAGAGG is described with additional reference to Figs. 9-15.

TAGTGTTAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGCCAGAAC encoded by the human genome.

CCTAGGGACG GAM336326 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTTTAAATTC GAM336326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
ACT GAM336326 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336326 precursor RNA is designated SEQ ID:5738, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5738 is located from position 8745924 to position 8746036 relative to chromosome 11 on the `+` strand.

GAM336326 precursor RNA folds onto itself, forming GAM336326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336326 precursor RNA, designated SEQ ID NO: 5738, and a schematic representation of a predicted secondary folding of GAM336326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336326 folded precursor RNA yielding a GAM336326 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336326 RNA, hereby incorporated herein.

GAM336326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336326 target RNA, herein designated GAM TARGET RNA.

GAM336326 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336326 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336326 RNA, herein designated GAM RNA, to target binding sites on GAM336326 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336326 target RNA into GAM336326 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336326 target genes. The mRNA of each one of this plurality of GAM336326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336326 RNA, herein designated GAM RNA, and which when bound by GAM336326 RNA causes inhibition of translation of the GAM336326 target mRNA into a corresponding GAM336326 target protein.

The mechanism of the translational inhibition exerted by GAM336326 RNA, herein designated GAM RNA, on one or more GAM336326 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336326 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336326 RNA, herein designated GAM RNA, of GAM336326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336326 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336326 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336326 RNA correlate with, and may be deduced from, the identity of the GAM336326 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336329 6935 GTTACCTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGCCTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCCCTTGTC Messenger 336329 (GAM336329) oligonucleotides modulates expression of respective target
TAGGGCGTGG genes whose function and utility is known in the art.

AGATGAGGTG GAM336329 is a novel bioinformatically detectable regulatory, non protein
TCCTTCCTAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336329 was detected
TCACAGGGTT is described with additional reference to Figs. 9-15.

GCTGCGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGT encoded by the human genome.

TGGC GAM336329 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336329 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336329 precursor RNA is designated SEQ ID:6935, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6935 is located from position 9095043 to position 9095136 relative to chromosome 17 on the `-` strand.

GAM336329 precursor RNA folds onto itself, forming GAM336329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336329 precursor RNA, designated SEQ ID NO: 6935, and a schematic representation of a predicted secondary folding of GAM336329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336329 folded precursor RNA yielding a GAM336329 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336329 RNA, hereby incorporated herein.

GAM336329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336329 target RNA, herein designated GAM TARGET RNA.

GAM336329 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336329 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336329 RNA, herein designated GAM RNA, to target binding sites on GAM336329 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336329 target RNA into GAM336329 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336329 target genes. The mRNA of each one of this plurality of GAM336329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336329 RNA, herein designated GAM RNA, and which when bound by GAM336329 RNA causes inhibition of translation of the GAM336329 target mRNA into a corresponding GAM336329 target protein.

The mechanism of the translational inhibition exerted by GAM336329 RNA, herein designated GAM RNA, on one or more GAM336329 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336329 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336329 RNA, herein designated GAM RNA, of GAM336329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336329 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336329 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336329 RNA correlate with, and may be deduced from, the identity of the GAM336329 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336330 5837 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336330 (GAM336330) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336330 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336330 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336330 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336330 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336330 precursor RNA is designated SEQ ID:5837, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5837 is located from position 9107249 to position 9107330 relative to chromosome 10 on the `+` strand.

GAM336330 precursor RNA folds onto itself, forming GAM336330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336330 precursor RNA, designated SEQ ID NO: 5837, and a schematic representation of a predicted secondary folding of GAM336330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336330 folded precursor RNA yielding a GAM336330 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336330 RNA, hereby incorporated herein.

GAM336330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336330 target RNA, herein designated GAM TARGET RNA.

GAM336330 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336330 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336330 RNA, herein designated GAM RNA, to target binding sites on GAM336330 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336330 target RNA into GAM336330 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336330 target genes. The mRNA of each one of this plurality of GAM336330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336330 RNA, herein designated GAM RNA, and which when bound by GAM336330 RNA causes inhibition of translation of the GAM336330 target mRNA into a corresponding GAM336330 target protein.

The mechanism of the translational inhibition exerted by GAM336330 RNA, herein designated GAM RNA, on one or more GAM336330 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336330 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336330 RNA, herein designated GAM RNA, of GAM336330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336330 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336330 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336330 RNA correlate with, and may be deduced from, the identity of the GAM336330 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336331 6227 CTGGCATACA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAGCCCGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTTCTGCCG Messenger 336331 (GAM336331) oligonucleotides modulates expression of respective target

ATTTGTCACT genes whose function and utility is known in the art.

GCAATCAACA GAM336331 is a novel bioinformatically detectable regulatory, non protein

ATACTCCCCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336331 was detected

GAACATCGGC is described with additional reference to Figs. 9-15.

AAGGATGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTTTCAGAT encoded by the human genome.

GCTGGTGTGC GAM336331 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTGGGAGCCA GAM336331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

G GAM336331 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336331 precursor RNA is designated SEQ

ID:6227, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6227 is located from position 9202641 to position 9202751 relative to chromosome 11 on the `-` strand.

GAM336331 precursor RNA folds onto itself, forming GAM336331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336331 precursor RNA, designated SEQ ID NO: 6227, and a schematic representation of a predicted secondary folding of GAM336331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336331 folded precursor RNA yielding a GAM336331 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336331 RNA, hereby incorporated herein.

GAM336331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336331 target RNA, herein designated GAM TARGET RNA.

GAM336331 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336331 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336331 RNA, herein designated GAM RNA, to target binding sites on GAM336331 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336331 target RNA into GAM336331 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336331 target genes. The mRNA of each one of this plurality of GAM336331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336331 RNA, herein designated GAM RNA, and which when bound by GAM336331 RNA causes inhibition of translation of the GAM336331 target mRNA into a corresponding GAM336331 target protein.

The mechanism of the translational inhibition exerted by GAM336331 RNA, herein designated GAM RNA, on one or more GAM336331 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336331 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336331 RNA, herein designated GAM RNA, of GAM336331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336331 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336331 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336331 RNA correlate with, and may be deduced from, the identity of the GAM336331 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336332 6221 CTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGATTGCAG Messenger 336332 (GAM336332) oligonucleotides modulates expression of respective target

TGAGTCAAGA genes whose function and utility is known in the art.

TGGCACTACT GAM336332 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336332 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

G GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336332 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336332 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336332 precursor RNA is designated SEQ ID:6221, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6221 is located from position 9215763 to position 9215833 relative to chromosome 11 on the `+` strand.

GAM336332 precursor RNA folds onto itself, forming GAM336332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336332 precursor RNA, designated SEQ ID NO: 6221, and a schematic representation of a predicted secondary folding of GAM336332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336332 folded precursor RNA yielding a GAM336332 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336332 RNA, hereby incorporated herein. Expression of GAM336332 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336332 target RNA, herein designated GAM TARGET RNA.

GAM336332 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336332 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336332 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336332 RNA, herein designated GAM RNA, to target binding sites on GAM336332 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336332 target RNA into GAM336332 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336332 target genes. The mRNA of each one of this plurality of GAM336332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336332 RNA, herein designated GAM RNA, and which when bound by GAM336332 RNA causes inhibition of translation of the GAM336332 target mRNA into a corresponding GAM336332 target protein.

The mechanism of the translational inhibition exerted by GAM336332 RNA, herein designated GAM RNA, on one or more GAM336332 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336332 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336332 RNA, herein designated GAM RNA, of GAM336332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336332 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336332 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336332 RNA correlate with, and may be deduced from, the identity of the GAM336332 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336334 7163 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336334 (GAM336334) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CGGTGAGCCG GAM336334 is a novel bioinformatically detectable regulatory, non protein
AGGTCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336334 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGA encoded by the human genome.

AACTCCGTCT GAM336334 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336334 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336334 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336334 precursor RNA is designated SEQ ID:7163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7163 is located from position 9504192 to position 9504293 relative to chromosome 11 on the `+` strand.

GAM336334 precursor RNA folds onto itself, forming GAM336334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336334 precursor RNA, designated SEQ ID NO: 7163, and a schematic representation of a predicted secondary folding of GAM336334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336334 folded precursor RNA yielding a GAM336334 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336334 RNA, hereby incorporated herein. Expression of GAM336334 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336334 target RNA, herein designated GAM TARGET RNA.

GAM336334 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336334 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336334 RNA, herein designated GAM RNA, to target binding sites on GAM336334 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336334 target RNA into GAM336334 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336334 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336334 target genes. The mRNA of each one of this plurality of GAM336334 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336334 RNA, herein designated GAM RNA, and which when bound by GAM336334 RNA causes inhibition of translation of the GAM336334 target mRNA into a corresponding GAM336334 target protein.

The mechanism of the translational inhibition exerted by GAM336334 RNA, herein designated GAM RNA, on one or more GAM336334 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336334 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336334 RNA, herein designated GAM RNA, of GAM336334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336334 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336334 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336334

RNA correlate with, and may be deduced from, the identity of the GAM336334 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336335 6421 GAGGCAGGAG AATTGCTTGA ACCCGGGAGG TGGAGGTTGC GGTGAGCCGA GGTCGCGCCA TTGCACTCCA GCCTGGGCAA CAAGAGCGAA ACTCCGTCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336335 (GAM336335) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336335 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336335 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336335 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336335 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336335 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336335 precursor RNA is designated SEQ ID:6421, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6421 is located from position 9504193 to position 9504292 relative to chromosome 11 on the `+` strand.

GAM336335 precursor RNA folds onto itself, forming GAM336335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336335 precursor RNA, designated SEQ ID NO: 6421, and a schematic representation of a predicted secondary folding of GAM336335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336335 folded precursor RNA yielding a GAM336335 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336335 RNA, hereby incorporated herein. Expression of GAM336335 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336335 target RNA, herein designated GAM TARGET RNA.

GAM336335 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336335 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336335 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336335 RNA, herein designated GAM RNA, to target binding sites on GAM336335 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336335 target RNA into GAM336335 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336335 target genes. The mRNA of each one of this plurality of GAM336335 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336335 RNA, herein designated GAM RNA, and which when bound by GAM336335 RNA causes inhibition of translation of the GAM336335 target mRNA into a corresponding GAM336335 target protein.

The mechanism of the translational inhibition exerted by GAM336335 RNA, herein designated GAM RNA, on one or more GAM336335 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336335 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336335 RNA, herein designated GAM RNA, of GAM336335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336335 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336335 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336335 RNA correlate with, and may be deduced from, the identity of the GAM336335 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336336 7139 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336336 (GAM336336) oligonucleotides modulates expression of respective target
GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336336 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336336 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCAG encoded by the human genome.

AACTCCGTCT GAM336336 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336336 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336336 precursor RNA is designated SEQ ID:7139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7139 is located from position 9554905 to position 9555006 relative to chromosome 2 on the `-` strand.

GAM336336 precursor RNA folds onto itself, forming GAM336336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336336 precursor RNA, designated SEQ ID NO: 7139, and a schematic representation of a predicted secondary folding of GAM336336 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336336 folded precursor RNA yielding a GAM336336 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336336 RNA, hereby incorporated herein. Expression of GAM336336 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336336 target RNA, herein designated GAM TARGET RNA.

GAM336336 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336336 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336336 RNA, herein designated GAM RNA, to target binding sites on GAM336336 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336336 target RNA into GAM336336 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336336 target genes. The mRNA of each one of this plurality of GAM336336 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336336 RNA, herein designated GAM RNA, and which when bound by GAM336336 RNA causes inhibition of translation of the GAM336336 target mRNA into a corresponding GAM336336 target protein.

The mechanism of the translational inhibition exerted by GAM336336 RNA, herein designated GAM RNA, on one or more GAM336336 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336336 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336336 RNA, herein designated GAM RNA, of GAM336336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336336 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336336 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336336 RNA correlate with, and may be deduced from, the identity of the GAM336336 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336337 6633 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336337 (GAM336337) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336337 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336337 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAACTCC encoded by the human genome.

GAM336337 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336337 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336337 precursor RNA is designated SEQ ID:6633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6633 is located from position 9554911 to position 9554999 relative to chromosome 2 on the `-` strand.

GAM336337 precursor RNA folds onto itself, forming GAM336337 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336337 precursor RNA, designated SEQ ID NO: 6633, and a schematic representation of a predicted secondary folding of GAM336337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336337 folded precursor RNA yielding a GAM336337 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336337 RNA, hereby incorporated herein. Expression of GAM336337 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336337 target RNA, herein designated GAM TARGET RNA.

GAM336337 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336337 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336337 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336337 RNA, herein designated GAM RNA, to target binding sites on GAM336337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336337 target RNA into GAM336337 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336337 target genes. The mRNA of each one of this

plurality of GAM336337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336337 RNA, herein designated GAM RNA, and which when bound by GAM336337 RNA causes inhibition of translation of the GAM336337 target mRNA into a corresponding GAM336337 target protein.

The mechanism of the translational inhibition exerted by GAM336337 RNA, herein designated GAM RNA, on one or more GAM336337 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336337 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336337 RNA, herein designated GAM RNA, of GAM336337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336337 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336337 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336337 RNA correlate with, and may be deduced from, the identity of the GAM336337 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336338 6927 GTGTGATATA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGGTCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GATCATGGCT Messenger 336338 (GAM336338) oligonucleotides modulates expression of respective target

GGACAAACAC genes whose function and utility is known in the art.

AATGCAGTAG GAM336338 is a novel bioinformatically detectable regulatory, non protein

GAAGAGTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336338 was detected

GGCTCTTGGT is described with additional reference to Figs. 9-15.

CACTGCTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGACCCAATG encoded by the human genome.

ATCTTGAGCA GAM336338 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCACCCGTCA GAM336338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TAC GAM336338 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336338 precursor RNA is designated SEQ ID:6927, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6927 is located from position 9584579 to position 9584691 relative to chromosome 18 on the `+` strand.

GAM336338 precursor RNA folds onto itself, forming GAM336338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336338 precursor RNA, designated SEQ ID NO: 6927, and a schematic representation of a predicted secondary folding of GAM336338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336338 folded precursor RNA yielding a GAM336338 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336338 RNA, hereby incorporated herein.

GAM336338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336338 target RNA, herein designated GAM TARGET RNA.

GAM336338 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336338 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336338 RNA, herein designated GAM RNA, to target binding sites on GAM336338 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336338 target RNA into GAM336338 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336338 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336338 target genes. The mRNA of each one of this plurality of GAM336338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336338 RNA, herein designated GAM RNA, and which when bound by GAM336338 RNA causes inhibition of translation of the GAM336338 target mRNA into a corresponding GAM336338 target protein.

The mechanism of the translational inhibition exerted by GAM336338 RNA, herein designated GAM RNA, on one or more GAM336338 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336338 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336338 RNA, herein designated GAM RNA, of GAM336338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336338 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336338 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336338 RNA correlate with, and may be deduced from, the identity of the GAM336338 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336339 6425 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGTGGG Messenger 336339 (GAM336339) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336339 is a novel bioinformatically detectable regulatory, non protein

AGATAACGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336339 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTAAA encoded by the human genome.

ACTCCGTCTC GAM336339 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336339 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336339 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336339 precursor RNA is designated SEQ ID:6425, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6425 is located from position 9731276 to position 9731375 relative to chromosome 18 on the `+` strand.

GAM336339 precursor RNA folds onto itself, forming GAM336339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336339 precursor RNA, designated SEQ ID NO: 6425, and a schematic representation of a predicted secondary folding of GAM336339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336339 folded precursor RNA yielding a GAM336339 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336339 RNA, hereby incorporated herein. Expression of GAM336339 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336339 target RNA, herein designated GAM TARGET RNA.

GAM336339 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336339 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336339 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336339 RNA, herein designated GAM RNA, to target binding sites on GAM336339 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336339 target RNA into GAM336339 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336339 target genes. The mRNA of each one of this plurality of GAM336339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336339 RNA, herein designated GAM RNA, and which when bound by GAM336339 RNA causes inhibition of translation of the GAM336339 target mRNA into a corresponding GAM336339 target protein.

The mechanism of the translational inhibition exerted by GAM336339 RNA, herein designated GAM RNA, on one or more GAM336339 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336339 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336339 RNA, herein designated GAM RNA, of GAM336339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336339 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336339 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336339 RNA correlate with, and may be deduced from, the identity of the GAM336339 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336340 6406 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAAG Messenger 336340 (GAM336340) oligonucleotides modulates expression of respective target
CGGAGGTTGC genes whose function and utility is known in the art.

CGTGAGTCGA GAM336340 is a novel bioinformatically detectable regulatory, non protein
GATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336340 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCGAA encoded by the human genome.

ACTCTCTC GAM336340 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336340 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336340 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336340 precursor RNA is designated SEQ ID:6406, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6406 is located from position 9732603 to position 9732700 relative to chromosome 3 on the `+` strand.

GAM336340 precursor RNA folds onto itself, forming GAM336340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336340 precursor RNA, designated SEQ ID NO: 6406, and a schematic representation of a predicted secondary folding of GAM336340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336340 folded precursor RNA yielding a GAM336340 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336340 RNA, hereby incorporated herein. Expression of GAM336340 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336340 target RNA, herein designated GAM TARGET RNA.

GAM336340 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336340 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336340 RNA, herein designated GAM RNA, to target binding sites on GAM336340 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336340 target RNA into GAM336340 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336340 target genes. The mRNA of each one of this plurality of GAM336340 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336340 RNA, herein designated GAM RNA, and which when bound by GAM336340 RNA causes inhibition of translation of the GAM336340 target mRNA into a corresponding GAM336340 target protein.

The mechanism of the translational inhibition exerted by GAM336340 RNA, herein designated GAM RNA, on one or more GAM336340 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336340 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336340 RNA, herein designated GAM RNA, of GAM336340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336340 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336340 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336340 RNA correlate with, and may be deduced from, the identity of the GAM336340 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336341 5718 AGAATTGCTC GAACCCGGGA GACAGAGGTT GCAGTGAGCC GAGATTGTGC CACTGCACTC CAGCCTGGGC AACAGAGCGA GACT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336341 (GAM336341) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336341 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336341 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336341 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336341 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336341 precursor RNA is designated SEQ ID:5718, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5718 is located from position 9793682 to position 9793765 relative to chromosome 3 on the `+` strand.

GAM336341 precursor RNA folds onto itself, forming GAM336341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336341 precursor RNA, designated SEQ ID NO: 5718, and a schematic representation of a predicted secondary folding of GAM336341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336341 folded precursor RNA yielding a GAM336341 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336341 RNA, hereby incorporated herein. Expression of GAM336341 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336341 target RNA, herein designated GAM TARGET RNA.

GAM336341 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336341 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336341 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336341 RNA, herein designated GAM RNA, to target binding sites on GAM336341 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336341 target RNA into GAM336341 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336341 target genes. The mRNA of each one of this plurality of GAM336341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336341 RNA, herein designated GAM RNA, and which when bound by GAM336341 RNA causes inhibition of translation of the GAM336341 target mRNA into a corresponding GAM336341 target protein.

The mechanism of the translational inhibition exerted by GAM336341 RNA, herein designated GAM RNA, on one or more GAM336341 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336341 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336341 RNA, herein designated GAM RNA, of GAM336341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336341 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336341 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336341 RNA correlate with, and may be deduced from, the identity of the GAM336341 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336342 7310 TTGCTCGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGACA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336342 (GAM336342) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TTGTGCCACT GAM336342 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336342 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336342 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336342 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336342 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336342 precursor RNA is designated SEQ ID:7310, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7310 is located from position 9793686 to position 9793761 relative to chromosome 3 on the `+` strand.

GAM336342 precursor RNA folds onto itself, forming GAM336342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336342 precursor RNA, designated SEQ ID NO: 7310, and a schematic representation of a predicted secondary folding of GAM336342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336342 folded precursor RNA yielding a GAM336342 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336342 RNA, hereby incorporated herein. Expression of GAM336342 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336342 target RNA, herein designated GAM TARGET RNA.

GAM336342 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336342 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336342 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336342 RNA, herein designated GAM RNA, to target binding sites on GAM336342 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336342 target RNA into GAM336342 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336342 target genes. The mRNA of each one of this plurality of GAM336342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336342 RNA, herein designated GAM RNA, and which when bound by GAM336342 RNA causes inhibition of translation of the GAM336342 target mRNA into a corresponding GAM336342 target protein.

The mechanism of the translational inhibition exerted by GAM336342 RNA, herein designated GAM RNA, on one or more GAM336342 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336342 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336342 RNA, herein designated GAM RNA, of GAM336342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336342 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336342 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336342 RNA correlate with, and may be deduced from, the identity of the GAM336342 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336343 6535 GCTCGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGAGACAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTTGCAGTG Messenger 336343 (GAM336343) oligonucleotides modulates expression of respective target
AGCCGAGATT genes whose function and utility is known in the art.

GTGCCACTGC GAM336343 is a novel bioinformatically detectable regulatory, non protein
ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336343 was detected
GGGCAACAGA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336343 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336343 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336343 precursor RNA is designated SEQ ID:6535, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6535 is located from position 9793688 to position 9793759 relative to chromosome 3 on the `+` strand.

GAM336343 precursor RNA folds onto itself, forming GAM336343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336343 precursor RNA, designated SEQ ID NO: 6535, and a schematic representation of a predicted secondary folding of GAM336343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336343 folded precursor RNA yielding a GAM336343 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336343 RNA, hereby incorporated herein. Expression of GAM336343 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336343 target RNA, herein designated GAM TARGET RNA.

GAM336343 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336343 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336343 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336343 RNA, herein designated GAM RNA, to target binding sites on GAM336343 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336343 target RNA into GAM336343 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336343 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336343 target genes. The mRNA of each one of this plurality of GAM336343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336343 RNA, herein designated GAM RNA, and which when bound by GAM336343 RNA causes inhibition of translation of the GAM336343 target mRNA into a corresponding GAM336343 target protein.

The mechanism of the translational inhibition exerted by GAM336343 RNA, herein designated GAM RNA, on one or more GAM336343 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336343 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336343 RNA, herein designated GAM RNA, of GAM336343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336343 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336343 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336343 RNA correlate with, and may be deduced from, the identity of the GAM336343 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336344 6803 GGGCGAGTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAACCTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAAAATAAAC Messenger 336344 (GAM336344) oligonucleotides modulates expression of respective target

TTCTGAATTT genes whose function and utility is known in the art.

ATTGAGACCT GAM336344 is a novel bioinformatically detectable regulatory, non protein

GTCTCAGGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336344 was detected

CTTTTTGGTT is described with additional reference to Figs. 9-15.

TACATGTGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTGAGGGCA encoded by the human genome.

GGCACC GAM336344 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336344 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336344 precursor RNA is designated SEQ ID:6803, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6803 is located from position 9881789 to position 9881884 relative to chromosome 11 on the `+` strand.

GAM336344 precursor RNA folds onto itself, forming GAM336344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336344 precursor RNA, designated SEQ ID NO: 6803, and a schematic representation of a predicted secondary folding of GAM336344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336344 folded precursor RNA yielding a GAM336344 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336344 RNA, hereby incorporated herein.

GAM336344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336344 target RNA, herein designated GAM TARGET RNA.

GAM336344 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336344 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336344 RNA, herein designated GAM RNA, to target binding sites on GAM336344 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336344 target RNA into GAM336344 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336344 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336344 target genes. The mRNA of each one of this plurality of GAM336344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336344 RNA, herein designated GAM RNA, and which when bound by GAM336344 RNA causes inhibition of translation of the GAM336344 target mRNA into a corresponding GAM336344 target protein.

The mechanism of the translational inhibition exerted by GAM336344 RNA, herein designated GAM RNA, on one or more GAM336344 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336344 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336344 RNA, herein designated GAM RNA, of GAM336344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336344 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336344 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336344 RNA correlate with, and may be deduced from, the identity of the GAM336344 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336347 5726 AGAGATGCTA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTTTAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGGGGCA Messenger 336347 (GAM336347) oligonucleotides modulates expression of respective target

GGACTGGATT genes whose function and utility is known in the art.

TTTAATTTCA TCTGGCTCCT GAGTCCTAGC TCCTAATCCT

GAM336347 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336347 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336347 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336347 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336347 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336347 precursor RNA is designated SEQ ID:5726, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5726 is located from position 10064670 to position 10064749 relative to chromosome 19 on the `+` strand.

GAM336347 precursor RNA folds onto itself, forming GAM336347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336347 precursor RNA, designated SEQ ID NO: 5726, and a schematic representation of a predicted secondary folding of GAM336347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336347 folded precursor RNA yielding a GAM336347 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336347 RNA, hereby incorporated herein.

GAM336347 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336347 target RNA, herein designated GAM TARGET RNA.

GAM336347 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336347 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336347 RNA, herein designated GAM RNA, to target binding sites on GAM336347 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336347 target RNA into GAM336347 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336347 target genes. The mRNA of each one of this plurality of GAM336347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336347 RNA, herein designated GAM RNA, and which when bound by GAM336347 RNA causes inhibition of translation of the GAM336347 target mRNA into a corresponding GAM336347 target protein.

The mechanism of the translational inhibition exerted by GAM336347 RNA, herein designated GAM RNA, on one or more GAM336347 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336347 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336347 RNA, herein designated GAM RNA, of GAM336347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336347 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336347 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336347 RNA correlate with, and may be deduced from, the identity of the GAM336347 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336348 5838 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336348 (GAM336348) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336348 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336348 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336348 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336348 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336348 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336348 precursor RNA is designated SEQ ID:5838, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5838 is located from position 10077912 to position 10077993 relative to chromosome 4 on the `-` strand.

GAM336348 precursor RNA folds onto itself, forming GAM336348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336348 precursor RNA, designated SEQ ID NO: 5838, and a schematic representation of a predicted secondary folding of GAM336348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336348 folded precursor RNA yielding a GAM336348 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336348 RNA, hereby incorporated herein.

GAM336348 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336348 target RNA, herein designated GAM TARGET RNA.

GAM336348 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336348 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336348 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336348 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336348 RNA, herein designated GAM RNA, to target binding sites on GAM336348 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336348 target RNA into GAM336348 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336348 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336348 target genes. The mRNA of each one of this plurality of GAM336348 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336348 RNA, herein designated GAM RNA, and which when bound by GAM336348 RNA causes inhibition of translation of the GAM336348 target mRNA into a corresponding GAM336348 target protein.

The mechanism of the translational inhibition exerted by GAM336348 RNA, herein designated GAM RNA, on one or more GAM336348 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336348 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336348 RNA, herein designated GAM RNA, of GAM336348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336348 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336348 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336348 RNA correlate with, and may be deduced from, the identity of the GAM336348 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336349 7088 TGAATTTGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
ACTTGTCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTGGCATCT Messenger 336349 (GAM336349) oligonucleotides modulates expression of respective target
CGAAGGGCTT genes whose function and utility is known in the art.

TCTCTACTGG GAM336349 is a novel bioinformatically detectable regulatory, non protein
GTCCAGGGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336349 was detected
CCACAGAACA is described with additional reference to Figs. 9-15.

GGTCAGCATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CA encoded by the human genome.

GAM336349 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336349 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336349 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336349 precursor RNA is designated SEQ ID:7088, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7088 is located from position 10202193 to position 10202274 relative to chromosome 7 on the `-` strand.

GAM336349 precursor RNA folds onto itself, forming GAM336349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336349 precursor RNA, designated SEQ ID NO: 7088, and a schematic representation of a predicted secondary folding of GAM336349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336349 folded precursor RNA yielding a GAM336349 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336349 RNA, hereby incorporated herein.

GAM336349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336349 target RNA, herein designated GAM TARGET RNA.

GAM336349 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336349 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336349 RNA, herein designated GAM RNA, to target binding sites on GAM336349 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336349 target RNA into GAM336349 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336349 target genes. The mRNA of each one of this plurality of GAM336349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336349 RNA, herein designated GAM RNA, and which when bound by GAM336349 RNA causes inhibition of translation of the GAM336349 target mRNA into a corresponding GAM336349 target protein.

The mechanism of the translational inhibition exerted by GAM336349 RNA, herein designated GAM RNA, on one or more GAM336349 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336349 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336349 RNA, herein designated GAM RNA, of GAM336349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336349 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336349 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336349 RNA correlate with, and may be deduced from, the identity of the GAM336349 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336350 6403 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCTAGGAAT Messenger 336350 (GAM336350) oligonucleotides modulates expression of respective target
CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336350 is a novel bioinformatically detectable regulatory, non protein
GGTCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336350 was detected
CTTGCACTCC is described with additional reference to Figs. 9-15.

ACAGCCTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGACAGAGTG encoded by the human genome.

AGACTGCCTC GAM336350 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336350 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336350 precursor RNA is designated SEQ ID:6403, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6403 is located from position 10212232 to position 10212331 relative to chromosome 19 on the `+` strand.

GAM336350 precursor RNA folds onto itself, forming GAM336350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336350 precursor RNA, designated SEQ ID NO: 6403, and a schematic representation of a predicted secondary folding of GAM336350 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336350 folded precursor RNA yielding a GAM336350 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336350 RNA, hereby incorporated herein.

GAM336350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336350 target RNA, herein designated GAM TARGET RNA.

GAM336350 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336350 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336350 RNA, herein designated GAM RNA, to target binding sites on GAM336350 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336350 target RNA into GAM336350 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336350 target genes. The mRNA of each one of this plurality of GAM336350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336350 RNA, herein designated GAM RNA, and which when bound by GAM336350 RNA causes inhibition of translation of the GAM336350 target mRNA into a corresponding GAM336350 target protein.

The mechanism of the translational inhibition exerted by GAM336350 RNA, herein designated GAM RNA, on one or more GAM336350 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336350 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336350 RNA, herein designated GAM RNA, of GAM336350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336350 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336350 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336350 RNA correlate with, and may be deduced from, the identity of the GAM336350 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336352 5839 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336352 (GAM336352) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336352 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336352 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336352 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336352 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336352 precursor RNA is designated SEQ ID:5839, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5839 is located from position 10343377 to position 10343458 relative to chromosome 8 on the `-` strand.

GAM336352 precursor RNA folds onto itself, forming GAM336352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336352 precursor RNA, designated SEQ ID NO: 5839, and a schematic representation of a predicted secondary folding of GAM336352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336352 folded precursor RNA yielding a GAM336352 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336352 RNA, hereby incorporated herein.

GAM336352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336352 target RNA, herein designated GAM TARGET RNA.

GAM336352 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336352 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336352 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336352 RNA, herein designated GAM RNA, to target binding sites on GAM336352 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336352 target RNA into GAM336352 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336352 target genes. The mRNA of each one of this plurality of GAM336352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336352 RNA, herein designated GAM RNA, and which when bound by GAM336352 RNA causes inhibition of translation of the GAM336352 target mRNA into a corresponding GAM336352 target protein.

The mechanism of the translational inhibition exerted by GAM336352 RNA, herein designated GAM RNA, on one or more GAM336352 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336352 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336352 RNA, herein designated GAM RNA, of GAM336352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336352 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336352 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336352 RNA correlate with, and may be deduced from, the identity of the GAM336352 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336353 6410 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGGCGCGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAAG Messenger 336353 (GAM336353) oligonucleotides modulates expression of respective target

TGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336353 is a novel bioinformatically detectable regulatory, non protein

GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336353 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCGAAA encoded by the human genome.

CTCCGTCTC GAM336353 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336353 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336353 precursor RNA is designated SEQ ID:6410, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6410 is located from position 10535996 to position 10536094 relative to chromosome 16 on the `+` strand.

GAM336353 precursor RNA folds onto itself, forming GAM336353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336353 precursor RNA, designated SEQ ID NO: 6410, and a schematic representation of a predicted secondary folding of GAM336353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336353 folded precursor RNA yielding a GAM336353 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336353 RNA, hereby incorporated herein. Expression of GAM336353 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336353 target RNA, herein designated GAM TARGET RNA.

GAM336353 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336353 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336353 RNA, herein designated GAM RNA, to target binding sites on GAM336353 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336353 target RNA into GAM336353 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336353 target genes. The mRNA of each one of this plurality of GAM336353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336353 RNA, herein designated GAM RNA, and which when bound by GAM336353 RNA causes inhibition of translation of the GAM336353 target mRNA into a corresponding GAM336353 target protein.

The mechanism of the translational inhibition exerted by GAM336353 RNA, herein designated GAM RNA, on one or more GAM336353 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336353 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336353 RNA, herein designated GAM RNA, of GAM336353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336353 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336353 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336353 RNA correlate with, and may be deduced from, the identity of the GAM336353 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336354 7097 TGAGACAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTCCGGAG Messenger 336354 (GAM336354) oligonucleotides modulates expression of respective target

GTTGAGGTTT genes whose function and utility is known in the art.

CAGTGGGCCG GAM336354 is a novel bioinformatically detectable regulatory, non protein

AGACCGAGCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336354 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCGAG encoded by the human genome.

ACTCCATTTC GAM336354 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336354 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336354 precursor RNA is designated SEQ ID:7097, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7097 is located from position 10593137 to position 10593237 relative to chromosome 19 on the `+` strand.

GAM336354 precursor RNA folds onto itself, forming GAM336354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336354 precursor RNA, designated SEQ ID NO: 7097, and a schematic representation of a predicted secondary folding of GAM336354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336354 folded precursor RNA yielding a GAM336354 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336354 RNA, hereby incorporated herein. Expression of GAM336354 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336354 target RNA, herein designated GAM TARGET RNA.

GAM336354 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336354 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336354 RNA, herein designated GAM RNA, to target binding sites on GAM336354 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336354 target RNA into GAM336354 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336354 target genes. The mRNA of each one of this plurality of GAM336354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336354 RNA, herein designated GAM RNA, and which when bound by GAM336354 RNA causes inhibition of translation of the GAM336354 target mRNA into a corresponding GAM336354 target protein.

The mechanism of the translational inhibition exerted by GAM336354 RNA, herein designated GAM RNA, on one or more GAM336354 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336354 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336354 RNA, herein designated GAM RNA, of GAM336354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336354 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336354 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336354 RNA correlate with, and may be deduced from, the identity of the GAM336354 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336357 7043 TCCTGCATGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTTCCATA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCAGAGCCA Messenger 336357 (GAM336357) oligonucleotides modulates expression of respective target
GAATCCATCC genes whose function and utility is known in the art.

TTGTTCCTTC GAM336357 is a novel bioinformatically detectable regulatory, non protein
TGCATTGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336357 was detected
GAAAATCCAT is described with additional reference to Figs. 9-15.

GGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336357 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336357 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336357 precursor RNA is designated SEQ ID:7043, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7043 is located from position 10669795 to position 10669870 relative to chromosome 17 on the `-` strand.

GAM336357 precursor RNA folds onto itself, forming GAM336357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336357 precursor RNA, designated SEQ ID NO: 7043, and a schematic representation of a predicted secondary folding of GAM336357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336357 folded precursor RNA yielding a GAM336357 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336357 RNA, hereby incorporated herein.

GAM336357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336357 target RNA, herein designated GAM TARGET RNA.

GAM336357 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336357 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336357 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336357 RNA, herein designated GAM RNA, to target binding sites on GAM336357 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336357 target RNA into GAM336357 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336357 target genes. The mRNA of each one of this plurality of GAM336357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336357 RNA, herein designated GAM RNA, and which when bound by GAM336357 RNA causes inhibition of translation of the GAM336357 target mRNA into a corresponding GAM336357 target protein.

The mechanism of the translational inhibition exerted by GAM336357 RNA, herein designated GAM RNA, on one or more GAM336357 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336357 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336357 RNA, herein designated GAM RNA, of GAM336357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336357 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336357 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336357

RNA correlate with, and may be deduced from, the identity of the GAM336357 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336359 7085 TGAACCCCGG AGACAGAGGT TGCAGTGAGC CGAGATACAT ACATATATAT GTATATATCA TGTGCAACTT GGCTCTGCTC CTTTGTAAGT TTGTGGGCTT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336359 (GAM336359) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336359 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336359 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336359 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336359 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336359 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336359 precursor RNA is designated SEQ ID:7085, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7085 is located from position 10822733 to position 10822833 relative to chromosome 8 on the `-` strand.

GAM336359 precursor RNA folds onto itself, forming GAM336359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336359 precursor RNA, designated SEQ ID NO: 7085, and a schematic representation of a predicted secondary folding of GAM336359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336359 folded precursor RNA yielding a GAM336359 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336359 RNA, hereby incorporated herein.

GAM336359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336359 target RNA, herein designated GAM TARGET RNA.

GAM336359 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336359 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336359 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336359 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336359 RNA, herein designated GAM RNA, to target binding sites on GAM336359 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336359 target RNA into GAM336359 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336359 target genes. The mRNA of each one of this plurality of GAM336359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336359 RNA, herein designated GAM RNA, and which when bound by GAM336359 RNA causes inhibition of translation of the GAM336359 target mRNA into a corresponding GAM336359 target protein.

The mechanism of the translational inhibition exerted by GAM336359 RNA, herein designated GAM RNA, on one or more GAM336359 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336359 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336359 RNA, herein designated GAM RNA, of GAM336359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336359 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336359 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336359 RNA correlate with, and may be deduced from, the identity of the GAM336359 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336360 5687 ACAGAGGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGTGAGCCG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATACATAC Messenger 336360 (GAM336360) oligonucleotides modulates expression of respective target
ATATATATGT genes whose function and utility is known in the art.

ATATATCATG GAM336360 is a novel bioinformatically detectable regulatory, non protein
TGCAACTTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336360 was detected
CTCTGCTCCT is described with additional reference to Figs. 9-15.

TTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336360 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336360 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336360 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336360 precursor RNA is designated SEQ ID:5687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5687 is located from position 10822748 to position 10822821 relative to chromosome 8 on the `-` strand.

GAM336360 precursor RNA folds onto itself, forming GAM336360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336360 precursor RNA, designated SEQ ID NO: 5687, and a schematic representation of a predicted secondary folding of GAM336360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336360 folded precursor RNA yielding a GAM336360 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336360 RNA, hereby incorporated herein.

GAM336360 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336360 target RNA, herein designated GAM TARGET RNA.

GAM336360 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336360 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336360 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336360 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336360 RNA, herein designated GAM RNA, to target binding sites on GAM336360 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336360 target RNA into GAM336360 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336360 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336360 target genes. The mRNA of each one of this plurality of GAM336360 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336360 RNA, herein designated GAM RNA, and which when bound by GAM336360 RNA causes inhibition of translation of the GAM336360 target mRNA into a corresponding GAM336360 target protein.

The mechanism of the translational inhibition exerted by GAM336360 RNA, herein designated GAM RNA, on one or more GAM336360 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336360 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336360 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336360 RNA, herein designated GAM RNA, of GAM336360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336360 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336360 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336360 RNA correlate with, and may be deduced from, the identity of the GAM336360 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336361 6684 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGAGG Messenger 336361 (GAM336361) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATAGC GAM336361 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336361 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336361 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336361 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336361 precursor RNA is designated SEQ ID:6684, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6684 is located from position 10939875 to position 10939962 relative to chromosome 2 on the `+` strand.

GAM336361 precursor RNA folds onto itself, forming GAM336361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336361 precursor RNA, designated SEQ ID NO: 6684, and a schematic representation of a predicted secondary folding of GAM336361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336361 folded precursor RNA yielding a GAM336361 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336361 RNA, hereby incorporated herein. Expression of GAM336361 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336361 target RNA, herein designated GAM TARGET RNA.

GAM336361 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336361 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336361 RNA, herein designated GAM RNA, to target binding sites on GAM336361 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336361 target RNA into GAM336361 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336361 target genes. The mRNA of each one of this plurality of GAM336361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336361 RNA, herein designated GAM RNA, and which when bound by GAM336361 RNA causes inhibition of translation of the GAM336361 target mRNA into a corresponding GAM336361 target protein.

The mechanism of the translational inhibition exerted by GAM336361 RNA, herein designated GAM RNA, on one or more GAM336361 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336361 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336361 RNA, herein designated GAM RNA, of GAM336361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336361 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336361 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336361 RNA correlate with, and may be deduced from, the identity of the GAM336361 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336362 6116 CCTGACTCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCACAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGAATAAA Messenger 336362 (GAM336362) oligonucleotides modulates expression of respective target

GTCTCATTTC genes whose function and utility is known in the art.

AATCCTGAGC GAM336362 is a novel bioinformatically detectable regulatory, non protein

TTCTCCTAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336362 was detected

TCTTGTGGAT is described with additional reference to Figs. 9-15.

CAGAGCTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336362 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336362 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336362 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336362 precursor RNA is designated SEQ

ID:6116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6116 is located from position 10975636 to position 10975715 relative to chromosome X on the `-` strand.

GAM336362 precursor RNA folds onto itself, forming GAM336362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336362 precursor RNA, designated SEQ ID NO: 6116, and a schematic representation of a predicted secondary folding of GAM336362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336362 folded precursor RNA yielding a GAM336362 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336362 RNA, hereby incorporated herein.

GAM336362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336362 target RNA, herein designated GAM TARGET RNA.

GAM336362 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336362 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336362 RNA, herein designated GAM RNA, to target binding sites on GAM336362 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336362 target RNA into GAM336362 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336362 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336362 target genes. The mRNA of each one of this plurality of GAM336362 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336362 RNA, herein designated GAM RNA, and which when bound by GAM336362 RNA causes inhibition of translation of the GAM336362 target mRNA into a corresponding GAM336362 target protein.

The mechanism of the translational inhibition exerted by GAM336362 RNA, herein designated GAM RNA, on one or more GAM336362 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336362 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336362 RNA, herein designated GAM RNA, of GAM336362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336362 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336362 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336362 RNA correlate with, and may be deduced from, the identity of the GAM336362 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336363 5742 AGCAGACTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTAAGACAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTCTGCCTG Messenger 336363 (GAM336363) oligonucleotides modulates expression of respective target

TGGTTGTCTT genes whose function and utility is known in the art.

GGCAAAGCCA GAM336363 is a novel bioinformatically detectable regulatory, non protein

GGTAATGCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336363 was detected

GAGAGGGGTG is described with additional reference to Figs. 9-15.

GACTCAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCT encoded by the human genome.

GAM336363 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336363 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336363 precursor RNA is designated SEQ ID:5742, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5742 is located from position 11000648 to position 11000730 relative to chromosome 16 on the `+` strand.

GAM336363 precursor RNA folds onto itself, forming GAM336363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336363 precursor RNA, designated SEQ ID NO: 5742, and a schematic representation of a predicted secondary folding of GAM336363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336363 folded precursor RNA yielding a GAM336363 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336363 RNA, hereby incorporated herein.

GAM336363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336363 target RNA, herein designated GAM TARGET RNA.

GAM336363 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336363 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336363 RNA, herein designated GAM RNA, to target binding sites on GAM336363 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336363 target RNA into GAM336363 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336363 target genes. The mRNA of each one of this plurality of GAM336363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336363 RNA, herein designated GAM RNA, and which when bound by GAM336363 RNA causes inhibition of translation of the GAM336363 target mRNA into a corresponding GAM336363 target protein.

The mechanism of the translational inhibition exerted by GAM336363 RNA, herein designated GAM RNA, on one or more GAM336363 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336363 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336363 RNA, herein designated GAM RNA, of GAM336363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336363 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336363 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336363 RNA correlate with, and may be deduced from, the identity of the GAM336363 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336364 7327 TTGCTTTAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTTGCAG Messenger 336364 (GAM336364) oligonucleotides modulates expression of respective target

TGAGCTATGA genes whose function and utility is known in the art.

TGGTGTCATT GAM336364 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336364 was detected
CTGGGCAATC is described with additional reference to Figs. 9-15.

AAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336364 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336364 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336364 precursor RNA is designated SEQ ID:7327, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7327 is located from position 11034593 to position 11034668 relative to chromosome 12 on the `-` strand.

GAM336364 precursor RNA folds onto itself, forming GAM336364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336364 precursor RNA, designated SEQ ID NO: 7327, and a schematic representation of a predicted secondary folding of GAM336364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336364 folded precursor RNA yielding a GAM336364 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336364 RNA, hereby incorporated herein.

GAM336364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336364 target RNA, herein designated GAM TARGET RNA.

GAM336364 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336364 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336364 RNA, herein designated GAM RNA, to target binding sites on GAM336364 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336364 target RNA into GAM336364 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336364 target genes. The mRNA of each one of this plurality of GAM336364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336364 RNA, herein designated GAM RNA, and which when bound by GAM336364 RNA causes inhibition of translation of the GAM336364 target mRNA into a corresponding GAM336364 target protein.

The mechanism of the translational inhibition exerted by GAM336364 RNA, herein designated GAM RNA, on one or more GAM336364 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336364 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336364 RNA, herein designated GAM RNA, of GAM336364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336364 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336364 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336364 RNA correlate with, and may be deduced from, the identity of the GAM336364 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336365 6020 CAGCTGGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCAGGGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATCACG Messenger 336365 (GAM336365) oligonucleotides modulates expression of respective target
CCTGGCTAAT genes whose function and utility is known in the art.

TTTTGTATTT GAM336365 is a novel bioinformatically detectable regulatory, non protein
TCTGTAGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336365 was detected
TAGGATTTCA is described with additional reference to Figs. 9-15.

CAGTGTTACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGGCTGGTC encoded by the human genome.

TCAAAATCCT GAM336365 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGGCTCAAAT GAM336365 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
G GAM336365 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336365 precursor RNA is designated SEQ ID:6020, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6020 is located from position 11079910 to position 11080020 relative to chromosome 12 on the `-` strand.

GAM336365 precursor RNA folds onto itself, forming GAM336365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336365 precursor RNA, designated SEQ ID NO: 6020, and a schematic representation of a predicted secondary folding of GAM336365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336365 folded precursor RNA yielding a GAM336365 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336365 RNA, hereby incorporated herein.

GAM336365 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336365 target RNA, herein designated GAM TARGET RNA.

GAM336365 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336365 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336365 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336365 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336365 RNA, herein designated GAM RNA, to target binding sites on GAM336365 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336365 target RNA into GAM336365 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336365 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336365 target genes. The mRNA of each one of this plurality of GAM336365 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336365 RNA, herein designated GAM RNA, and which when bound by GAM336365 RNA causes inhibition of translation of the GAM336365 target mRNA into a corresponding GAM336365 target protein.

The mechanism of the translational inhibition exerted by GAM336365 RNA, herein designated GAM RNA, on one or more GAM336365 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336365 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336365 RNA, herein designated GAM RNA, of GAM336365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336365 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336365 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336365 RNA correlate with, and may be deduced from, the identity of the GAM336365 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336368 6242 CTGTGACTAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCGCTGAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTTGCAACT Messenger 336368 (GAM336368) oligonucleotides modulates expression of respective target
CTGAGAGGTC genes whose function and utility is known in the art.

AGTACTTTTA GAM336368 is a novel bioinformatically detectable regulatory, non protein
TTTTACCCAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336368 was detected
TTTGTAGGTG is described with additional reference to Figs. 9-15.

AGAAAACTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCTCAGAAA encoded by the human genome.

GGGTAACACA GAM336368 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTGACACAG GAM336368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336368 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336368 precursor RNA is designated SEQ ID:6242, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6242 is located from position 11301473 to position 11301581 relative to chromosome 11 on the `+` strand.

GAM336368 precursor RNA folds onto itself, forming GAM336368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336368 precursor RNA, designated SEQ ID NO: 6242, and a schematic representation of a predicted secondary folding of GAM336368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336368 folded precursor RNA yielding a GAM336368 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336368 RNA, hereby incorporated herein.

GAM336368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336368 target RNA, herein designated GAM TARGET RNA.

GAM336368 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336368 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336368 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336368 RNA, herein designated GAM RNA, to target binding sites on GAM336368 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336368 target RNA into GAM336368 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336368 target genes. The mRNA of each one of this plurality of GAM336368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336368 RNA, herein designated GAM RNA, and which when bound by GAM336368 RNA causes inhibition of translation of the GAM336368 target mRNA into a corresponding GAM336368 target protein.

The mechanism of the translational inhibition exerted by GAM336368 RNA, herein designated GAM RNA, on one or more GAM336368 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336368 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336368 RNA, herein designated GAM RNA, of

GAM336368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336368 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336368 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336368 RNA correlate with, and may be deduced from, the identity of the GAM336368 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336369 6219 CTGCCTCCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCAAGCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTAAGGACG Messenger 336369 (GAM336369) oligonucleotides modulates expression of respective target

CAAAGAGGGC genes whose function and utility is known in the art.

AAGGCCACGA GAM336369 is a novel bioinformatically detectable regulatory, non protein

AGGACTCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336369 was detected

CTGGCCCATC is described with additional reference to Figs. 9-15.

GTGTCCCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGCCCCAG encoded by the human genome.

TGCCAGAGCC GAM336369 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AG GAM336369 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336369 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336369 precursor RNA is designated SEQ ID:6219, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6219 is located from position 11451765 to position 11451866 relative to chromosome 19 on the `+` strand.

GAM336369 precursor RNA folds onto itself, forming GAM336369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336369 precursor RNA, designated SEQ ID NO: 6219, and a schematic representation of a predicted secondary folding of GAM336369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336369 folded precursor RNA yielding a GAM336369 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336369 RNA, hereby incorporated herein.

GAM336369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336369 target RNA, herein designated GAM TARGET RNA.

GAM336369 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336369 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336369 RNA, herein designated GAM RNA, to target binding sites on GAM336369 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336369 target RNA into GAM336369 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336369 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336369 target genes. The mRNA of each one of this plurality of GAM336369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336369 RNA, herein designated GAM RNA, and which when bound by GAM336369 RNA causes inhibition of translation of the GAM336369 target mRNA into a corresponding GAM336369 target protein.

The mechanism of the translational inhibition exerted by GAM336369 RNA, herein designated GAM RNA, on one or more GAM336369 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336369 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336369 RNA, herein designated GAM RNA, of GAM336369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336369 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336369 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336369 RNA correlate with, and may be deduced from, the identity of the GAM336369 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336372 6271 CTTTCTCTCG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAATGGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTTTTCTTC Messenger 336372 (GAM336372) oligonucleotides modulates expression of respective target
AGAGCCTTTG genes whose function and utility is known in the art.

CTCTGAAACA GAM336372 is a novel bioinformatically detectable regulatory, non protein
TCACGCTCCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336372 was detected
CTGTATGGGG is described with additional reference to Figs. 9-15.

AGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336372 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336372 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336372 precursor RNA is designated SEQ ID:6271, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6271 is located from position 11647684 to position 11647758 relative to chromosome 10 on the `-` strand.

GAM336372 precursor RNA folds onto itself, forming GAM336372 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336372 precursor RNA, designated SEQ ID NO: 6271, and a schematic representation of a predicted secondary folding of GAM336372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336372 folded precursor RNA yielding a GAM336372 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336372 RNA, hereby incorporated herein.

GAM336372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336372 target RNA, herein designated GAM TARGET RNA.

GAM336372 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336372 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336372 RNA, herein designated GAM RNA, to target binding sites on GAM336372 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336372 target RNA into GAM336372 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336372 target genes. The mRNA of each one of this plurality of GAM336372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336372 RNA,

herein designated GAM RNA, and which when bound by GAM336372 RNA causes inhibition of translation of the GAM336372 target mRNA into a corresponding GAM336372 target protein.

The mechanism of the translational inhibition exerted by GAM336372 RNA, herein designated GAM RNA, on one or more GAM336372 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336372 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336372 RNA, herein designated GAM RNA, of GAM336372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336372 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336372 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336372 RNA correlate with, and may be deduced from, the identity of the GAM336372 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336373 7143 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336373 (GAM336373) oligonucleotides modulates expression of respective target

GCGGAGGTCG genes whose function and utility is known in the art.

TGGTGAGCCA GAM336373 is a novel bioinformatically detectable regulatory, non protein

AAATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336373 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGTGA encoded by the human genome.

AACTCTGTCT GAM336373 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336373 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336373 precursor RNA is designated SEQ ID:7143, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7143 is located from position 11686899 to position 11687000 relative to chromosome 1 on the `-` strand.

GAM336373 precursor RNA folds onto itself, forming GAM336373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336373 precursor RNA, designated SEQ ID NO: 7143, and a schematic representation of a predicted secondary folding of GAM336373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336373 folded precursor RNA yielding a GAM336373 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336373 RNA, hereby incorporated herein. Expression of GAM336373 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336373 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336373 target RNA, herein designated GAM TARGET RNA.

GAM336373 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336373 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336373 RNA, herein designated GAM RNA, to target binding sites on GAM336373 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336373 target RNA into GAM336373 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336373 target genes. The mRNA of each one of this plurality of GAM336373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336373 RNA, herein designated GAM RNA, and which when bound by GAM336373 RNA causes inhibition of translation of the GAM336373 target mRNA into a corresponding GAM336373 target protein.

The mechanism of the translational inhibition exerted by GAM336373 RNA, herein designated GAM RNA, on one or more GAM336373 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336373 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336373 RNA, herein designated GAM RNA, of GAM336373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336373 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336373 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336373 RNA correlate with, and may be deduced from, the identity of the GAM336373 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336374 6396 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 336374 (GAM336374) oligonucleotides modulates expression of respective target

CGGAGGTCGT genes whose function and utility is known in the art.

GGTGAGCCAA GAM336374 is a novel bioinformatically detectable regulatory, non protein

AATCGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336374 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGTGAA encoded by the human genome.

ACTCTGTCTC GAM336374 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336374 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336374 precursor RNA is designated SEQ ID:6396, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6396 is located from position 11686900 to position 11686999 relative to chromosome 1 on the `-` strand.

GAM336374 precursor RNA folds onto itself, forming GAM336374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336374 precursor RNA, designated SEQ ID NO: 6396, and a schematic representation of a predicted secondary folding of GAM336374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336374 folded precursor RNA yielding a GAM336374 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336374 RNA, hereby incorporated herein. Expression of GAM336374 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336374 target RNA, herein designated GAM TARGET RNA.

GAM336374 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336374 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336374 RNA, herein designated GAM RNA, to target binding sites on GAM336374 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336374 target RNA into GAM336374 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336374 target genes. The mRNA of each one of this plurality of GAM336374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336374 RNA, herein designated GAM RNA, and which when bound by GAM336374 RNA causes inhibition of translation of the GAM336374 target mRNA into a corresponding GAM336374 target protein.

The mechanism of the translational inhibition exerted by GAM336374 RNA, herein designated GAM RNA, on one or more GAM336374 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336374 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336374 RNA, herein designated GAM RNA, of GAM336374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336374 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336374 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336374 RNA correlate with, and may be deduced from, the identity of the GAM336374 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336375 5969 ATGCATGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTACACAGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GACACAATGC Messenger 336375 (GAM336375) oligonucleotides modulates expression of respective target
AGTGTTGGTG genes whose function and utility is known in the art.

GGAAATAGTC GAM336375 is a novel bioinformatically detectable regulatory, non protein
ATTGAGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336375 was detected
TCTCCTTTCC is described with additional reference to Figs. 9-15.

TCTCATGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATGTTCAGA encoded by the human genome.

GAATCACCAC GAM336375 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CAGACACTCC GAM336375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CGTGTGAAAA GAM336375 precursor RNA does not encode a protein. A nucleotide sequence identical or

TTTGTATGCA highly similar to the nucleotide sequence of GAM336375 precursor RNA is designated SEQ

T ID:5969, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5969 is located from position 11850038 to position 11850168 relative to chromosome 19 on the `+` strand.

GAM336375 precursor RNA folds onto itself, forming GAM336375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336375 precursor RNA, designated SEQ ID NO: 5969, and a schematic representation of a predicted secondary folding of GAM336375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336375 folded precursor RNA yielding a GAM336375 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336375 RNA, hereby incorporated herein.

GAM336375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336375 target RNA, herein designated GAM TARGET RNA.

GAM336375 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336375 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336375 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336375 RNA, herein designated GAM RNA, to target binding sites on GAM336375 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336375 target RNA into GAM336375 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336375 target genes. The mRNA of each one of this plurality of GAM336375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336375 RNA, herein designated GAM RNA, and which when bound by GAM336375 RNA causes inhibition of translation of the GAM336375 target mRNA into a corresponding GAM336375 target protein.

The mechanism of the translational inhibition exerted by GAM336375 RNA, herein designated GAM RNA, on one or more GAM336375 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336375 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336375 RNA, herein designated GAM RNA, of GAM336375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336375 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336375 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336375 RNA correlate with, and may be deduced from, the identity of the GAM336375 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336376 6232 CTGGGATTAC ATGTGTGAGC CACCGCGCCT GGCCTCAAAT TGTTTTTGAA GTAGTTAGGT TGTAGCTCAT AAGACTGTCT TTCAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336376 (GAM336376) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336376 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336376 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336376 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336376 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336376 precursor RNA is designated SEQ ID:6232, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6232 is located from position 11968201 to position 11968285 relative to chromosome 16 on the `-` strand.

GAM336376 precursor RNA folds onto itself, forming GAM336376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336376 precursor RNA, designated SEQ ID NO: 6232, and a schematic representation of a predicted secondary folding of GAM336376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336376 folded precursor RNA yielding a GAM336376 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336376 RNA, hereby incorporated herein.

GAM336376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336376 target RNA, herein designated GAM TARGET RNA.

GAM336376 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336376 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336376 RNA, herein designated GAM RNA, to target binding sites on GAM336376 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336376 target RNA into GAM336376 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336376 target genes. The mRNA of each one of this plurality of GAM336376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336376 RNA, herein designated GAM RNA, and which when bound by GAM336376 RNA causes inhibition of translation of the GAM336376 target mRNA into a corresponding GAM336376 target protein.

The mechanism of the translational inhibition exerted by GAM336376 RNA, herein designated GAM RNA, on one or more GAM336376 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336376 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336376 RNA, herein designated GAM RNA, of GAM336376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336376 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336376 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336376 RNA correlate with, and may be deduced from, the identity of the GAM336376 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336377 7269 TGTGAGCCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CGCGCCTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCAAATTGT Messenger 336377 (GAM336377) oligonucleotides modulates expression of respective target
TTTTGAAGTA genes whose function and utility is known in the art.

GTTAGGTTGT GAM336377 is a novel bioinformatically detectable regulatory, non protein
AGCTCATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336377 was detected
is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336377 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336377 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336377 precursor RNA is designated SEQ ID:7269, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7269 is located from position 11968215 to position 11968272 relative to chromosome 16 on the `-` strand.

GAM336377 precursor RNA folds onto itself, forming GAM336377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336377 precursor RNA, designated SEQ ID NO: 7269, and a schematic representation of a predicted secondary folding of GAM336377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336377 folded precursor RNA yielding a GAM336377 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336377 RNA, hereby incorporated herein.

GAM336377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336377 target RNA, herein designated GAM TARGET RNA.

GAM336377 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336377 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336377 RNA, herein designated GAM RNA, to target binding sites on GAM336377 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336377 target RNA into GAM336377 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336377 target genes. The mRNA of each one of this plurality of GAM336377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336377 RNA, herein designated GAM RNA, and which when bound by GAM336377 RNA causes inhibition of translation of the GAM336377 target mRNA into a corresponding GAM336377 target protein.

The mechanism of the translational inhibition exerted by GAM336377 RNA, herein designated GAM RNA, on one or more GAM336377 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336377 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336377 RNA, herein designated GAM RNA, of GAM336377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336377 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336377 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336377 RNA correlate with, and may be deduced from, the identity of the GAM336377 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336378 5840 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336378 (GAM336378) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336378 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336378 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336378 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336378 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336378 precursor RNA is designated SEQ ID:5840, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5840 is located from position 12026100 to position 12026181 relative to chromosome 17 on the `+` strand.

GAM336378 precursor RNA folds onto itself, forming GAM336378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336378 precursor RNA, designated SEQ ID NO: 5840, and a schematic representation of a predicted secondary folding of GAM336378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336378 folded precursor RNA yielding a GAM336378 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336378 RNA, hereby incorporated herein.

GAM336378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336378 target RNA, herein designated GAM TARGET RNA.

GAM336378 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336378 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336378 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336378 RNA, herein designated GAM RNA, to target binding sites on GAM336378 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336378 target RNA into GAM336378 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336378 target genes. The mRNA of each one of this plurality of GAM336378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336378 RNA, herein designated GAM RNA, and which when bound by GAM336378 RNA causes inhibition of translation of the GAM336378 target mRNA into a corresponding GAM336378 target protein.

The mechanism of the translational inhibition exerted by GAM336378 RNA, herein designated GAM RNA, on one or more GAM336378 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336378 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336378 RNA, herein designated GAM RNA, of GAM336378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336378 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336378 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336378 RNA correlate with, and may be deduced from, the identity of the GAM336378 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336380 6230 CTGGGATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGAGCAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGAAGAT Messenger 336380 (GAM336380) oligonucleotides modulates expression of respective target

CTTGGAGTCT genes whose function and utility is known in the art.

GGAATCAGAC GAM336380 is a novel bioinformatically detectable regulatory, non protein

CACCTGGATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336380 was detected

TTCATCCTAG is described with additional reference to Figs. 9-15.

TTCCCCGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGG encoded by the human genome.

GAM336380 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336380 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336380 precursor RNA is designated SEQ ID:6230, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6230 is located from position 12103390 to position 12103473 relative to chromosome 16 on the `+` strand.

GAM336380 precursor RNA folds onto itself, forming GAM336380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336380 precursor RNA, designated SEQ ID NO: 6230, and a schematic representation of a predicted secondary folding of GAM336380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336380 folded precursor RNA yielding a GAM336380 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336380 RNA, hereby incorporated herein.

GAM336380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336380 target RNA, herein designated GAM TARGET RNA.

GAM336380 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336380 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336380 RNA, herein designated GAM RNA, to target binding sites on GAM336380 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336380 target RNA into GAM336380 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336380 target genes. The mRNA of each one of this plurality of GAM336380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336380 RNA, herein designated GAM RNA, and which when bound by GAM336380 RNA causes inhibition of translation of the GAM336380 target mRNA into a corresponding GAM336380 target protein.

The mechanism of the translational inhibition exerted by GAM336380 RNA, herein designated GAM RNA, on one or more GAM336380 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336380 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336380 RNA, herein designated GAM RNA, of GAM336380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336380 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336380 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336380 RNA correlate with, and may be deduced from, the identity of the GAM336380 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336381 6474 GATGGGATGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCAAGAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGATCTTG Messenger 336381 (GAM336381) oligonucleotides modulates expression of respective target

GAGTCTGGAA genes whose function and utility is known in the art.

TCAGACCACC GAM336381 is a novel bioinformatically detectable regulatory, non protein

TGGATTTTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336381 was detected

TCCTAGTTCC is described with additional reference to Figs. 9-15.

CCGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336381 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336381 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336381 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336381 precursor RNA is designated SEQ ID:6474, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6474 is located from position 12103394 to position 12103469 relative to chromosome 16 on the `+` strand.

GAM336381 precursor RNA folds onto itself, forming GAM336381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336381 precursor RNA, designated SEQ ID NO: 6474, and a schematic representation of a predicted secondary folding of GAM336381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336381 folded precursor RNA yielding a GAM336381 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336381 RNA, hereby incorporated herein.

GAM336381 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336381 target RNA, herein designated GAM TARGET RNA.

GAM336381 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336381 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336381 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336381 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336381 RNA, herein designated GAM RNA, to target binding sites on GAM336381 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336381 target RNA into GAM336381 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336381 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336381 target genes. The mRNA of each one of this plurality of GAM336381 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336381 RNA, herein designated GAM RNA, and which when bound by GAM336381 RNA causes inhibition of translation of the GAM336381 target mRNA into a corresponding GAM336381 target protein.

The mechanism of the translational inhibition exerted by GAM336381 RNA, herein designated GAM RNA, on one or more GAM336381 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336381 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336381 RNA, herein designated GAM RNA, of GAM336381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336381 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336381 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336381 RNA correlate with, and may be deduced from, the identity of the GAM336381 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336382 6617 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACTCGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 336382 (GAM336382) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCCC GAM336382 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336382 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336382 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336382 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336382 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336382 precursor RNA is designated SEQ ID:6617, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6617 is located from position 12118809 to position 12118896 relative to chromosome 16 on the `-` strand.

GAM336382 precursor RNA folds onto itself, forming GAM336382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336382 precursor RNA, designated SEQ ID NO: 6617, and a schematic representation of a predicted secondary folding of GAM336382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336382 folded precursor RNA yielding a GAM336382 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336382 RNA, hereby incorporated herein.

GAM336382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336382 target RNA, herein designated GAM TARGET RNA.

GAM336382 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336382 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336382 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336382 RNA, herein designated GAM RNA, to target binding sites on GAM336382 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336382 target RNA into GAM336382 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336382 target genes. The mRNA of each one of this plurality of GAM336382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336382 RNA, herein designated GAM RNA, and which when bound by GAM336382 RNA causes inhibition of translation of the GAM336382 target mRNA into a corresponding GAM336382 target protein.

The mechanism of the translational inhibition exerted by GAM336382 RNA, herein designated GAM RNA, on one or more GAM336382 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336382 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336382 RNA, herein designated GAM RNA, of GAM336382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336382 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336382 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336382 RNA correlate with, and may be deduced from, the identity of the GAM336382 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336384 7341 TTGTTGATTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTTGAGGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
ATATCCCTAT Messenger 336384 (GAM336384) oligonucleotides modulates expression of respective target
GATGTCCCTG genes whose function and utility is known in the art.

GGAAGCGATG GAM336384 is a novel bioinformatically detectable regulatory, non protein
GGGCATTCCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336384 was detected
AGTCATCTGG is described with additional reference to Figs. 9-15.

GATGTGCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCTAAATAT encoded by the human genome.

TATCAATGG GAM336384 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336384 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336384 precursor RNA is designated SEQ ID:7341, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7341 is located from position 12348835 to position 12348933 relative to chromosome 20 on the `-` strand.

GAM336384 precursor RNA folds onto itself, forming GAM336384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336384 precursor RNA, designated SEQ ID NO: 7341, and a schematic representation of a predicted secondary folding of GAM336384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336384 folded precursor RNA yielding a GAM336384 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336384 RNA, hereby incorporated herein.

GAM336384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336384 target RNA, herein designated GAM TARGET RNA.

GAM336384 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336384 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336384 RNA, herein designated GAM RNA, to target binding sites on GAM336384 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336384 target RNA into GAM336384 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336384 target genes. The mRNA of each one of this plurality of GAM336384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336384 RNA, herein designated GAM RNA, and which when bound by GAM336384 RNA causes inhibition of translation of the GAM336384 target mRNA into a corresponding GAM336384 target protein.

The mechanism of the translational inhibition exerted by GAM336384 RNA, herein designated GAM RNA, on one or more GAM336384 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336384 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336384 RNA, herein designated GAM RNA, of GAM336384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336384 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336384 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336384 RNA correlate with, and may be deduced from, the identity of the GAM336384 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336385 6478 GATTCTGTTG AGGATATATC CCTATGATGT CCCTGGGAAG CGATGGGGCA TTCCCAGTCA TCTGGGATGT GCAGTTTCTA AATATTATC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336385 (GAM336385) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336385 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336385 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336385 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336385 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336385 precursor RNA is designated SEQ ID:6478, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6478 is located from position 12348840 to position 12348928 relative to chromosome 20 on the `-` strand.

GAM336385 precursor RNA folds onto itself, forming GAM336385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336385 precursor RNA, designated SEQ ID NO: 6478, and a schematic representation of a predicted secondary folding of GAM336385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336385 folded precursor RNA yielding a GAM336385 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336385 RNA, hereby incorporated herein.

GAM336385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336385 target RNA, herein designated GAM TARGET RNA.

GAM336385 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336385 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336385 RNA, herein designated GAM RNA, to target binding sites on GAM336385 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336385 target RNA into GAM336385 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336385 target genes. The mRNA of each one of this plurality of GAM336385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336385 RNA, herein designated GAM RNA, and which when bound by GAM336385 RNA causes inhibition of translation of the GAM336385 target mRNA into a corresponding GAM336385 target protein.

The mechanism of the translational inhibition exerted by GAM336385 RNA, herein designated GAM RNA, on one or more GAM336385 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336385 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336385 RNA, herein designated GAM RNA, of GAM336385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336385 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336385 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336385 RNA correlate with, and may be deduced from, the identity of the GAM336385 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336386 5680 ACAAATGTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGCCTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCCTTTCCT Messenger 336386 (GAM336386) oligonucleotides modulates expression of respective target
CAGACTTTCA genes whose function and utility is known in the art.

GGCCCATTGT GAM336386 is a novel bioinformatically detectable regulatory, non protein
GAGAGAGCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336386 was detected
GGAAGATACA is described with additional reference to Figs. 9-15.

GGGTTGTCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTGACACAT encoded by the human genome.

GT GAM336386 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336386 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336386 precursor RNA is designated SEQ ID:5680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5680 is located from position 12401666 to position 12401757 relative to chromosome 16 on the `+` strand.

GAM336386 precursor RNA folds onto itself, forming GAM336386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336386 precursor RNA, designated SEQ ID NO: 5680, and a schematic representation of a predicted secondary folding of GAM336386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336386 folded precursor RNA yielding a GAM336386 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336386 RNA, hereby incorporated herein.

GAM336386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336386 target RNA, herein designated GAM TARGET RNA.

GAM336386 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336386 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336386 RNA, herein designated GAM RNA, to target binding sites on GAM336386 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336386 target RNA into GAM336386 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336386 target genes. The mRNA of each one of this plurality of GAM336386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336386 RNA, herein designated GAM RNA, and which when bound by GAM336386 RNA causes inhibition of translation of the GAM336386 target mRNA into a corresponding GAM336386 target protein.

The mechanism of the translational inhibition exerted by GAM336386 RNA, herein designated GAM RNA, on one or more GAM336386 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336386 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336386 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336386 RNA, herein designated GAM RNA, of GAM336386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336386 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336386 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336386 RNA correlate with, and may be deduced from, the identity of the GAM336386 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336387 7324 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTGCAG Messenger 336387 (GAM336387) oligonucleotides modulates expression of respective target
TGAGCCAAGA genes whose function and utility is known in the art.

TCATGCCACT GAM336387 is a novel bioinformatically detectable regulatory, non protein
GCACTGTAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336387 was detected
CTCCTGGGTG is described with additional reference to Figs. 9-15.

ACAGAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336387 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336387 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336387 precursor RNA is designated SEQ ID:7324, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7324 is located from position 12619567 to position 12619645 relative to chromosome X on the `+` strand.

GAM336387 precursor RNA folds onto itself, forming GAM336387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336387 precursor RNA, designated SEQ ID NO: 7324, and a schematic representation of a predicted secondary folding of GAM336387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336387 folded precursor RNA yielding a GAM336387 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336387 RNA, hereby incorporated herein.

GAM336387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336387 target RNA, herein designated GAM TARGET RNA.

GAM336387 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336387 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336387 RNA, herein designated GAM RNA, to target binding sites on GAM336387 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336387 target RNA into GAM336387 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336387 target genes. The mRNA of each one of this plurality of GAM336387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336387 RNA, herein designated GAM RNA, and which when bound by GAM336387 RNA causes inhibition of translation of the GAM336387 target mRNA into a corresponding GAM336387 target protein.

The mechanism of the translational inhibition exerted by GAM336387 RNA, herein

designated GAM RNA, on one or more GAM336387 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336387 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336387 RNA, herein designated GAM RNA, of GAM336387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336387 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336387 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336387 RNA correlate with, and may be deduced from, the identity of the GAM336387 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336388 6938 GTTCCTCTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCATTGGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTGCTCTG Messenger 336388 (GAM336388) oligonucleotides modulates expression of respective target

TGGCATCTGT genes whose function and utility is known in the art.

CACAGGTTTT GAM336388 is a novel bioinformatically detectable regulatory, non protein

AATTGAAGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336388 was detected

CAGCAGTGGC is described with additional reference to Figs. 9-15.

AGGTAAGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCAGCATCAT encoded by the human genome.

CAGCTTCTTT GAM336388 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAGCCTTTTG GAM336388 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAAC GAM336388 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336388 precursor RNA is designated SEQ ID:6938, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6938 is located from position 12778141 to position 12778254 relative to chromosome 10 on the `+` strand.

GAM336388 precursor RNA folds onto itself, forming GAM336388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336388 precursor RNA, designated SEQ ID NO: 6938, and a schematic representation of a predicted secondary folding of GAM336388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336388 folded precursor RNA yielding a GAM336388 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336388 RNA, hereby incorporated herein.

GAM336388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336388 target RNA, herein designated GAM TARGET RNA.

GAM336388 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336388 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336388 RNA, herein designated GAM RNA, to target binding sites on GAM336388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336388 target RNA into GAM336388 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336388 target genes. The mRNA of each one of this plurality of GAM336388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336388 RNA, herein designated GAM RNA, and which when bound by GAM336388 RNA causes inhibition of translation of the GAM336388 target mRNA into a corresponding GAM336388 target protein.

The mechanism of the translational inhibition exerted by GAM336388 RNA, herein designated GAM RNA, on one or more GAM336388 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336388 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336388 RNA, herein designated GAM RNA, of GAM336388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336388 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336388 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336388 RNA correlate with, and may be deduced from, the identity of the GAM336388 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336389 6763 GGCTGATGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCTGTGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTGTCACAG Messenger 336389 (GAM336389) oligonucleotides modulates expression of respective target

GTTTTAATTG genes whose function and utility is known in the art.

AAGGTCAGCA GAM336389 is a novel bioinformatically detectable regulatory, non protein

GTGGCAGGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336389 was detected

AGCCACCAGC is described with additional reference to Figs. 9-15.

ATCATCAGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336389 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336389 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336389 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336389 precursor RNA is designated SEQ ID:6763, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6763 is located from position 12778156 to position 12778235 relative to chromosome 10 on the `+` strand.

GAM336389 precursor RNA folds onto itself, forming GAM336389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336389 precursor RNA, designated SEQ ID NO: 6763, and a schematic representation of a predicted secondary folding of GAM336389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336389 folded precursor RNA yielding a GAM336389 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336389 RNA, hereby incorporated herein.

GAM336389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336389 target RNA, herein designated GAM TARGET RNA.

GAM336389 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336389 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336389 RNA, herein designated GAM RNA, to target binding sites on GAM336389 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336389 target RNA into GAM336389 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336389 target genes. The mRNA of each one of this plurality of GAM336389 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336389 RNA, herein designated GAM RNA, and which when bound by GAM336389 RNA causes inhibition of translation of the GAM336389 target mRNA into a corresponding GAM336389 target protein.

The mechanism of the translational inhibition exerted by GAM336389 RNA, herein designated GAM RNA, on one or more GAM336389 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336389 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336389 RNA, herein designated GAM RNA, of GAM336389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336389 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336389 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336389 RNA correlate with, and may be deduced from, the identity of the GAM336389 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336390 7112 TGAGGCAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCTCTTA detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336390 (GAM336390) oligonucleotides modulates expression of respective target

GCGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336390 is a novel bioinformatically detectable regulatory, non protein

AGATTGCGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336390 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCGAG encoded by the human genome.

ACTCCGTTTC GAM336390 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336390 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336390 precursor RNA is designated SEQ ID:7112, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7112 is located from position 12791804 to position 12791904 relative to chromosome 19 on the `-` strand.

GAM336390 precursor RNA folds onto itself, forming GAM336390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336390 precursor RNA, designated SEQ ID NO: 7112, and a schematic representation of a predicted secondary folding of GAM336390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336390 folded precursor RNA yielding a GAM336390 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336390 RNA, hereby incorporated herein. Expression of GAM336390 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336390 target RNA, herein designated GAM TARGET RNA.

GAM336390 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336390 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336390 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336390 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336390 RNA, herein designated GAM RNA, to target binding sites on GAM336390 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336390 target RNA into GAM336390 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336390 target genes. The mRNA of each one of this plurality of GAM336390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336390 RNA, herein designated GAM RNA, and which when bound by GAM336390 RNA causes inhibition of translation of the GAM336390 target mRNA into a corresponding GAM336390 target protein.

The mechanism of the translational inhibition exerted by GAM336390 RNA, herein designated GAM RNA, on one or more GAM336390 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336390 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336390 RNA, herein designated GAM RNA, of GAM336390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336390 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336390 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336390 RNA correlate with, and may be deduced from, the identity of the GAM336390 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336391 6294 GAAGAATCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTAAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGAGG Messenger 336391 (GAM336391) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATTGC GAM336391 is a novel bioinformatically detectable regulatory, non protein
GTCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336391 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCCGT encoded by the human genome.

TTC GAM336391 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336391 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336391 precursor RNA is designated SEQ ID:6294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6294 is located from position 12791805 to position 12791897 relative to chromosome 19 on the `-` strand.

GAM336391 precursor RNA folds onto itself, forming GAM336391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336391 precursor RNA, designated SEQ ID NO: 6294, and a schematic representation of a predicted secondary folding of GAM336391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336391 folded precursor RNA yielding a GAM336391 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336391 RNA, hereby incorporated herein. Expression of GAM336391 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336391 target RNA, herein designated GAM TARGET RNA.

GAM336391 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336391 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336391 RNA, herein designated GAM RNA, to target binding sites on GAM336391 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336391 target RNA into GAM336391 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336391 target genes. The mRNA of each one of this plurality of GAM336391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336391 RNA, herein designated GAM RNA, and which when bound by GAM336391 RNA causes inhibition of translation of the GAM336391 target mRNA into a corresponding GAM336391 target protein.

The mechanism of the translational inhibition exerted by GAM336391 RNA, herein designated GAM RNA, on one or more GAM336391 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336391 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336391 RNA, herein designated GAM RNA, of GAM336391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336391 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336391 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336391 RNA correlate with, and may be deduced from, the identity of the GAM336391 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336392 6180 CTCTTAAACC Fig. 8 further provides a conceptual description of another novel bioinformatically
CGGGAGGCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTTGCAGT Messenger 336392 (GAM336392) oligonucleotides modulates expression of respective target
GAGCCGAGAT genes whose function and utility is known in the art.
TGCGTCACTG GAM336392 is a novel bioinformatically detectable regulatory, non protein
CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336392 was detected
TGGGCAACAG is described with additional reference to Figs. 9-15.
AG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336392 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336392 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336392 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336392 precursor RNA is designated SEQ ID:6180, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6180 is located from position 12791819 to position 12791890 relative to chromosome 19 on the `-` strand.

GAM336392 precursor RNA folds onto itself, forming GAM336392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336392 precursor RNA, designated SEQ ID NO: 6180, and a schematic representation of a predicted secondary folding of GAM336392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336392 folded precursor RNA yielding a GAM336392 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336392 RNA, hereby incorporated herein. Expression of GAM336392 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336392 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336392 target RNA, herein designated GAM TARGET RNA.

GAM336392 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336392 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336392 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336392 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336392 RNA, herein designated GAM RNA, to target binding sites on GAM336392 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336392 target RNA into GAM336392 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336392 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336392 target genes. The mRNA of each one of this plurality of GAM336392 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336392 RNA, herein designated GAM RNA, and which when bound by GAM336392 RNA causes inhibition of translation of the GAM336392 target mRNA into a corresponding GAM336392 target protein.

The mechanism of the translational inhibition exerted by GAM336392 RNA, herein designated GAM RNA, on one or more GAM336392 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336392 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336392 RNA, herein designated GAM RNA, of GAM336392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336392 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336392 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336392 RNA correlate with, and may be deduced from, the identity of the GAM336392 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336393 7079 TCTTTCACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACATC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCAGCTCCT Messenger 336393 (GAM336393) oligonucleotides modulates expression of respective target

CCCCCTCCGC genes whose function and utility is known in the art.

CCTCCCTCAG GAM336393 is a novel bioinformatically detectable regulatory, non protein

GCTTAGACCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336393 was detected

TGGAGCTGTA is described with additional reference to Figs. 9-15.

ACAGATCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTTCGTGTG encoded by the human genome.

AGA GAM336393 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336393 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336393 precursor RNA is designated SEQ ID:7079, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7079 is located from position 12833782 to position 12833874 relative to chromosome 17 on the `+` strand.

GAM336393 precursor RNA folds onto itself, forming GAM336393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336393 precursor RNA, designated SEQ ID NO: 7079, and a schematic representation of a predicted secondary folding of GAM336393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336393 folded precursor RNA yielding a GAM336393 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336393 RNA, hereby incorporated herein.

GAM336393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336393 target RNA, herein designated GAM TARGET RNA.

GAM336393 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336393 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336393 RNA, herein designated GAM RNA, to target binding sites on GAM336393 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336393 target RNA into GAM336393 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336393 target genes. The mRNA of each one of this plurality of GAM336393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336393 RNA, herein designated GAM RNA, and which when bound by GAM336393 RNA causes inhibition of translation of the GAM336393 target mRNA into a corresponding GAM336393 target protein.

The mechanism of the translational inhibition exerted by GAM336393 RNA, herein designated GAM RNA, on one or more GAM336393 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336393 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336393 RNA, herein designated GAM RNA, of GAM336393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336393 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336393 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336393 RNA correlate with, and may be deduced from, the identity of the GAM336393 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336394 6214 CTGCCAGCCG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTGTCTCTA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTTTTTCC Messenger 336394 (GAM336394) oligonucleotides modulates expression of respective target

AAATGACATC genes whose function and utility is known in the art.

CAGGGCTCTG GAM336394 is a novel bioinformatically detectable regulatory, non protein

GCCGTGGAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336394 was detected

CCCTGATGTG is described with additional reference to Figs. 9-15.

ATCGCTAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACCTCCGGA encoded by the human genome.

GAGGGGCTCG GAM336394 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAG GAM336394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336394 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336394 precursor RNA is designated SEQ

ID:6214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6214 is located from position 12908963 to position 12909065 relative to chromosome 8 on the `+` strand.

GAM336394 precursor RNA folds onto itself, forming GAM336394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336394 precursor RNA, designated SEQ ID NO: 6214, and a schematic representation of a predicted secondary folding of GAM336394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336394 folded precursor RNA yielding a GAM336394 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336394 RNA, hereby incorporated herein.

GAM336394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336394 target RNA, herein designated GAM TARGET RNA.

GAM336394 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336394 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336394 RNA, herein designated GAM RNA, to target binding sites on GAM336394 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336394 target RNA into GAM336394 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336394 target genes. The mRNA of each one of this plurality of GAM336394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336394 RNA, herein designated GAM RNA, and which when bound by GAM336394 RNA causes inhibition of translation of the GAM336394 target mRNA into a corresponding GAM336394 target protein.

The mechanism of the translational inhibition exerted by GAM336394 RNA, herein designated GAM RNA, on one or more GAM336394 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336394 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336394 RNA, herein designated GAM RNA, of GAM336394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336394 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336394 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336394 RNA correlate with, and may be deduced from, the identity of the GAM336394 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336395 6891 GTCTGTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGTTTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAAATGACAT Messenger 336395 (GAM336395) oligonucleotides modulates expression of respective target

CCAGGGCTCT genes whose function and utility is known in the art.

GGCCGTGGAG GAM336395 is a novel bioinformatically detectable regulatory, non protein

TCCCTGATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336395 was detected

GATCGCTAAA is described with additional reference to Figs. 9-15.

GGACCTCCGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGGGGC encoded by the human genome.

GAM336395 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336395 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336395 precursor RNA is designated SEQ ID:6891, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6891 is located from position 12908972 to position 12909059 relative to chromosome 8 on the `+` strand.

GAM336395 precursor RNA folds onto itself, forming GAM336395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336395 precursor RNA, designated SEQ ID NO: 6891, and a schematic representation of a predicted secondary folding of GAM336395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336395 folded precursor RNA yielding a GAM336395 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336395 RNA, hereby incorporated herein.

GAM336395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336395 target RNA, herein designated GAM TARGET RNA.

GAM336395 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336395 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336395 RNA, herein designated GAM RNA, to target binding sites on GAM336395 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336395 target RNA into GAM336395 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336395 target genes. The mRNA of each one of this plurality of GAM336395 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336395 RNA, herein designated GAM RNA, and which when bound by GAM336395 RNA causes inhibition of translation of the GAM336395 target mRNA into a corresponding GAM336395 target protein.

The mechanism of the translational inhibition exerted by GAM336395 RNA, herein designated GAM RNA, on one or more GAM336395 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336395 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336395 RNA, herein designated GAM RNA, of GAM336395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336395 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336395 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336395 RNA correlate with, and may be deduced from, the identity of the GAM336395 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336397 6520 GCGTTCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAAACCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGATTTCAT Messenger 336397 (GAM336397) oligonucleotides modulates expression of respective target

TCTCCTTCCT genes whose function and utility is known in the art.

TTCTCTGACA GAM336397 is a novel bioinformatically detectable regulatory, non protein
GAAGCTGCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336397 was detected
GTGAGGAAGG is described with additional reference to Figs. 9-15.

TAATGATCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATCAAACCA encoded by the human genome.

TCCCCAGAAT GAM336397 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GC GAM336397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336397 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336397 precursor RNA is designated SEQ ID:6520, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6520 is located from position 13120513 to position 13120614 relative to chromosome 16 on the `+` strand.

GAM336397 precursor RNA folds onto itself, forming GAM336397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336397 precursor RNA, designated SEQ ID NO: 6520, and a schematic representation of a predicted secondary folding of GAM336397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336397 folded precursor RNA yielding a GAM336397 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336397 RNA, hereby incorporated herein.

GAM336397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336397 target RNA, herein designated GAM TARGET RNA.

GAM336397 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336397 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336397 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336397 RNA, herein designated GAM RNA, to target binding sites on GAM336397 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336397 target RNA into GAM336397 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336397 target genes. The mRNA of each one of this plurality of GAM336397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336397 RNA, herein designated GAM RNA, and which when bound by GAM336397 RNA causes inhibition of translation of the GAM336397 target mRNA into a corresponding GAM336397 target protein.

The mechanism of the translational inhibition exerted by GAM336397 RNA, herein designated GAM RNA, on one or more GAM336397 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336397 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336397 RNA, herein designated GAM RNA, of GAM336397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336397 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336397 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336397 RNA correlate with, and may be deduced from, the identity of the GAM336397 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336399 6044 CATTTTAGTA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGCTCAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGACCAGTGT Messenger 336399 (GAM336399) oligonucleotides modulates expression of respective target
TAGTTATATT genes whose function and utility is known in the art.

TGAGTCAGAA GAM336399 is a novel bioinformatically detectable regulatory, non protein
AAATGTTGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336399 was detected
TTTCAACTTG is described with additional reference to Figs. 9-15.

CTTTATAATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCTGCATCT encoded by the human genome.

ATCTCCTGCT GAM336399 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTAGCATCAC GAM336399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAAGGTG GAM336399 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336399 precursor RNA is designated SEQ ID:6044, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6044 is located from position 13641031 to position 13641147 relative to chromosome 18 on the `+` strand.

GAM336399 precursor RNA folds onto itself, forming GAM336399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336399 precursor RNA, designated SEQ ID NO: 6044, and a schematic representation of a predicted secondary folding of GAM336399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336399 folded precursor RNA yielding a GAM336399 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336399 RNA, hereby incorporated herein.

GAM336399 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336399 target RNA, herein designated GAM TARGET RNA.

GAM336399 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336399 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336399 RNA, herein designated GAM RNA, to target binding sites on GAM336399 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336399 target RNA into GAM336399 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336399 target genes. The mRNA of each one of this plurality of GAM336399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336399 RNA, herein designated GAM RNA, and which when bound by GAM336399 RNA causes inhibition of translation of the GAM336399 target mRNA into a corresponding GAM336399 target protein.

The mechanism of the translational inhibition exerted by GAM336399 RNA, herein designated GAM RNA, on one or more GAM336399 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336399 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336399 RNA, herein designated GAM RNA, of GAM336399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336399 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336399 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336399 RNA correlate with, and may be deduced from, the identity of the GAM336399 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336400 5841 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336400 (GAM336400) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336400 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336400 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336400 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336400 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336400 precursor RNA is designated SEQ ID:5841, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5841 is located from position 13789635 to position 13789716 relative to chromosome 3 on the `+` strand.

GAM336400 precursor RNA folds onto itself, forming GAM336400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336400 precursor RNA, designated SEQ ID NO: 5841, and a schematic representation of a predicted secondary folding of GAM336400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336400 folded precursor RNA yielding a GAM336400 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336400 RNA, hereby incorporated herein.

GAM336400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336400 target RNA, herein designated GAM TARGET RNA.

GAM336400 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336400 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336400 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336400 RNA, herein designated GAM RNA, to target binding sites on GAM336400 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336400 target RNA into GAM336400 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336400 target genes. The mRNA of each one of this plurality of GAM336400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336400 RNA, herein designated GAM RNA, and which when bound by GAM336400 RNA causes inhibition of translation of the GAM336400 target mRNA into a corresponding GAM336400 target protein.

The mechanism of the translational inhibition exerted by GAM336400 RNA, herein designated GAM RNA, on one or more GAM336400 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336400 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336400 RNA, herein designated GAM RNA, of GAM336400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336400 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336400 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336400 RNA correlate with, and may be deduced from, the identity of the GAM336400 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336403 6267 CTTGCCATGC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCCTTTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGGAGCAAG Messenger 336403 (GAM336403) oligonucleotides modulates expression of respective target

TCACAATACA genes whose function and utility is known in the art.

GCAGCTTGCT GAM336403 is a novel bioinformatically detectable regulatory, non protein

TCATTAGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336403 was detected

AAGCAAGCAA is described with additional reference to Figs. 9-15.

G GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336403 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336403 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336403 precursor RNA is designated SEQ ID:6267, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6267 is located from position 14113783 to position 14113853 relative to chromosome Y on the `+` strand.

GAM336403 precursor RNA folds onto itself, forming GAM336403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336403 precursor RNA, designated SEQ ID NO: 6267, and a schematic representation of a predicted secondary folding of GAM336403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336403 folded precursor RNA yielding a GAM336403 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336403 RNA, hereby incorporated herein.

GAM336403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336403 target RNA, herein designated GAM TARGET RNA.

GAM336403 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336403 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336403 RNA, herein designated GAM RNA, to target binding sites on GAM336403 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336403 target RNA into GAM336403 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336403 target genes. The mRNA of each one of this plurality of GAM336403 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336403 RNA, herein designated GAM RNA, and which when bound by GAM336403 RNA causes inhibition of translation of the GAM336403 target mRNA into a corresponding GAM336403 target protein.

The mechanism of the translational inhibition exerted by GAM336403 RNA, herein designated GAM RNA, on one or more GAM336403 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336403 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336403 RNA, herein designated GAM RNA, of GAM336403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336403 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336403 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336403 RNA correlate with, and may be deduced from, the identity of the GAM336403 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336404 6841 GGTGAAACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCTTTCCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTGTTCTAT Messenger 336404 (GAM336404) oligonucleotides modulates expression of respective target

GAGTGTGATG genes whose function and utility is known in the art.

GTGTTTGAGA GAM336404 is a novel bioinformatically detectable regulatory, non protein

AAATGTGGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336404 was detected

CTATGGTTCA is described with additional reference to Figs. 9-15.

GGCGCACTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACATGTGCAA encoded by the human genome.

AGATGGAGAA GAM336404 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AGCACTCACC GAM336404 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336404 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336404 precursor RNA is designated SEQ ID:6841, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6841 is located from position 14534146 to position 14534255 relative to chromosome 22 on the `-` strand.

GAM336404 precursor RNA folds onto itself, forming GAM336404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336404 precursor RNA, designated SEQ ID NO: 6841, and a schematic representation of a predicted secondary folding of GAM336404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336404 folded precursor RNA yielding a GAM336404 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336404 RNA, hereby incorporated herein.

GAM336404 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336404 target RNA, herein designated GAM TARGET RNA.

GAM336404 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336404 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336404 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336404 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336404 RNA, herein designated GAM RNA, to target binding sites on GAM336404 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336404 target RNA into GAM336404 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336404 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336404 target genes. The mRNA of each one of this plurality of GAM336404 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336404 RNA, herein designated GAM RNA, and which when bound by GAM336404 RNA causes inhibition of translation of the GAM336404 target mRNA into a corresponding GAM336404 target protein.

The mechanism of the translational inhibition exerted by GAM336404 RNA, herein designated GAM RNA, on one or more GAM336404 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336404 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336404 RNA, herein designated GAM RNA, of GAM336404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336404 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336404 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336404 RNA correlate with, and may be deduced from, the identity of the GAM336404 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336405 7244 TGGGTACTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTCACACT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGATTTCTT Messenger 336405 (GAM336405) oligonucleotides modulates expression of respective target

GCTTCGTGGG genes whose function and utility is known in the art.

AAACAGACTG GAM336405 is a novel bioinformatically detectable regulatory, non protein

TAATATTGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336405 was detected

AGCA is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336405 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336405 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336405 precursor RNA is designated SEQ ID:7244, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7244 is located from position 14872165 to position 14872228 relative to chromosome 18 on the `+` strand.

GAM336405 precursor RNA folds onto itself, forming GAM336405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336405 precursor RNA, designated SEQ ID NO: 7244, and a schematic representation of a predicted secondary folding of GAM336405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336405 folded precursor RNA yielding a GAM336405 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336405 RNA, hereby incorporated herein.

GAM336405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336405 target RNA, herein designated GAM TARGET RNA.

GAM336405 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336405 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336405 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336405 RNA, herein designated GAM RNA, to target binding sites on GAM336405 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336405 target RNA

into GAM336405 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336405 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336405 target genes. The mRNA of each one of this plurality of GAM336405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336405 RNA, herein designated GAM RNA, and which when bound by GAM336405 RNA causes inhibition of translation of the GAM336405 target mRNA into a corresponding GAM336405 target protein.

The mechanism of the translational inhibition exerted by GAM336405 RNA, herein designated GAM RNA, on one or more GAM336405 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336405 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336405 RNA, herein designated GAM RNA, of GAM336405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336405 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336405 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336405 RNA correlate with, and may be deduced from, the identity of the GAM336405 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336406 7271 TGTGCATTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCAGAGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTGTGAGGA Messenger 336406 (GAM336406) oligonucleotides modulates expression of respective target

GTGTTCAGCT genes whose function and utility is known in the art.

GCTGCAAACA GAM336406 is a novel bioinformatically detectable regulatory, non protein

TCCCATGAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336406 was detected

CCTCAGCTAC is described with additional reference to Figs. 9-15.

TTGGAACAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTACA encoded by the human genome.

GAM336406 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336406 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336406 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336406 precursor RNA is designated SEQ ID:7271, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7271 is located from position 14912408 to position 14912493 relative to chromosome 17 on the `+` strand.

GAM336406 precursor RNA folds onto itself, forming GAM336406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336406 precursor RNA, designated SEQ ID NO: 7271, and a schematic representation of a predicted secondary folding of GAM336406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336406 folded precursor RNA yielding a GAM336406 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336406 RNA, hereby incorporated herein.

GAM336406 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336406 target RNA, herein designated GAM TARGET RNA.

GAM336406 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336406 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336406 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336406 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336406 RNA, herein designated GAM RNA, to target binding sites on GAM336406 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336406 target RNA into GAM336406 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336406 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336406 target genes. The mRNA of each one of this plurality of GAM336406 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336406 RNA, herein designated GAM RNA, and which when bound by GAM336406 RNA causes inhibition of translation of the GAM336406 target mRNA into a corresponding GAM336406 target protein.

The mechanism of the translational inhibition exerted by GAM336406 RNA, herein designated GAM RNA, on one or more GAM336406 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336406 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336406 RNA, herein designated GAM RNA, of GAM336406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336406 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336406 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336406 RNA correlate with, and may be deduced from, the identity of the GAM336406 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336407 6788 GGGAGGACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGAGCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGGTGGAG Messenger 336407 (GAM336407) oligonucleotides modulates expression of respective target

TCTGTAGTGA genes whose function and utility is known in the art.

GCTGTGATCC GAM336407 is a novel bioinformatically detectable regulatory, non protein
TGCCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336407 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGACCCTG encoded by the human genome.

CC GAM336407 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336407 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336407 precursor RNA is designated SEQ ID:6788, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6788 is located from position 15010865 to position 15010956 relative to chromosome 10 on the `-` strand.

GAM336407 precursor RNA folds onto itself, forming GAM336407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336407 precursor RNA, designated SEQ ID NO: 6788, and a schematic representation of a predicted secondary folding of GAM336407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336407 folded precursor RNA yielding a GAM336407 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336407 RNA, hereby incorporated herein. Expression of GAM336407 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336407 target RNA, herein designated GAM TARGET RNA.

GAM336407 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336407 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336407 RNA, herein designated GAM RNA, to target binding sites on GAM336407 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336407 target RNA into GAM336407 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336407 target genes. The mRNA of each one of this plurality of GAM336407 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336407 RNA, herein designated GAM RNA, and which when bound by GAM336407 RNA causes inhibition of translation of the GAM336407 target mRNA into a corresponding GAM336407 target protein.

The mechanism of the translational inhibition exerted by GAM336407 RNA, herein designated GAM RNA, on one or more GAM336407 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336407 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336407 RNA, herein designated GAM RNA, of GAM336407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336407 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336407 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336407 RNA correlate with, and may be deduced from, the identity of the GAM336407 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336408 6848 GGTGGGAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGCTTGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAGGAGGTG Messenger 336408 (GAM336408) oligonucleotides modulates expression of respective target
GAGTCTGTAG genes whose function and utility is known in the art.

TGAGCTGTGA GAM336408 is a novel bioinformatically detectable regulatory, non protein
TCCTGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336408 was detected
GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGCAAGACC encoded by the human genome.

CTGCC GAM336408 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336408 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336408 precursor RNA is designated SEQ ID:6848, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6848 is located from position 15010865 to position 15010959 relative to chromosome 10 on the `-` strand.

GAM336408 precursor RNA folds onto itself, forming GAM336408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336408 precursor RNA, designated SEQ ID NO: 6848, and a schematic representation of a predicted secondary folding of GAM336408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336408 folded precursor RNA yielding a GAM336408 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336408 RNA, hereby incorporated herein.

Expression of GAM336408 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336408 target RNA, herein designated GAM TARGET RNA.

GAM336408 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336408 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336408 RNA, herein designated GAM RNA, to target binding sites on GAM336408 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336408 target RNA into GAM336408 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336408 target genes. The mRNA of each one of this plurality of GAM336408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336408 RNA, herein designated GAM RNA, and which when bound by GAM336408 RNA causes inhibition of translation of the GAM336408 target mRNA into a corresponding GAM336408 target protein.

The mechanism of the translational inhibition exerted by GAM336408 RNA, herein designated GAM RNA, on one or more GAM336408 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336408 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336408 RNA, herein designated GAM RNA, of GAM336408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336408 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336408 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336408 RNA correlate with, and may be deduced from, the identity of the GAM336408 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336409 6598 GGACTGCTTG AGCCCAGGAG GTGGAGTCTG TAGTGAGCTG TGATCCTGCC ACTGCACTCC AGCCTGGGCA ACAGAGCAAG ACC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336409 (GAM336409) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336409 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336409 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336409 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336409 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336409 precursor RNA is designated SEQ ID:6598, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6598 is located from position 15010870 to position 15010952 relative to chromosome 10 on the `-` strand.

GAM336409 precursor RNA folds onto itself, forming GAM336409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336409 precursor RNA, designated SEQ ID NO: 6598, and a schematic representation of a predicted secondary folding of GAM336409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336409 folded precursor RNA yielding a GAM336409 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336409 RNA, hereby incorporated herein. Expression of GAM336409 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336409 target RNA, herein designated GAM TARGET RNA.

GAM336409 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336409 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336409 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336409 RNA, herein designated GAM RNA, to target binding sites on GAM336409 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336409 target RNA into GAM336409 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336409 target genes. The mRNA of each one of this plurality of GAM336409 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336409 RNA, herein designated GAM RNA, and which when bound by GAM336409 RNA causes inhibition of translation of the GAM336409 target mRNA into a corresponding GAM336409 target protein.

The mechanism of the translational inhibition exerted by GAM336409 RNA, herein designated GAM RNA, on one or more GAM336409 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336409 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336409 RNA, herein designated GAM RNA, of GAM336409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336409 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336409 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336409 RNA correlate with, and may be deduced from, the identity of the GAM336409 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336412 6117 CCTGAGACAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTTGCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTTGCCCAG Messenger 336412 (GAM336412) oligonucleotides modulates expression of respective target
GCTGGAGTTT genes whose function and utility is known in the art.

AATGGCACGA GAM336412 is a novel bioinformatically detectable regulatory, non protein
TCTTGGCTTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336412 was detected
CCACAACCTC is described with additional reference to Figs. 9-15.

TGCCTCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTCAAGCAA encoded by the human genome.

TTCTCCTGCC GAM336412 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCAGG GAM336412 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336412 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336412 precursor RNA is designated SEQ ID:6117, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6117 is located from position 15155243 to position 15155347 relative to chromosome 9 on the `-` strand.

GAM336412 precursor RNA folds onto itself, forming GAM336412 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336412 precursor RNA, designated SEQ ID NO: 6117, and a schematic representation of a predicted secondary folding of GAM336412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336412 folded precursor RNA yielding a GAM336412 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336412 RNA, hereby incorporated herein.

GAM336412 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336412 target RNA, herein designated GAM TARGET RNA.

GAM336412 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336412 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336412 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336412 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336412 RNA, herein designated GAM RNA, to target binding sites on GAM336412 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336412 target RNA into GAM336412 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336412 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336412 target genes. The mRNA of each one of this plurality of GAM336412 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336412 RNA,

herein designated GAM RNA, and which when bound by GAM336412 RNA causes inhibition of translation of the GAM336412 target mRNA into a corresponding GAM336412 target protein.

The mechanism of the translational inhibition exerted by GAM336412 RNA, herein designated GAM RNA, on one or more GAM336412 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336412 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336412 RNA, herein designated GAM RNA, of GAM336412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336412 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336412 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336412 RNA correlate with, and may be deduced from, the identity of the GAM336412 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336413 6383 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGA Messenger 336413 (GAM336413) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336413 is a novel bioinformatically detectable regulatory, non protein

GATGGCGCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336413 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAATGGAGA encoded by the human genome.

CTCTGTCTC GAM336413 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336413 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336413 precursor RNA is designated SEQ ID:6383, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6383 is located from position 15476401 to position 15476499 relative to chromosome 16 on the `+` strand.

GAM336413 precursor RNA folds onto itself, forming GAM336413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336413 precursor RNA, designated SEQ ID NO: 6383, and a schematic representation of a predicted secondary folding of GAM336413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336413 folded precursor RNA yielding a GAM336413 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336413 RNA, hereby incorporated herein. Expression of GAM336413 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336413 target RNA, herein designated GAM TARGET RNA.

GAM336413 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336413 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336413 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336413 RNA, herein designated GAM RNA, to target binding sites on GAM336413 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336413 target RNA into GAM336413 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336413 target genes. The mRNA of each one of this plurality of GAM336413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336413 RNA, herein designated GAM RNA, and which when bound by GAM336413 RNA causes inhibition of translation of the GAM336413 target mRNA into a corresponding GAM336413 target protein.

The mechanism of the translational inhibition exerted by GAM336413 RNA, herein designated GAM RNA, on one or more GAM336413 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336413 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336413 RNA, herein designated GAM RNA, of GAM336413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336413 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336413 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336413 RNA correlate with, and may be deduced from, the identity of the GAM336413 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336414 5754 AGGAAGAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGCTGTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GATGAGAGCA Messenger 336414 (GAM336414) oligonucleotides modulates expression of respective target
ACTTGCTTTT genes whose function and utility is known in the art.

TACAATAATT GAM336414 is a novel bioinformatically detectable regulatory, non protein
ATTTGTTATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336414 was detected
GTAAATTAAC is described with additional reference to Figs. 9-15.

AATTTGCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGGTATTA encoded by the human genome.

TATGGAAGTA GAM336414 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTTGATCCT GAM336414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336414 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336414 precursor RNA is designated SEQ ID:5754, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5754 is located from position 15591278 to position 15591386 relative to chromosome 7 on the `-` strand.

GAM336414 precursor RNA folds onto itself, forming GAM336414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336414 precursor RNA, designated SEQ ID NO: 5754, and a schematic representation of a predicted secondary folding of GAM336414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336414 folded precursor RNA yielding a GAM336414 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336414 RNA, hereby incorporated herein.

GAM336414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336414 target RNA, herein designated GAM TARGET RNA.

GAM336414 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336414 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336414 RNA, herein designated GAM RNA, to target binding sites on GAM336414 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336414 target RNA into GAM336414 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336414 target genes. The mRNA of each one of this plurality of GAM336414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336414 RNA, herein designated GAM RNA, and which when bound by GAM336414 RNA causes inhibition of translation of the GAM336414 target mRNA into a corresponding GAM336414 target protein.

The mechanism of the translational inhibition exerted by GAM336414 RNA, herein designated GAM RNA, on one or more GAM336414 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336414 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336414 RNA, herein designated GAM RNA, of GAM336414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336414 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336414 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336414 RNA correlate with, and may be deduced from, the identity of the GAM336414 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336420 5842 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336420 (GAM336420) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336420 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336420 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336420 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336420 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336420 precursor RNA is designated SEQ ID:5842, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5842 is located from position 16256343 to position 16256424 relative to chromosome 10 on the `+` strand.

GAM336420 precursor RNA folds onto itself, forming GAM336420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336420 precursor RNA, designated SEQ ID NO: 5842, and a schematic representation of a predicted secondary folding of GAM336420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336420 folded precursor RNA yielding a GAM336420 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336420 RNA, hereby incorporated herein.

GAM336420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336420 target RNA, herein designated GAM TARGET RNA.

GAM336420 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336420 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336420 RNA, herein designated GAM RNA, to target binding sites on GAM336420 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336420 target RNA into GAM336420 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336420 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336420 target genes. The mRNA of each one of this plurality of GAM336420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336420 RNA, herein designated GAM RNA, and which when bound by GAM336420 RNA causes inhibition of translation of the GAM336420 target mRNA into a corresponding GAM336420 target protein.

The mechanism of the translational inhibition exerted by GAM336420 RNA, herein designated GAM RNA, on one or more GAM336420 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336420 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336420 RNA, herein designated GAM RNA, of GAM336420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336420 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336420 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336420 RNA correlate with, and may be deduced from, the identity of the GAM336420 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336422 6333 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAACCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTGGAGGT Messenger 336422 (GAM336422) oligonucleotides modulates expression of respective target
TGTGGTGAGC genes whose function and utility is known in the art.

CGAAATTGTG GAM336422 is a novel bioinformatically detectable regulatory, non protein
CCATTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336422 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAACTC encoded by the human genome.

GAM336422 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336422 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336422 precursor RNA is designated SEQ ID:6333, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6333 is located from position 16344259 to position 16344345 relative to chromosome 3 on the `+` strand.

GAM336422 precursor RNA folds onto itself, forming GAM336422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336422 precursor RNA, designated SEQ ID NO: 6333, and a schematic representation of a predicted secondary folding of GAM336422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336422 folded precursor RNA yielding a GAM336422 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336422 RNA, hereby incorporated herein. Expression of GAM336422 RNA was experimentally validated in HeLa cells using the methods

described with reference to Figs.22 to 24.

GAM336422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336422 target RNA, herein designated GAM TARGET RNA.

GAM336422 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336422 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336422 RNA, herein designated GAM RNA, to target binding sites on GAM336422 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336422 target RNA into GAM336422 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336422 target genes. The mRNA of each one of this plurality of GAM336422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336422 RNA, herein designated GAM RNA, and which when bound by GAM336422 RNA causes inhibition of translation of the GAM336422 target mRNA into a corresponding GAM336422 target protein.

The mechanism of the translational inhibition exerted by GAM336422 RNA, herein designated GAM RNA, on one or more GAM336422 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336422 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336422 RNA, herein designated GAM RNA, of GAM336422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336422 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336422 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336422 RNA correlate with, and may be deduced from, the identity of the GAM336422 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336424 6461 GAGTAGCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATTACAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGTGCCACC Messenger 336424 (GAM336424) oligonucleotides modulates expression of respective target
ATGTCTGGCT genes whose function and utility is known in the art.

GATTTTTGTA GAM336424 is a novel bioinformatically detectable regulatory, non protein
TTTTTAGTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336424 was detected
AGGTGGGGTT is described with additional reference to Figs. 9-15.

TCACCATGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCCAGGCTG encoded by the human genome.

GTC GAM336424 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336424 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336424 precursor RNA is designated SEQ ID:6461, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6461 is located from position 16592675 to position 16592767 relative to chromosome 16 on the `+` strand.

GAM336424 precursor RNA folds onto itself, forming GAM336424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336424 precursor RNA, designated SEQ ID NO: 6461, and a schematic representation of a predicted secondary folding of GAM336424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336424 folded precursor RNA yielding a GAM336424 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336424 RNA, hereby incorporated herein.

GAM336424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336424 target RNA, herein designated GAM TARGET RNA.

GAM336424 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336424 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336424 RNA, herein designated GAM RNA, to target binding sites on GAM336424 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336424 target RNA into GAM336424 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336424 target genes. The mRNA of each one of this plurality of GAM336424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336424 RNA, herein designated GAM RNA, and which when bound by GAM336424 RNA causes inhibition of translation of the GAM336424 target mRNA into a corresponding GAM336424 target protein.

The mechanism of the translational inhibition exerted by GAM336424 RNA, herein designated GAM RNA, on one or more GAM336424 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336424 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336424 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336424 RNA, herein designated GAM RNA, of GAM336424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336424 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336424 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336424 RNA correlate with, and may be deduced from, the identity of the GAM336424 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336426 5843 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336426 (GAM336426) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336426 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336426 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336426 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336426 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336426 precursor RNA is designated SEQ ID:5843, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5843 is located from position 16815249 to position 16815330 relative to chromosome 3 on the `-` strand.

GAM336426 precursor RNA folds onto itself, forming GAM336426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336426 precursor RNA, designated SEQ ID NO: 5843, and a schematic representation of a predicted secondary folding of GAM336426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336426 folded precursor RNA yielding a GAM336426 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336426 RNA, hereby incorporated herein.

GAM336426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336426 target RNA, herein designated GAM TARGET RNA.

GAM336426 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336426 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336426 RNA, herein designated GAM RNA, to target binding sites on GAM336426 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336426 target RNA into GAM336426 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336426 target genes. The mRNA of each one of this plurality of GAM336426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336426 RNA, herein designated GAM RNA, and which when bound by GAM336426 RNA causes inhibition of translation of the GAM336426 target mRNA into a corresponding GAM336426 target protein.

The mechanism of the translational inhibition exerted by GAM336426 RNA, herein

designated GAM RNA, on one or more GAM336426 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336426 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336426 RNA, herein designated GAM RNA, of GAM336426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336426 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336426 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336426 RNA correlate with, and may be deduced from, the identity of the GAM336426 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336428 6931 GTGTTCGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
ACACACCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCAGTGGC Messenger 336428 (GAM336428) oligonucleotides modulates expression of respective target
TTCAGCACCC genes whose function and utility is known in the art.

AGGTCTCCGG GAM336428 is a novel bioinformatically detectable regulatory, non protein
GAGCCAGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336428 was detected
AGGAACCAAG is described with additional reference to Figs. 9-15.

TGTTGGATAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336428 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336428 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336428 precursor RNA is designated SEQ ID:6931, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6931 is located from position 16882174 to position 16882253

relative to chromosome 22 on the `+` strand.

GAM336428 precursor RNA folds onto itself, forming GAM336428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336428 precursor RNA, designated SEQ ID NO: 6931, and a schematic representation of a predicted secondary folding of GAM336428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336428 folded precursor RNA yielding a GAM336428 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336428 RNA, hereby incorporated herein.

GAM336428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336428 target RNA, herein designated GAM TARGET RNA.

GAM336428 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336428 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336428 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336428 RNA, herein designated GAM RNA, to target binding sites on GAM336428 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336428 target RNA into GAM336428 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336428 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336428 target genes. The mRNA of each one of this plurality of GAM336428 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336428 RNA, herein designated GAM RNA, and which when bound by GAM336428 RNA causes inhibition of translation of the GAM336428 target mRNA into a corresponding GAM336428 target protein.

The mechanism of the translational inhibition exerted by GAM336428 RNA, herein designated GAM RNA, on one or more GAM336428 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336428 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336428 RNA, herein designated GAM RNA, of GAM336428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336428 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336428 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336428 RNA correlate with, and may be deduced from, the identity of the GAM336428 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336429 6591 GGACCTGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCATCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGACCAGA Messenger 336429 (GAM336429) oligonucleotides modulates expression of respective target
TAGGAGTTTT genes whose function and utility is known in the art.

TGCCTCGTGT GAM336429 is a novel bioinformatically detectable regulatory, non protein
CTGGGTGCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336429 was detected
CGATTTTGTG is described with additional reference to Figs. 9-15.

CCGTTCTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGTCC encoded by the human genome.

GAM336429 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336429 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336429 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336429 precursor RNA is designated SEQ ID:6591, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6591 is located from position 17033275 to position 17033360 relative to chromosome 17 on the `+` strand.

GAM336429 precursor RNA folds onto itself, forming GAM336429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336429 precursor RNA, designated SEQ ID NO: 6591, and a schematic representation of a predicted secondary folding of GAM336429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336429 folded precursor RNA yielding a GAM336429 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336429 RNA, hereby incorporated herein.

GAM336429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336429 target RNA, herein designated GAM TARGET RNA.

GAM336429 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336429 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336429 RNA, herein designated GAM RNA, to target

binding sites on GAM336429 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336429 target RNA into GAM336429 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336429 target genes. The mRNA of each one of this plurality of GAM336429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336429 RNA, herein designated GAM RNA, and which when bound by GAM336429 RNA causes inhibition of translation of the GAM336429 target mRNA into a corresponding GAM336429 target protein.

The mechanism of the translational inhibition exerted by GAM336429 RNA, herein designated GAM RNA, on one or more GAM336429 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336429 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336429 RNA, herein designated GAM RNA, of GAM336429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336429 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336429 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336429 RNA correlate with, and may be deduced from, the identity of the GAM336429 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336430 6750 GGCCTCCTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGCGTCACG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAATGCTGTC Messenger 336430 (GAM336430) oligonucleotides modulates expression of respective target

CTGATCCCTA genes whose function and utility is known in the art.

GCATTTACTC GAM336430 is a novel bioinformatically detectable regulatory, non protein

ACATGCTGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336430 was detected

CTTAGTGCTT is described with additional reference to Figs. 9-15.

GACCATGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGCAGATTC encoded by the human genome.

TGTGATGTGT GAM336430 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAGACGTGGT GAM336430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TGCC GAM336430 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336430 precursor RNA is designated SEQ ID:6750, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6750 is located from position 17062054 to position 17062167 relative to chromosome 7 on the `+` strand.

GAM336430 precursor RNA folds onto itself, forming GAM336430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336430 precursor RNA, designated SEQ ID NO: 6750, and a schematic representation of a predicted secondary folding of GAM336430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336430 folded precursor RNA yielding a GAM336430 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336430 RNA, hereby incorporated herein.

GAM336430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336430 target RNA, herein designated GAM TARGET RNA.

GAM336430 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336430 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336430 RNA, herein designated GAM RNA, to target binding sites on GAM336430 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336430 target RNA into GAM336430 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336430 target genes. The mRNA of each one of this plurality of GAM336430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336430 RNA, herein designated GAM RNA, and which when bound by GAM336430 RNA causes inhibition of translation of the GAM336430 target mRNA into a corresponding GAM336430 target protein.

The mechanism of the translational inhibition exerted by GAM336430 RNA, herein designated GAM RNA, on one or more GAM336430 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336430 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336430 RNA, herein designated GAM RNA, of GAM336430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336430 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336430 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336430 RNA correlate with, and may be deduced from, the identity of the GAM336430 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336431 6164 CTCCCAGCGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CACGGAATGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTCCTGATC Messenger 336431 (GAM336431) oligonucleotides modulates expression of respective target
CCTAGCATTT genes whose function and utility is known in the art.

ACTCACATGC GAM336431 is a novel bioinformatically detectable regulatory, non protein
TGTGCTTAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336431 was detected
GCTTGACCAT is described with additional reference to Figs. 9-15.

GTGGTGGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTCTGTGAT encoded by the human genome.

GTGTAAG GAM336431 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336431 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336431 precursor RNA is designated SEQ ID:6164, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6164 is located from position 17062060 to position 17062156 relative to chromosome 7 on the `+` strand.

GAM336431 precursor RNA folds onto itself, forming GAM336431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336431 precursor RNA, designated SEQ ID NO: 6164, and a schematic representation of a predicted secondary folding of GAM336431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336431 folded precursor RNA yielding a GAM336431 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336431 RNA, hereby incorporated herein.

GAM336431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336431 target RNA, herein designated GAM TARGET RNA.

GAM336431 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336431 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336431 RNA, herein designated GAM RNA, to target binding sites on GAM336431 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336431 target RNA into GAM336431 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336431 target genes. The mRNA of each one of this plurality of GAM336431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336431 RNA, herein designated GAM RNA, and which when bound by GAM336431 RNA causes inhibition of translation of the GAM336431 target mRNA into a corresponding GAM336431 target protein.

The mechanism of the translational inhibition exerted by GAM336431 RNA, herein designated GAM RNA, on one or more GAM336431 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336431 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336431 RNA, herein designated GAM RNA, of GAM336431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336431 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336431 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336431 RNA correlate with, and may be deduced from, the identity of the GAM336431 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336432 6518 GCGTCACGGA ATGCTGTCCT GATCCCTAGC ATTTACTCAC ATGCTGTGCT TAGTGCTTGA CCATGTGGTG GCAGATTCTG TGATGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336432 (GAM336432) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336432 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336432 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336432 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336432 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336432 precursor RNA is designated SEQ ID:6518, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6518 is located from position 17062066 to position 17062151 relative to chromosome 7 on the `+` strand.

GAM336432 precursor RNA folds onto itself, forming GAM336432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336432 precursor RNA, designated SEQ ID NO: 6518, and a schematic representation of a predicted secondary folding of GAM336432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336432 folded precursor RNA yielding a GAM336432 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336432 RNA, hereby incorporated herein.

GAM336432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336432 target RNA, herein designated GAM TARGET RNA.

GAM336432 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336432 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336432 RNA, herein designated GAM RNA, to target binding sites on GAM336432 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336432 target RNA into GAM336432 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336432 target genes. The mRNA of each one of this plurality of GAM336432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336432 RNA, herein designated GAM RNA, and which when bound by GAM336432 RNA causes inhibition of translation of the GAM336432 target mRNA into a corresponding GAM336432 target protein.

The mechanism of the translational inhibition exerted by GAM336432 RNA, herein designated GAM RNA, on one or more GAM336432 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336432 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336432 RNA, herein designated GAM RNA, of GAM336432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336432 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336432 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336432 RNA correlate with, and may be deduced from, the identity of the GAM336432 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336433 6148 CGTCACGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCTGTCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCCCTAGCA Messenger 336433 (GAM336433) oligonucleotides modulates expression of respective target
TTTACTCACA genes whose function and utility is known in the art.

TGCTGTGCTT GAM336433 is a novel bioinformatically detectable regulatory, non protein
AGTGCTTGAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336433 was detected
CATGTGGTGG is described with additional reference to Figs. 9-15.

CAGATTCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATG encoded by the human genome.

GAM336433 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336433 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336433 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336433 precursor RNA is designated SEQ ID:6148, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6148 is located from position 17062067 to position 17062150 relative to chromosome 7 on the `+` strand.

GAM336433 precursor RNA folds onto itself, forming GAM336433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336433 precursor RNA, designated SEQ ID NO: 6148, and a schematic representation of a predicted secondary folding of GAM336433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336433 folded precursor RNA yielding a GAM336433 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336433 RNA, hereby incorporated herein.

GAM336433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336433 target RNA, herein designated GAM TARGET RNA.

GAM336433 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336433 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336433 RNA, herein designated GAM RNA, to target binding sites on GAM336433 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336433 target RNA into GAM336433 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336433 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336433 target genes. The mRNA of each one of this plurality of GAM336433 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336433 RNA, herein designated GAM RNA, and which when bound by GAM336433 RNA causes inhibition of translation of the GAM336433 target mRNA into a corresponding GAM336433 target protein.

The mechanism of the translational inhibition exerted by GAM336433 RNA, herein designated GAM RNA, on one or more GAM336433 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336433 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336433 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336433 RNA, herein designated GAM RNA, of GAM336433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336433 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336433 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336433 RNA correlate with, and may be deduced from, the identity of the GAM336433 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336434 6317 GAGAACTGTA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGCAAGGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGCCAACTT Messenger 336434 (GAM336434) oligonucleotides modulates expression of respective target
TTTGACCAGA genes whose function and utility is known in the art.

ATCCTCGGTG GAM336434 is a novel bioinformatically detectable regulatory, non protein
AGTAATAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336434 was detected
TTTGCACTGC is described with additional reference to Figs. 9-15.

AGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336434 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336434 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336434 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336434 precursor RNA is designated SEQ ID:6317, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6317 is located from position 17392534 to position 17392608 relative to chromosome 20 on the `+` strand.

GAM336434 precursor RNA folds onto itself, forming GAM336434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336434 precursor RNA, designated SEQ ID NO: 6317, and a schematic representation of a predicted secondary folding of GAM336434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336434 folded precursor RNA yielding a GAM336434 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336434 RNA, hereby incorporated herein.

GAM336434 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336434 target RNA, herein designated GAM TARGET RNA.

GAM336434 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336434 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336434 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336434 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336434 RNA, herein designated GAM RNA, to target binding sites on GAM336434 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336434 target RNA into GAM336434 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336434 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336434 target genes. The mRNA of each one of this plurality of GAM336434 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336434 RNA, herein designated GAM RNA, and which when bound by GAM336434 RNA causes inhibition of translation of the GAM336434 target mRNA into a corresponding GAM336434 target protein.

The mechanism of the translational inhibition exerted by GAM336434 RNA, herein

designated GAM RNA, on one or more GAM336434 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336434 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336434 RNA, herein designated GAM RNA, of GAM336434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336434 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336434 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336434 RNA correlate with, and may be deduced from, the identity of the GAM336434 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336435 6969 TAGCTGCACA Fig. 8 further provides a conceptual description of another novel bioinformatically
ACACAAGCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACAGGCAAAC Messenger 336435 (GAM336435) oligonucleotides modulates expression of respective target
ACACAGACTC genes whose function and utility is known in the art.

CTGCAGTGTC GAM336435 is a novel bioinformatically detectable regulatory, non protein
TAGAGCAGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336435 was detected
ACTGGGATAT is described with additional reference to Figs. 9-15.

GAAGACTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTGGAGGCT encoded by the human genome.

GGGCAGCTA GAM336435 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336435 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336435 precursor RNA is designated SEQ ID:6969, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6969 is located from position 17533127 to position 17533225 relative to chromosome 10 on the `-` strand.

GAM336435 precursor RNA folds onto itself, forming GAM336435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336435 precursor RNA, designated SEQ ID NO: 6969, and a schematic representation of a predicted secondary folding of GAM336435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336435 folded precursor RNA yielding a GAM336435 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336435 RNA, hereby incorporated herein.

GAM336435 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336435 target RNA, herein designated GAM TARGET RNA.

GAM336435 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336435 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336435 RNA, herein designated GAM RNA, to target binding sites on GAM336435 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336435 target RNA into GAM336435 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336435 target genes. The mRNA of each one of this plurality of GAM336435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336435 RNA, herein designated GAM RNA, and which when bound by GAM336435 RNA causes inhibition of translation of the GAM336435 target mRNA into a corresponding GAM336435 target protein.

The mechanism of the translational inhibition exerted by GAM336435 RNA, herein designated GAM RNA, on one or more GAM336435 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336435 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336435 RNA, herein designated GAM RNA, of GAM336435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336435 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336435 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336435 RNA correlate with, and may be deduced from, the identity of the GAM336435 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336439 7335 TTGGGGGTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTACATGCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGCTGAGG Messenger 336439 (GAM336439) oligonucleotides modulates expression of respective target

TTTGGGAATA genes whose function and utility is known in the art.

TGGATGGTCC GAM336439 is a novel bioinformatically detectable regulatory, non protein

CATCACCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336439 was detected

GTGATGTATG is described with additional reference to Figs. 9-15.

TAGTACCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336439 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336439 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336439 precursor RNA is designated SEQ ID:7335, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7335 is located from position 18148992 to position 18149071 relative to chromosome 11 on the `+` strand.

GAM336439 precursor RNA folds onto itself, forming GAM336439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336439 precursor RNA, designated SEQ ID NO: 7335, and a schematic representation of a predicted secondary folding of GAM336439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336439 folded precursor RNA yielding a GAM336439 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336439 RNA, hereby incorporated herein.

GAM336439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336439 target RNA, herein designated GAM TARGET RNA.

GAM336439 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336439 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336439 RNA, herein designated GAM RNA, to target binding sites on GAM336439 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336439 target RNA into GAM336439 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336439 target genes. The mRNA of each one of this plurality of GAM336439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336439 RNA, herein designated GAM RNA, and which when bound by GAM336439 RNA causes inhibition of translation of the GAM336439 target mRNA into a corresponding GAM336439 target protein.

The mechanism of the translational inhibition exerted by GAM336439 RNA, herein designated GAM RNA, on one or more GAM336439 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336439 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336439 RNA, herein designated GAM RNA, of GAM336439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336439 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336439 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336439 RNA correlate with, and may be deduced from, the identity of the GAM336439 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336440 6828 GGGTTGTTAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGCATGATG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGAGGTTTG Messenger 336440 (GAM336440) oligonucleotides modulates expression of respective target

GGAATATGGA genes whose function and utility is known in the art.

TGGTCCCATC GAM336440 is a novel bioinformatically detectable regulatory, non protein

ACCCAGGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336440 was detected

TGTATGTAGT is described with additional reference to Figs. 9-15.

ACCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336440 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336440 precursor RNA is designated SEQ ID:6828, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6828 is located from position 18148996 to position 18149069 relative to chromosome 11 on the `+` strand.

GAM336440 precursor RNA folds onto itself, forming GAM336440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336440 precursor RNA, designated SEQ ID NO: 6828, and a schematic representation of a predicted secondary folding of GAM336440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336440 folded precursor RNA yielding a GAM336440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336440 RNA, hereby incorporated herein.

GAM336440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336440 target RNA, herein designated GAM TARGET RNA.

GAM336440 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336440 RNA, herein designated GAM RNA, to target binding sites on GAM336440 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336440 target RNA into GAM336440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336440 target genes. The mRNA of each one of this plurality of GAM336440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336440 RNA, herein designated GAM RNA, and which when bound by GAM336440 RNA causes inhibition of translation of the GAM336440 target mRNA into a corresponding GAM336440 target protein.

The mechanism of the translational inhibition exerted by GAM336440 RNA, herein designated GAM RNA, on one or more GAM336440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336440 RNA, herein designated GAM RNA, of GAM336440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336440 RNA correlate with, and may be deduced from, the identity of the GAM336440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336441 6730 GGCAGGAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCTTCACC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGGAGGTGG Messenger 336441 (GAM336441) oligonucleotides modulates expression of respective target
AGGTTGCAGT genes whose function and utility is known in the art.

GAGCCAAGAT GAM336441 is a novel bioinformatically detectable regulatory, non protein
TGCACCACTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336441 was detected
CACTCCTAGG is described with additional reference to Figs. 9-15.

CAATGGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACCTTGTC encoded by the human genome.

GAM336441 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336441 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336441 precursor RNA is designated SEQ ID:6730, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6730 is located from position 18229150 to position 18229239 relative to chromosome Y on the `+` strand.

GAM336441 precursor RNA folds onto itself, forming GAM336441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336441 precursor RNA, designated SEQ ID NO: 6730, and a schematic representation of a predicted secondary folding of GAM336441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336441 folded precursor RNA yielding a GAM336441 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336441 RNA, hereby incorporated herein.

GAM336441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336441 target RNA, herein designated GAM TARGET RNA.

GAM336441 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336441 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336441 RNA, herein designated GAM RNA, to target binding sites on GAM336441 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336441 target RNA into GAM336441 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336441 target genes. The mRNA of each one of this plurality of GAM336441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336441 RNA, herein designated GAM RNA, and which when bound by GAM336441 RNA causes inhibition of translation of the GAM336441 target mRNA into a corresponding GAM336441 target protein.

The mechanism of the translational inhibition exerted by GAM336441 RNA, herein designated GAM RNA, on one or more GAM336441 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336441 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336441 RNA, herein designated GAM RNA, of GAM336441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336441 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336441 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336441

RNA correlate with, and may be deduced from, the identity of the GAM336441 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336442 6540 GCTCTTTAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGTAAGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTGTTTTG Messenger 336442 (GAM336442) oligonucleotides modulates expression of respective target
TTTTCTGTGC genes whose function and utility is known in the art.

TGCTTAGTGC GAM336442 is a novel bioinformatically detectable regulatory, non protein
AGGACAATAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336442 was detected
AGAGCAGATC is described with additional reference to Figs. 9-15.

TGGCTCTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTTAGCAGC encoded by the human genome.

GAM336442 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336442 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336442 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336442 precursor RNA is designated SEQ ID:6540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6540 is located from position 18307900 to position 18307989 relative to chromosome 9 on the `+` strand.

GAM336442 precursor RNA folds onto itself, forming GAM336442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336442 precursor RNA, designated SEQ ID NO: 6540, and a schematic representation of a predicted secondary folding of GAM336442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336442 folded precursor RNA yielding a GAM336442 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336442 RNA, hereby incorporated herein.

GAM336442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336442 target RNA, herein designated GAM TARGET RNA.

GAM336442 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336442 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336442 RNA, herein designated GAM RNA, to target binding sites on GAM336442 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336442 target RNA into GAM336442 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336442 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336442 target genes. The mRNA of each one of this plurality of GAM336442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336442 RNA, herein designated GAM RNA, and which when bound by GAM336442 RNA causes inhibition of translation of the GAM336442 target mRNA into a corresponding GAM336442 target protein.

The mechanism of the translational inhibition exerted by GAM336442 RNA, herein designated GAM RNA, on one or more GAM336442 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336442 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336442 RNA, herein designated GAM RNA, of GAM336442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336442 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336442 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336442 RNA correlate with, and may be deduced from, the identity of the GAM336442 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336445 6158 CTCAGAGGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGTCACCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGCCATGAG Messenger 336445 (GAM336445) oligonucleotides modulates expression of respective target
GCTGGACTGC genes whose function and utility is known in the art.

AGCTGTGGTG GAM336445 is a novel bioinformatically detectable regulatory, non protein
GCAAGTGACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336445 was detected
AGATGTCACT is described with additional reference to Figs. 9-15.

GAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336445 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336445 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336445 precursor RNA is designated SEQ ID:6158, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6158 is located from position 18488728 to position 18488800 relative to chromosome 22 on the `+` strand.

GAM336445 precursor RNA folds onto itself, forming GAM336445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336445 precursor RNA, designated SEQ ID NO: 6158, and a schematic representation of a predicted secondary folding of GAM336445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336445 folded precursor RNA yielding a GAM336445 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336445 RNA, hereby incorporated herein.

GAM336445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336445 target RNA, herein designated GAM TARGET RNA.

GAM336445 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336445 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336445 RNA, herein designated GAM RNA, to target binding sites on GAM336445 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336445 target RNA into GAM336445 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336445 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336445 target genes. The mRNA of each one of this plurality of GAM336445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336445 RNA, herein designated GAM RNA, and which when bound by GAM336445 RNA causes inhibition of translation of the GAM336445 target mRNA into a corresponding GAM336445 target protein.

The mechanism of the translational inhibition exerted by GAM336445 RNA, herein designated GAM RNA, on one or more GAM336445 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336445 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336445 RNA, herein designated GAM RNA, of GAM336445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336445 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336445 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336445 RNA correlate with, and may be deduced from, the identity of the GAM336445 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336447 5712 AGAAAAATTA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTAATATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAAAACTGT Messenger 336447 (GAM336447) oligonucleotides modulates expression of respective target
ATTGTGCATT genes whose function and utility is known in the art.

TTGGCTTCAC GAM336447 is a novel bioinformatically detectable regulatory, non protein
ATGTTTAACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336447 was detected
TTTTTTAAGA is described with additional reference to Figs. 9-15.

AAAAAGTTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATGAATGGAA encoded by the human genome.

AAAAAATCTG GAM336447 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TATACAGTAT GAM336447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CTGTAAAAAC GAM336447 precursor RNA does not encode a protein. A nucleotide sequence identical or

TGTCTTATCT highly similar to the nucleotide sequence of GAM336447 precursor RNA is designated SEQ

ID:5712, and is provided hereinbelow with reference to the sequence listing part.
Nucleotide sequence SEQ ID:5712 is located from position 18512666 to position 18512795 relative to chromosome 17 on the `-` strand.

GAM336447 precursor RNA folds onto itself, forming GAM336447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336447 precursor RNA, designated SEQ ID NO: 5712, and a schematic representation of a predicted secondary folding of GAM336447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336447 folded precursor RNA yielding a GAM336447 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336447 RNA, hereby incorporated herein.

GAM336447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336447 target RNA, herein designated GAM TARGET RNA.

GAM336447 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336447 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336447 RNA, herein designated GAM RNA, to target binding sites on GAM336447 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336447 target RNA into GAM336447 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336447 target genes. The mRNA of each one of this plurality of GAM336447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336447 RNA, herein designated GAM RNA, and which when bound by GAM336447 RNA causes inhibition of translation of the GAM336447 target mRNA into a corresponding GAM336447 target protein.

The mechanism of the translational inhibition exerted by GAM336447 RNA, herein designated GAM RNA, on one or more GAM336447 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336447 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336447 RNA, herein designated GAM RNA, of GAM336447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336447 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336447 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336447 RNA correlate with, and may be deduced from, the identity of the GAM336447 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336448 6462 GAGTAGCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTACAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTGCCACC Messenger 336448 (GAM336448) oligonucleotides modulates expression of respective target

ATGTCTGGCT genes whose function and utility is known in the art.

GATTTTTGTA GAM336448 is a novel bioinformatically detectable regulatory, non protein

TTTTTAGTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336448 was detected

AGGTGGGGTT is described with additional reference to Figs. 9-15.

TCACCATGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCCAGGCTG encoded by the human genome.

GTC GAM336448 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336448 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336448 precursor RNA is designated SEQ

ID:6462, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6462 is located from position 18720857 to position 18720949 relative to chromosome 16 on the `-` strand.

GAM336448 precursor RNA folds onto itself, forming GAM336448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336448 precursor RNA, designated SEQ ID NO: 6462, and a schematic representation of a predicted secondary folding of GAM336448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336448 folded precursor RNA yielding a GAM336448 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336448 RNA, hereby incorporated herein.

GAM336448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336448 target RNA, herein designated GAM TARGET RNA.

GAM336448 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336448 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336448 RNA, herein designated GAM RNA, to target binding sites on GAM336448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336448 target RNA into GAM336448 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336448 target genes. The mRNA of each one of this plurality of GAM336448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336448 RNA, herein designated GAM RNA, and which when bound by GAM336448 RNA causes inhibition of translation of the GAM336448 target mRNA into a corresponding GAM336448 target protein.

The mechanism of the translational inhibition exerted by GAM336448 RNA, herein designated GAM RNA, on one or more GAM336448 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336448 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336448 RNA, herein designated GAM RNA, of GAM336448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336448 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336448 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336448 RNA correlate with, and may be deduced from, the identity of the GAM336448 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336450 6177 CTCTGTAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTGCGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTACACTATT Messenger 336450 (GAM336450) oligonucleotides modulates expression of respective target

TTACATGGTC genes whose function and utility is known in the art.

ACTATCAGCT GAM336450 is a novel bioinformatically detectable regulatory, non protein

TAGTTGTTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336450 was detected

TCACTTGTTG is described with additional reference to Figs. 9-15.

GTGACTGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAAGGTAGAT encoded by the human genome.

TTGAGATGTC GAM336450 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAGGGACTGC GAM336450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AGAG GAM336450 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336450 precursor RNA is designated SEQ ID:6177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6177 is located from position 18853144 to position 18853257 relative to chromosome 10 on the `+` strand.

GAM336450 precursor RNA folds onto itself, forming GAM336450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336450 precursor RNA, designated SEQ ID NO: 6177, and a schematic representation of a predicted secondary folding of GAM336450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336450 folded precursor RNA yielding a GAM336450 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336450 RNA, hereby incorporated herein.

GAM336450 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336450 target RNA, herein designated GAM TARGET RNA.

GAM336450 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336450 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336450 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336450 RNA, herein designated GAM RNA, to target binding sites on GAM336450 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336450 target RNA into GAM336450 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336450 target genes. The mRNA of each one of this plurality of GAM336450 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336450 RNA, herein designated GAM RNA, and which when bound by GAM336450 RNA causes inhibition of translation of the GAM336450 target mRNA into a corresponding GAM336450 target protein.

The mechanism of the translational inhibition exerted by GAM336450 RNA, herein designated GAM RNA, on one or more GAM336450 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336450 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336450 RNA, herein designated GAM RNA, of GAM336450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336450 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336450 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336450 RNA correlate with, and may be deduced from, the identity of the GAM336450 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336451 6506 GCCCTAAACG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGGGGCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAAGTTACGA Messenger 336451 (GAM336451) oligonucleotides modulates expression of respective target

CTTCTCAAGG genes whose function and utility is known in the art.

CAGTGACATC GAM336451 is a novel bioinformatically detectable regulatory, non protein
TTCCTCAATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336451 was detected
GGTATGAGTA is described with additional reference to Figs. 9-15.

GCTGCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAGTACG encoded by the human genome.

TATAAGAGTG GAM336451 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCCCATATTC GAM336451 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TGGC GAM336451 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336451 precursor RNA is designated SEQ ID:6506, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6506 is located from position 18960647 to position 18960760 relative to chromosome 18 on the `+` strand.

GAM336451 precursor RNA folds onto itself, forming GAM336451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336451 precursor RNA, designated SEQ ID NO: 6506, and a schematic representation of a predicted secondary folding of GAM336451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336451 folded precursor RNA yielding a GAM336451 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336451 RNA, hereby incorporated herein.

GAM336451 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336451 target RNA, herein designated GAM TARGET RNA.

GAM336451 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336451 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336451 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336451 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336451 RNA, herein designated GAM RNA, to target binding sites on GAM336451 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336451 target RNA into GAM336451 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336451 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336451 target genes. The mRNA of each one of this plurality of GAM336451 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336451 RNA, herein designated GAM RNA, and which when bound by GAM336451 RNA causes inhibition of translation of the GAM336451 target mRNA into a corresponding GAM336451 target protein.

The mechanism of the translational inhibition exerted by GAM336451 RNA, herein designated GAM RNA, on one or more GAM336451 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336451 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336451 RNA, herein designated GAM RNA, of GAM336451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336451 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336451 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336451 RNA correlate with, and may be deduced from, the identity of the GAM336451 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336452 6812 GGGGCCTCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTACGACTT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCAAGGCAG Messenger 336452 (GAM336452) oligonucleotides modulates expression of respective target
TGACATCTTC genes whose function and utility is known in the art.

CTCAATTGGT GAM336452 is a novel bioinformatically detectable regulatory, non protein
ATGAGTAGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336452 was detected
GCCAGGCAAC is described with additional reference to Figs. 9-15.

AAGTACGTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGAGTGTCC encoded by the human genome.

C GAM336452 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336452 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336452 precursor RNA is designated SEQ ID:6812, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6812 is located from position 18960660 to position 18960750 relative to chromosome 18 on the `+` strand.

GAM336452 precursor RNA folds onto itself, forming GAM336452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336452 precursor RNA, designated SEQ ID NO: 6812, and a schematic representation of a predicted secondary folding of GAM336452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336452 folded precursor RNA yielding a GAM336452 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336452 RNA, hereby incorporated herein.

GAM336452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336452 target RNA, herein designated GAM TARGET RNA.

GAM336452 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336452 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336452 RNA, herein designated GAM RNA, to target binding sites on GAM336452 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336452 target RNA into GAM336452 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336452 target genes. The mRNA of each one of this plurality of GAM336452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336452 RNA, herein designated GAM RNA, and which when bound by GAM336452 RNA causes inhibition of translation of the GAM336452 target mRNA into a corresponding GAM336452 target protein.

The mechanism of the translational inhibition exerted by GAM336452 RNA, herein designated GAM RNA, on one or more GAM336452 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336452 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336452 RNA, herein designated GAM RNA, of GAM336452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336452 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336452 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336452 RNA correlate with, and may be deduced from, the identity of the GAM336452 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336453 7195 TGCACCTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGGGACAAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTCTTATTG Messenger 336453 (GAM336453) oligonucleotides modulates expression of respective target
ATGGGTCTTG genes whose function and utility is known in the art.

TGTTTAATTA GAM336453 is a novel bioinformatically detectable regulatory, non protein
ATGAGAGTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336453 was detected
GTTTTAGGGG is described with additional reference to Figs. 9-15.

TATGGGCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGTGCA encoded by the human genome.

GAM336453 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336453 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336453 precursor RNA is designated SEQ ID:7195, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7195 is located from position 19104724 to position 19104809 relative to chromosome 15 on the `-` strand.

GAM336453 precursor RNA folds onto itself, forming GAM336453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336453 precursor RNA, designated SEQ ID NO: 7195, and a schematic representation of a predicted secondary folding of GAM336453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336453 folded precursor RNA yielding a GAM336453 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336453 RNA, hereby incorporated herein.

GAM336453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336453 target RNA, herein designated GAM TARGET RNA.

GAM336453 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336453 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336453 RNA, herein designated GAM RNA, to target binding sites on GAM336453 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336453 target RNA into GAM336453 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336453 target genes. The mRNA of each one of this plurality of GAM336453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336453 RNA, herein designated GAM RNA, and which when bound by GAM336453 RNA causes inhibition of translation of the GAM336453 target mRNA into a corresponding GAM336453 target protein.

The mechanism of the translational inhibition exerted by GAM336453 RNA, herein designated GAM RNA, on one or more GAM336453 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336453 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336453 RNA, herein designated GAM RNA, of GAM336453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336453 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336453 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336453 RNA correlate with, and may be deduced from, the identity of the GAM336453 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336454 7125 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAAGGCGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 336454 (GAM336454) oligonucleotides modulates expression of respective target
CGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCAGA GAM336454 is a novel bioinformatically detectable regulatory, non protein
GATCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336454 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCCGTCTCA GAM336454 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336454 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336454 precursor RNA is designated SEQ ID:7125, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7125 is located from position 19125660 to position 19125759 relative to chromosome 1 on the `+` strand.

GAM336454 precursor RNA folds onto itself, forming GAM336454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336454 precursor RNA, designated SEQ ID NO: 7125, and a schematic representation of a predicted secondary folding of GAM336454 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336454 folded precursor RNA yielding a GAM336454 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336454 RNA, hereby incorporated herein. Expression of GAM336454 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336454 target RNA, herein designated GAM TARGET RNA.

GAM336454 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336454 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336454 RNA, herein designated GAM RNA, to target binding sites on GAM336454 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336454 target RNA into GAM336454 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336454 target genes. The mRNA of each one of this plurality of GAM336454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336454 RNA, herein designated GAM RNA, and which when bound by GAM336454 RNA causes inhibition of translation of the GAM336454 target mRNA into a corresponding GAM336454 target protein.

The mechanism of the translational inhibition exerted by GAM336454 RNA, herein designated GAM RNA, on one or more GAM336454 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336454 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336454 RNA, herein designated GAM RNA, of GAM336454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336454 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336454 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336454 RNA correlate with, and may be deduced from, the identity of the GAM336454 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336455 6476 GATGTGTTCA AGAAAATTTA TTGCAGCATT GTTTGCAATA GTGAAAAAAC TGAACTCATC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336455 (GAM336455) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336455 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336455 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336455 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336455 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336455 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336455 precursor RNA is designated SEQ ID:6476, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6476 is located from position 19182411 to position 19182470 relative to chromosome 17 on the `+` strand.

GAM336455 precursor RNA folds onto itself, forming GAM336455 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336455 precursor RNA, designated SEQ ID NO: 6476, and a schematic representation of a predicted secondary folding of GAM336455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336455 folded precursor RNA yielding a GAM336455 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336455 RNA, hereby incorporated herein.

GAM336455 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336455 target RNA, herein designated GAM TARGET RNA.

GAM336455 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336455 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336455 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336455 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336455 RNA, herein designated GAM RNA, to target binding sites on GAM336455 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336455 target RNA into GAM336455 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336455 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336455 target genes. The mRNA of each one of this plurality of GAM336455 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336455 RNA,

herein designated GAM RNA, and which when bound by GAM336455 RNA causes inhibition of translation of the GAM336455 target mRNA into a corresponding GAM336455 target protein.

The mechanism of the translational inhibition exerted by GAM336455 RNA, herein designated GAM RNA, on one or more GAM336455 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336455 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336455 RNA, herein designated GAM RNA, of GAM336455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336455 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336455 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336455 RNA correlate with, and may be deduced from, the identity of the GAM336455 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336456 6514 GCCTTGGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCAAAGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGGAATACA Messenger 336456 (GAM336456) oligonucleotides modulates expression of respective target

GGTGTGAGCC genes whose function and utility is known in the art.

AACATGCCTG GAM336456 is a novel bioinformatically detectable regulatory, non protein

TCCTGTAAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336456 was detected

ATTTTTTAAA is described with additional reference to Figs. 9-15.

ACAAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336456 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336456 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336456 precursor RNA is designated SEQ ID:6514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6514 is located from position 19183141 to position 19183217 relative to chromosome 13 on the `+` strand.

GAM336456 precursor RNA folds onto itself, forming GAM336456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336456 precursor RNA, designated SEQ ID NO: 6514, and a schematic representation of a predicted secondary folding of GAM336456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336456 folded precursor RNA yielding a GAM336456 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336456 RNA, hereby incorporated herein.

GAM336456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336456 target RNA, herein designated GAM TARGET RNA.

GAM336456 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336456 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336456 RNA, herein designated GAM RNA, to target binding sites on GAM336456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336456 target RNA

into GAM336456 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336456 target genes. The mRNA of each one of this plurality of GAM336456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336456 RNA, herein designated GAM RNA, and which when bound by GAM336456 RNA causes inhibition of translation of the GAM336456 target mRNA into a corresponding GAM336456 target protein.

The mechanism of the translational inhibition exerted by GAM336456 RNA, herein designated GAM RNA, on one or more GAM336456 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336456 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336456 RNA, herein designated GAM RNA, of GAM336456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336456 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336456 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336456 RNA correlate with, and may be deduced from, the identity of the GAM336456 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336458 6610 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTAGAGG Messenger 336458 (GAM336458) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCCAAAATCA GAM336458 is a novel bioinformatically detectable regulatory, non protein

CACCACTGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336458 was detected

CTCCAGCCTG is described with additional reference to Figs. 9-15.

CCTGGGTAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGTGAGAT encoded by the human genome.

TCC GAM336458 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336458 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336458 precursor RNA is designated SEQ ID:6610, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6610 is located from position 19294864 to position 19294956 relative to chromosome 12 on the `+` strand.

GAM336458 precursor RNA folds onto itself, forming GAM336458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336458 precursor RNA, designated SEQ ID NO: 6610, and a schematic representation of a predicted secondary folding of GAM336458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336458 folded precursor RNA yielding a GAM336458 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336458 RNA, hereby incorporated herein.

GAM336458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336458 target RNA, herein designated GAM TARGET RNA.

GAM336458 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336458 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336458 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336458 RNA, herein designated GAM RNA, to target binding sites on GAM336458 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336458 target RNA into GAM336458 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336458 target genes. The mRNA of each one of this plurality of GAM336458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336458 RNA, herein designated GAM RNA, and which when bound by GAM336458 RNA causes inhibition of translation of the GAM336458 target mRNA into a corresponding GAM336458 target protein.

The mechanism of the translational inhibition exerted by GAM336458 RNA, herein designated GAM RNA, on one or more GAM336458 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336458 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336458 RNA, herein designated GAM RNA, of GAM336458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336458 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336458 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336458 RNA correlate with, and may be deduced from, the identity of the GAM336458 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336460 5701 ACCTTGCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTGGTAAT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTAGTGTGA Messenger 336460 (GAM336460) oligonucleotides modulates expression of respective target

AAGGCATAGT genes whose function and utility is known in the art.

GTCCTCTTGC GAM336460 is a novel bioinformatically detectable regulatory, non protein
TTAATCATGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336460 was detected
GATACAGACT is described with additional reference to Figs. 9-15.

GCTCACTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAAATGGTTA encoded by the human genome.

CCTTTGCAGT GAM336460 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTAAGAGGT GAM336460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336460 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336460 precursor RNA is designated SEQ ID:5701, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5701 is located from position 19464207 to position 19464315 relative to chromosome 16 on the `+` strand.

GAM336460 precursor RNA folds onto itself, forming GAM336460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336460 precursor RNA, designated SEQ ID NO: 5701, and a schematic representation of a predicted secondary folding of GAM336460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336460 folded precursor RNA yielding a GAM336460 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336460 RNA, hereby incorporated herein.

GAM336460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336460 target RNA, herein designated GAM TARGET RNA.

GAM336460 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336460 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336460 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336460 RNA, herein designated GAM RNA, to target binding sites on GAM336460 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336460 target RNA into GAM336460 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336460 target genes. The mRNA of each one of this plurality of GAM336460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336460 RNA, herein designated GAM RNA, and which when bound by GAM336460 RNA causes inhibition of translation of the GAM336460 target mRNA into a corresponding GAM336460 target protein.

The mechanism of the translational inhibition exerted by GAM336460 RNA, herein designated GAM RNA, on one or more GAM336460 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336460 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336460 RNA, herein designated GAM RNA, of GAM336460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336460 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336460 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336460 RNA correlate with, and may be deduced from, the identity of the GAM336460 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336461 6513 GCCTTGCAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAAGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGATCACC Messenger 336461 (GAM336461) oligonucleotides modulates expression of respective target
ATCAAAGTCT genes whose function and utility is known in the art.

TCTGCTCTGG GAM336461 is a novel bioinformatically detectable regulatory, non protein
GAAGGATCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336461 was detected
ACAGTCGTCC is described with additional reference to Figs. 9-15.

TTCAGCCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGGGGC encoded by the human genome.

GAM336461 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336461 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336461 precursor RNA is designated SEQ ID:6513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6513 is located from position 19661582 to position 19661668 relative to chromosome 18 on the `+` strand.

GAM336461 precursor RNA folds onto itself, forming GAM336461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336461 precursor RNA, designated SEQ ID NO: 6513, and a schematic representation of a predicted secondary folding of GAM336461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336461 folded precursor RNA yielding a GAM336461 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336461 RNA, hereby incorporated herein.

GAM336461 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336461 target RNA, herein designated GAM TARGET RNA.

GAM336461 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336461 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336461 RNA, herein designated GAM RNA, to target binding sites on GAM336461 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336461 target RNA into GAM336461 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336461 target genes. The mRNA of each one of this plurality of GAM336461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336461 RNA, herein designated GAM RNA, and which when bound by GAM336461 RNA causes inhibition of translation of the GAM336461 target mRNA into a corresponding GAM336461 target protein.

The mechanism of the translational inhibition exerted by GAM336461 RNA, herein designated GAM RNA, on one or more GAM336461 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336461 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336461 RNA, herein designated GAM RNA, of GAM336461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336461 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336461 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336461 RNA correlate with, and may be deduced from, the identity of the GAM336461 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336462 6854 GGTGTCTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGTTGATCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAATGATGG Messenger 336462 (GAM336462) oligonucleotides modulates expression of respective target
CAAGTGGGCA genes whose function and utility is known in the art.

CTTTTCAGGT GAM336462 is a novel bioinformatically detectable regulatory, non protein
AACTATTGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336462 was detected
GATTAACTGA is described with additional reference to Figs. 9-15.

CAAAGATCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAAGGCTAC encoded by the human genome.

ACTTTGTCAC GAM336462 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTCAGAGTGC GAM336462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CAGAGATACC GAM336462 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336462 precursor RNA is designated SEQ ID:6854, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6854 is located from position 19699736 to position 19699855 relative to chromosome 13 on the `+` strand.

GAM336462 precursor RNA folds onto itself, forming GAM336462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336462 precursor RNA, designated SEQ ID NO: 6854, and a schematic representation of a predicted secondary folding of GAM336462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336462 folded precursor RNA yielding a GAM336462 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336462 RNA, hereby incorporated herein.

GAM336462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336462 target RNA, herein designated GAM TARGET RNA.

GAM336462 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336462 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336462 RNA, herein designated GAM RNA, to target binding sites on GAM336462 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336462 target RNA into GAM336462 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336462 target genes. The mRNA of each one of this plurality of GAM336462 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336462 RNA, herein designated GAM RNA, and which when bound by GAM336462 RNA causes inhibition of translation of the GAM336462 target mRNA into a corresponding GAM336462 target protein.

The mechanism of the translational inhibition exerted by GAM336462 RNA, herein designated GAM RNA, on one or more GAM336462 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336462 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336462 RNA, herein designated GAM RNA, of GAM336462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336462 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336462 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336462 RNA correlate with, and may be deduced from, the identity of the GAM336462 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336465 6605 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGACGGAGG Messenger 336465 (GAM336465) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCCAGATCGC GAM336465 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336465 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGACTCC encoded by the human genome.

GAM336465 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336465 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336465 precursor RNA is designated SEQ ID:6605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6605 is located from position 19884809 to position 19884896 relative to chromosome 20 on the `+` strand.

GAM336465 precursor RNA folds onto itself, forming GAM336465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336465 precursor RNA, designated SEQ ID NO: 6605, and a schematic representation of a predicted secondary folding of GAM336465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336465 folded precursor RNA yielding a GAM336465 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336465 RNA, hereby incorporated herein. Expression of GAM336465 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336465 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336465 target RNA, herein designated GAM TARGET RNA.

GAM336465 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336465 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336465 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336465 RNA, herein designated GAM RNA, to target binding sites on GAM336465 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336465 target RNA into GAM336465 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336465 target genes. The mRNA of each one of this plurality of GAM336465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336465 RNA, herein designated GAM RNA, and which when bound by GAM336465 RNA causes inhibition of translation of the GAM336465 target mRNA into a corresponding GAM336465 target protein.

The mechanism of the translational inhibition exerted by GAM336465 RNA, herein designated GAM RNA, on one or more GAM336465 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336465 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336465 RNA, herein designated GAM RNA, of GAM336465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336465 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336465 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336465 RNA correlate with, and may be deduced from, the identity of the GAM336465 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336468 6965 TAGAAATGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATGAGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCTCTGGGT Messenger 336468 (GAM336468) oligonucleotides modulates expression of respective target

AAGTGGGGAA genes whose function and utility is known in the art.

CTGTTTGGTC GAM336468 is a novel bioinformatically detectable regulatory, non protein

TCATCGCCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336468 was detected

CATTTCTACA is described with additional reference to Figs. 9-15.

TCTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336468 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336468 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336468 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336468 precursor RNA is designated SEQ ID:6965, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6965 is located from position 19896011 to position 19896086 relative to chromosome 8 on the `+` strand.

GAM336468 precursor RNA folds onto itself, forming GAM336468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336468 precursor RNA, designated SEQ ID NO: 6965, and a schematic representation of a predicted secondary folding of GAM336468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336468 folded precursor RNA yielding a GAM336468 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336468 RNA, hereby incorporated herein.

GAM336468 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336468 target RNA, herein designated GAM TARGET RNA.

GAM336468 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336468 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336468 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336468 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336468 RNA, herein designated GAM RNA, to target binding sites on GAM336468 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336468 target RNA into GAM336468 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336468 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336468 target genes. The mRNA of each one of this plurality of GAM336468 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336468 RNA, herein designated GAM RNA, and which when bound by GAM336468 RNA causes inhibition of translation of the GAM336468 target mRNA into a corresponding GAM336468 target protein.

The mechanism of the translational inhibition exerted by GAM336468 RNA, herein designated GAM RNA, on one or more GAM336468 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336468 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336468 RNA, herein designated GAM RNA, of GAM336468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336468 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336468 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336468 RNA correlate with, and may be deduced from, the identity of the GAM336468 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336469 5792 AGGTCTCATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTTGCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTGGGGTA Messenger 336469 (GAM336469) oligonucleotides modulates expression of respective target

CAGTGGTGCA genes whose function and utility is known in the art.

AGTATGGCTC GAM336469 is a novel bioinformatically detectable regulatory, non protein

ACTGCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336469 was detected

TGAACTCTTT is described with additional reference to Figs. 9-15.

CTGGGCTCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGATCCT encoded by the human genome.

GAM336469 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336469 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336469 precursor RNA is designated SEQ ID:5792, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5792 is located from position 20036295 to position 20036382 relative to chromosome 20 on the `+` strand.

GAM336469 precursor RNA folds onto itself, forming GAM336469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336469 precursor RNA, designated SEQ ID NO: 5792, and a schematic representation of a predicted secondary folding of GAM336469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336469 folded precursor RNA yielding a GAM336469 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336469 RNA, hereby incorporated herein.

GAM336469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336469 target RNA, herein designated GAM TARGET RNA.

GAM336469 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336469 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336469 RNA, herein designated GAM RNA, to target binding sites on GAM336469 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336469 target RNA into GAM336469 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336469 target genes. The mRNA of each one of this plurality of GAM336469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336469 RNA, herein designated GAM RNA, and which when bound by GAM336469 RNA causes inhibition of translation of the GAM336469 target mRNA into a corresponding GAM336469 target protein.

The mechanism of the translational inhibition exerted by GAM336469 RNA, herein designated GAM RNA, on one or more GAM336469 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336469 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336469 RNA, herein designated GAM RNA, of GAM336469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336469 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336469 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336469 RNA correlate with, and may be deduced from, the identity of the GAM336469 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336470 5793 AGGTCTCATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTTGCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTGGGGTA Messenger 336470 (GAM336470) oligonucleotides modulates expression of respective target

CAGTGGTGCA genes whose function and utility is known in the art.

AGTATGGCTC GAM336470 is a novel bioinformatically detectable regulatory, non protein

ACTGCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336470 was detected

TGAACTCTTT is described with additional reference to Figs. 9-15.

CTGGGCTCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGATCCTCC encoded by the human genome.

T GAM336470 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336470 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336470 precursor RNA is designated SEQ ID:5793, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5793 is located from position 20036295 to position 20036385 relative to chromosome 20 on the `+` strand.

GAM336470 precursor RNA folds onto itself, forming GAM336470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336470 precursor RNA, designated SEQ ID NO: 5793, and a schematic representation of a predicted secondary folding of GAM336470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336470 folded precursor RNA yielding a GAM336470 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336470 RNA, hereby incorporated herein.

GAM336470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336470 target RNA, herein designated GAM TARGET RNA.

GAM336470 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336470 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336470 RNA, herein designated GAM RNA, to target binding sites on GAM336470 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336470 target RNA into GAM336470 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336470 target genes. The mRNA of each one of this plurality of GAM336470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336470 RNA, herein designated GAM RNA, and which when bound by GAM336470 RNA causes inhibition of translation of the GAM336470 target mRNA into a corresponding GAM336470 target protein.

The mechanism of the translational inhibition exerted by GAM336470 RNA, herein designated GAM RNA, on one or more GAM336470 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336470 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336470 RNA, herein designated GAM RNA, of GAM336470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336470 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336470 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336470 RNA correlate with, and may be deduced from, the identity of the GAM336470 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336472 6014 CAGATGCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTCGGGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
CACAGGATCC Messenger 336472 (GAM336472) oligonucleotides modulates expression of respective target
AGAGAGTCAA genes whose function and utility is known in the art.

TGAAAGTAAA GAM336472 is a novel bioinformatically detectable regulatory, non protein
ACTTCAGGAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336472 was detected
TGTCTGGATT is described with additional reference to Figs. 9-15.

TATTACGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGAGGAAGT encoded by the human genome.

TG GAM336472 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336472 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336472 precursor RNA is designated SEQ ID:6014, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6014 is located from position 20299247 to position 20299338 relative to chromosome 15 on the `+` strand.

GAM336472 precursor RNA folds onto itself, forming GAM336472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336472 precursor RNA, designated SEQ ID NO: 6014, and a schematic representation of a predicted secondary folding of GAM336472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336472 folded precursor RNA yielding a GAM336472 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336472 RNA, hereby incorporated herein.

GAM336472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336472 target RNA, herein designated GAM TARGET RNA.

GAM336472 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336472 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336472 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336472 RNA, herein designated GAM RNA, to target binding sites on GAM336472 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336472 target RNA into GAM336472 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336472 target genes. The mRNA of each one of this plurality of GAM336472 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336472 RNA, herein designated GAM RNA, and which when bound by GAM336472 RNA causes inhibition of translation of the GAM336472 target mRNA into a corresponding GAM336472 target protein.

The mechanism of the translational inhibition exerted by GAM336472 RNA, herein designated GAM RNA, on one or more GAM336472 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336472 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336472 RNA, herein designated GAM RNA, of GAM336472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336472 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336472 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336472

RNA correlate with, and may be deduced from, the identity of the GAM336472 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336474 6034 CATAGCTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGAGGCGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTTTCAGAA Messenger 336474 (GAM336474) oligonucleotides modulates expression of respective target
ACCATAGACA genes whose function and utility is known in the art.

TCTGAGAAAT GAM336474 is a novel bioinformatically detectable regulatory, non protein
ATGTTTCTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336474 was detected
CTTTTATG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336474 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336474 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336474 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336474 precursor RNA is designated SEQ ID:6034, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6034 is located from position 20354510 to position 20354577 relative to chromosome Y on the `-` strand.

GAM336474 precursor RNA folds onto itself, forming GAM336474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336474 precursor RNA, designated SEQ ID NO: 6034, and a schematic representation of a predicted secondary folding of GAM336474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336474 folded precursor RNA yielding a GAM336474 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336474 RNA, hereby incorporated herein.

GAM336474 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336474 target RNA, herein designated GAM TARGET RNA.

GAM336474 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336474 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336474 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336474 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336474 RNA, herein designated GAM RNA, to target binding sites on GAM336474 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336474 target RNA into GAM336474 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336474 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336474 target genes. The mRNA of each one of this plurality of GAM336474 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336474 RNA, herein designated GAM RNA, and which when bound by GAM336474 RNA causes inhibition of translation of the GAM336474 target mRNA into a corresponding GAM336474 target protein.

The mechanism of the translational inhibition exerted by GAM336474 RNA, herein designated GAM RNA, on one or more GAM336474 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336474 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336474 RNA, herein designated GAM RNA, of GAM336474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336474 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336474 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336474 RNA correlate with, and may be deduced from, the identity of the GAM336474 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336475 6672 GGAGAATGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGAGG Messenger 336475 (GAM336475) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATTGT GAM336475 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336475 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336475 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336475 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336475 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336475 precursor RNA is designated SEQ ID:6672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6672 is located from position 20384897 to position 20384984 relative to chromosome 15 on the `+` strand.

GAM336475 precursor RNA folds onto itself, forming GAM336475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336475 precursor RNA, designated SEQ ID NO: 6672, and a schematic representation of a predicted secondary folding of GAM336475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336475 folded precursor RNA yielding a GAM336475 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336475 RNA, hereby incorporated herein. Expression of GAM336475 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336475 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336475 target RNA, herein designated GAM TARGET RNA.

GAM336475 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336475 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336475 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336475 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336475 RNA, herein designated GAM RNA, to target binding sites on GAM336475 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336475 target RNA into GAM336475 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336475 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336475 target genes. The mRNA of each one of this plurality of GAM336475 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336475 RNA, herein designated GAM RNA, and which when bound by GAM336475 RNA causes inhibition of translation of the GAM336475 target mRNA into a corresponding GAM336475 target protein.

The mechanism of the translational inhibition exerted by GAM336475 RNA, herein designated GAM RNA, on one or more GAM336475 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336475 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336475 RNA, herein designated GAM RNA, of GAM336475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336475 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336475 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336475 RNA correlate with, and may be deduced from, the identity of the GAM336475 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336476 6902 GTGCACTACA Fig. 8 further provides a conceptual description of another novel bioinformatically
GACTCCAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCCTTTGAA Messenger 336476 (GAM336476) oligonucleotides modulates expression of respective target
GCCAGGTTCC genes whose function and utility is known in the art.

AGAGCTTCCT GAM336476 is a novel bioinformatically detectable regulatory, non protein
CCCTTTGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336476 was detected
TGGAACCTCA is described with additional reference to Figs. 9-15.

ACAGCAGGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGGATGAGG encoded by the human genome.

ATGGAAGTGT GAM336476 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AC GAM336476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336476 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336476 precursor RNA is designated SEQ ID:6902, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6902 is located from position 20417307 to position 20417408 relative to chromosome 17 on the `-` strand.

GAM336476 precursor RNA folds onto itself, forming GAM336476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336476 precursor RNA, designated SEQ ID NO: 6902, and a schematic representation of a predicted secondary folding of GAM336476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336476 folded precursor RNA yielding a GAM336476 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336476 RNA, hereby incorporated herein.

GAM336476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336476 target RNA, herein designated GAM TARGET RNA.

GAM336476 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336476 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336476 RNA, herein designated GAM RNA, to target binding sites on GAM336476 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336476 target RNA into GAM336476 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336476 target genes. The mRNA of each one of this plurality of GAM336476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336476 RNA, herein designated GAM RNA, and which when bound by GAM336476 RNA causes inhibition of translation of the GAM336476 target mRNA into a corresponding GAM336476 target protein.

The mechanism of the translational inhibition exerted by GAM336476 RNA, herein designated GAM RNA, on one or more GAM336476 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336476 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336476 RNA, herein designated GAM RNA, of GAM336476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336476 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336476 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336476 RNA correlate with, and may be deduced from, the identity of the GAM336476 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336477 6910 GTGGACTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTGTGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGAAAATAT Messenger 336477 (GAM336477) oligonucleotides modulates expression of respective target

TAAGGTGGGA genes whose function and utility is known in the art.

TGTGTGGATC GAM336477 is a novel bioinformatically detectable regulatory, non protein

AGTGTCCTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336477 was detected

CACATTCCCG is described with additional reference to Figs. 9-15.

CAGGGTGTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCTGGCACT encoded by the human genome.

ATCATAC GAM336477 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336477 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336477 precursor RNA is designated SEQ ID:6910, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6910 is located from position 20421189 to position 20421285 relative to chromosome 16 on the `+` strand.

GAM336477 precursor RNA folds onto itself, forming GAM336477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336477 precursor RNA, designated SEQ ID NO: 6910, and a schematic representation of a predicted secondary folding of GAM336477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336477 folded precursor RNA yielding a GAM336477 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336477 RNA, hereby incorporated herein.

GAM336477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336477 target RNA, herein designated GAM TARGET RNA.

GAM336477 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336477 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336477 RNA, herein designated GAM RNA, to target binding sites on GAM336477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336477 target RNA into GAM336477 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336477 target genes. The mRNA of each one of this plurality of GAM336477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336477 RNA, herein designated GAM RNA, and which when bound by GAM336477 RNA causes inhibition of translation of the GAM336477 target mRNA into a corresponding GAM336477 target protein.

The mechanism of the translational inhibition exerted by GAM336477 RNA, herein designated GAM RNA, on one or more GAM336477 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336477 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336477 RNA, herein designated GAM RNA, of GAM336477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336477 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336477 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336477 RNA correlate with, and may be deduced from, the identity of the GAM336477 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336478 7192 TGATGTGTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAGGAAAAT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTAAGGTGG Messenger 336478 (GAM336478) oligonucleotides modulates expression of respective target

GATGTGTGGA genes whose function and utility is known in the art.

TCAGTGTCCT GAM336478 is a novel bioinformatically detectable regulatory, non protein

AGCACATTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336478 was detected

CGCAGGGTGT is described with additional reference to Figs. 9-15.

AAGCCTGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTATCA encoded by the human genome.

GAM336478 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336478 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336478 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336478 precursor RNA is designated SEQ ID:7192, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7192 is located from position 20421197 to position 20421282 relative to chromosome 16 on the `+` strand.

GAM336478 precursor RNA folds onto itself, forming GAM336478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336478 precursor RNA, designated SEQ ID NO: 7192, and a schematic representation of a predicted secondary folding of GAM336478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336478 folded precursor RNA yielding a GAM336478 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336478 RNA, hereby incorporated herein.

GAM336478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336478 target RNA, herein designated GAM TARGET RNA.

GAM336478 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336478 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336478 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336478 RNA, herein designated GAM RNA, to target binding sites on GAM336478 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336478 target RNA into GAM336478 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336478 target genes. The mRNA of each one of this plurality of GAM336478 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336478 RNA, herein designated GAM RNA, and which when bound by GAM336478 RNA causes inhibition of translation of the GAM336478 target mRNA into a corresponding GAM336478 target protein.

The mechanism of the translational inhibition exerted by GAM336478 RNA, herein designated GAM RNA, on one or more GAM336478 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336478 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336478 RNA, herein designated GAM RNA, of GAM336478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336478 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336478 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336478 RNA correlate with, and may be deduced from, the identity of the GAM336478 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336479 6911 GTGGACTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTGTGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGAAAATAT Messenger 336479 (GAM336479) oligonucleotides modulates expression of respective target

TAAGGTGGGA genes whose function and utility is known in the art.

TGTGTGGATC GAM336479 is a novel bioinformatically detectable regulatory, non protein
AGTGTCCTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336479 was detected
CACATTCCCG is described with additional reference to Figs. 9-15.

CAGGGTGTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCTGGCACT encoded by the human genome.

ATCATAC GAM336479 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336479 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336479 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336479 precursor RNA is designated SEQ ID:6911, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6911 is located from position 20480066 to position 20480162 relative to chromosome 16 on the `-` strand.

GAM336479 precursor RNA folds onto itself, forming GAM336479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336479 precursor RNA, designated SEQ ID NO: 6911, and a schematic representation of a predicted secondary folding of GAM336479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336479 folded precursor RNA yielding a GAM336479 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336479 RNA, hereby incorporated herein.

GAM336479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336479 target RNA, herein designated GAM TARGET RNA.

GAM336479 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336479 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336479 RNA, herein designated GAM RNA, to target binding sites on GAM336479 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336479 target RNA into GAM336479 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336479 target genes. The mRNA of each one of this plurality of GAM336479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336479 RNA, herein designated GAM RNA, and which when bound by GAM336479 RNA causes inhibition of translation of the GAM336479 target mRNA into a corresponding GAM336479 target protein.

The mechanism of the translational inhibition exerted by GAM336479 RNA, herein designated GAM RNA, on one or more GAM336479 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336479 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336479 RNA, herein designated GAM RNA, of GAM336479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336479 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336479 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336479 RNA correlate with, and may be deduced from, the identity of the GAM336479 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336480 7193 TGATGTGTGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTAGGAAAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTAAGGTGG Messenger 336480 (GAM336480) oligonucleotides modulates expression of respective target
GATGTGTGGA genes whose function and utility is known in the art.

TCAGTGTCCT GAM336480 is a novel bioinformatically detectable regulatory, non protein
AGCACATTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336480 was detected
CGCAGGGTGT is described with additional reference to Figs. 9-15.

AAGCCTGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTATCA encoded by the human genome.

GAM336480 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336480 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336480 precursor RNA is designated SEQ ID:7193, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7193 is located from position 20480069 to position 20480154 relative to chromosome 16 on the `-` strand.

GAM336480 precursor RNA folds onto itself, forming GAM336480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336480 precursor RNA, designated SEQ ID NO: 7193, and a schematic representation of a predicted secondary folding of GAM336480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336480 folded precursor RNA yielding a GAM336480 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336480 RNA, hereby incorporated herein.

GAM336480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336480 target RNA, herein designated GAM TARGET RNA.

GAM336480 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336480 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336480 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336480 RNA, herein designated GAM RNA, to target binding sites on GAM336480 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336480 target RNA into GAM336480 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336480 target genes. The mRNA of each one of this plurality of GAM336480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336480 RNA, herein designated GAM RNA, and which when bound by GAM336480 RNA causes inhibition of translation of the GAM336480 target mRNA into a corresponding GAM336480 target protein.

The mechanism of the translational inhibition exerted by GAM336480 RNA, herein designated GAM RNA, on one or more GAM336480 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336480 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336480 RNA, herein designated GAM RNA, of GAM336480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336480 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336480 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336480 RNA correlate with, and may be deduced from, the identity of the GAM336480 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336483 7331 TTGGCCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGAGTCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGAGTAGGT Messenger 336483 (GAM336483) oligonucleotides modulates expression of respective target
GTGCAATAAG genes whose function and utility is known in the art.

AGTTAACATT GAM336483 is a novel bioinformatically detectable regulatory, non protein
TGCTAACTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336483 was detected
CAGTCTTATG is described with additional reference to Figs. 9-15.

GCTCCTTACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGCTGA encoded by the human genome.

GAM336483 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336483 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336483 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336483 precursor RNA is designated SEQ ID:7331, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7331 is located from position 20641538 to position 20641624 relative to chromosome 8 on the `+` strand.

GAM336483 precursor RNA folds onto itself, forming GAM336483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336483 precursor RNA, designated SEQ ID NO: 7331, and a schematic representation of a predicted secondary folding of GAM336483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336483 folded precursor RNA yielding a GAM336483 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336483 RNA, hereby incorporated herein.

GAM336483 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336483 target RNA, herein designated GAM TARGET RNA.

GAM336483 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336483 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336483 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336483 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336483 RNA, herein designated GAM RNA, to target binding sites on GAM336483 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336483 target RNA into GAM336483 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336483 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336483 target genes. The mRNA of each one of this plurality of GAM336483 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336483 RNA, herein designated GAM RNA, and which when bound by GAM336483 RNA causes inhibition of translation of the GAM336483 target mRNA into a corresponding GAM336483 target protein.

The mechanism of the translational inhibition exerted by GAM336483 RNA, herein designated GAM RNA, on one or more GAM336483 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336483 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336483 RNA, herein designated GAM RNA, of GAM336483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336483 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336483 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336483 RNA correlate with, and may be deduced from, the identity of the GAM336483 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336484 5737 AGATCCGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCTTGGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTTAGGGAA Messenger 336484 (GAM336484) oligonucleotides modulates expression of respective target
TGAACAAATA genes whose function and utility is known in the art.

GAGGCCAGTA GAM336484 is a novel bioinformatically detectable regulatory, non protein
TTAGGAGGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336484 was detected
TAGCTCCAGA is described with additional reference to Figs. 9-15.

GATTCTAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTGGGGTCA encoded by the human genome.

GGGATCT GAM336484 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336484 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336484 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336484 precursor RNA is designated SEQ ID:5737, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5737 is located from position 20790820 to position 20790916 relative to chromosome 12 on the `+` strand.

GAM336484 precursor RNA folds onto itself, forming GAM336484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336484 precursor RNA, designated SEQ ID NO: 5737, and a schematic representation of a predicted secondary folding of GAM336484 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336484 folded precursor RNA yielding a GAM336484 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336484 RNA, hereby incorporated herein.

GAM336484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336484 target RNA, herein designated GAM TARGET RNA.

GAM336484 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336484 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336484 RNA, herein designated GAM RNA, to target binding sites on GAM336484 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336484 target RNA into GAM336484 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336484 target genes. The mRNA of each one of this plurality of GAM336484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336484 RNA, herein designated GAM RNA, and which when bound by GAM336484 RNA causes inhibition of translation of the GAM336484 target mRNA into a corresponding GAM336484 target protein.

The mechanism of the translational inhibition exerted by GAM336484 RNA, herein designated GAM RNA, on one or more GAM336484 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336484 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336484 RNA, herein designated GAM RNA, of GAM336484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336484 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336484 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336484 RNA correlate with, and may be deduced from, the identity of the GAM336484 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336486 5799 AGGTTGGTAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGTGGTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TAACACAGTA Messenger 336486 (GAM336486) oligonucleotides modulates expression of respective target

TCTCTTCTTT genes whose function and utility is known in the art.

TAGGTGTTCA GAM336486 is a novel bioinformatically detectable regulatory, non protein

GTGGAATCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336486 was detected

ACTTACAAAA is described with additional reference to Figs. 9-15.

TTTGGAGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGTGGTGTT encoded by the human genome.

GGCTTTTGCC GAM336486 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAATCT GAM336486 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336486 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336486 precursor RNA is designated SEQ ID:5799, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5799 is located from position 21001411 to position 21001516 relative to chromosome 18 on the `-` strand.

GAM336486 precursor RNA folds onto itself, forming GAM336486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336486 precursor RNA, designated SEQ ID NO: 5799, and a schematic representation of a predicted secondary folding of GAM336486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336486 folded precursor RNA yielding a GAM336486 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336486 RNA, hereby incorporated herein.

GAM336486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336486 target RNA, herein designated GAM TARGET RNA.

GAM336486 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336486 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336486 RNA, herein designated GAM RNA, to target binding sites on GAM336486 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336486 target RNA into GAM336486 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336486 target genes. The mRNA of each one of this plurality of GAM336486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336486 RNA, herein designated GAM RNA, and which when bound by GAM336486 RNA causes inhibition of translation of the GAM336486 target mRNA into a corresponding GAM336486 target protein.

The mechanism of the translational inhibition exerted by GAM336486 RNA, herein designated GAM RNA, on one or more GAM336486 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336486 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336486 RNA, herein designated GAM RNA, of GAM336486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336486 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336486 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336486 RNA correlate with, and may be deduced from, the identity of the GAM336486 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336487 5676 AATGGCTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TAAGGGAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCATTCATT Messenger 336487 (GAM336487) oligonucleotides modulates expression of respective target

TATTCATTCA genes whose function and utility is known in the art.

ACTAATATT GAM336487 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336487 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336487 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336487 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336487 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336487 precursor RNA is designated SEQ ID:5676, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:5676 is located from position 21104974 to position 21105023 relative to chromosome 5 on the `-` strand.

GAM336487 precursor RNA folds onto itself, forming GAM336487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336487 precursor RNA, designated SEQ ID NO: 5676, and a schematic representation of a predicted secondary folding of GAM336487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336487 folded precursor RNA yielding a GAM336487 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336487 RNA, hereby incorporated herein. Expression of GAM336487 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336487 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336487 target RNA, herein designated GAM TARGET RNA.

GAM336487 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336487 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336487 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336487 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336487 RNA, herein designated GAM RNA, to target binding sites on GAM336487 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336487 target RNA into GAM336487 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336487 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336487 target genes. The mRNA of each one of this plurality of GAM336487 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336487 RNA, herein designated GAM RNA, and which when bound by GAM336487 RNA causes inhibition of translation of the GAM336487 target mRNA into a corresponding GAM336487 target protein.

The mechanism of the translational inhibition exerted by GAM336487 RNA, herein designated GAM RNA, on one or more GAM336487 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336487 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336487 RNA, herein designated GAM RNA, of GAM336487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336487 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336487 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336487 RNA correlate with, and may be deduced from, the identity of the GAM336487 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336488 5749 AGCCCTAATA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTATAATTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GAACTGTACT Messenger 336488 (GAM336488) oligonucleotides modulates expression of respective target

GGACCCATAG genes whose function and utility is known in the art.

TTTTAACTGA GAM336488 is a novel bioinformatically detectable regulatory, non protein

AAAGGGCCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336488 was detected

ACAAGTGGTG is described with additional reference to Figs. 9-15.

TCTGTCCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCTGGACTG encoded by the human genome.

GGCT GAM336488 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336488 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336488 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336488 precursor RNA is designated SEQ ID:5749, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5749 is located from position 21165273 to position 21165366 relative to chromosome 22 on the `-` strand.

GAM336488 precursor RNA folds onto itself, forming GAM336488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336488 precursor RNA, designated SEQ ID NO: 5749, and a schematic representation of a predicted secondary folding of GAM336488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336488 folded precursor RNA yielding a GAM336488 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336488 RNA, hereby incorporated herein.

GAM336488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336488 target RNA, herein designated GAM TARGET RNA.

GAM336488 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336488 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336488 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336488 RNA, herein designated GAM RNA, to target binding sites on GAM336488 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336488 target RNA into GAM336488 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336488 target genes. The mRNA of each one of this plurality of GAM336488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336488 RNA, herein designated GAM RNA, and which when bound by GAM336488 RNA causes inhibition of translation of the GAM336488 target mRNA into a corresponding GAM336488 target protein.

The mechanism of the translational inhibition exerted by GAM336488 RNA, herein designated GAM RNA, on one or more GAM336488 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336488 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336488 RNA, herein designated GAM RNA, of GAM336488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336488 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336488 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336488 RNA correlate with, and may be deduced from, the identity of the GAM336488 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336489 5844 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336489 (GAM336489) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336489 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336489 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336489 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336489 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336489 precursor RNA is designated SEQ ID:5844, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5844 is located from position 21185062 to position 21185143 relative to chromosome 12 on the `+` strand.

GAM336489 precursor RNA folds onto itself, forming GAM336489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336489 precursor RNA, designated SEQ ID NO: 5844, and a schematic representation of a predicted secondary folding of GAM336489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336489 folded precursor RNA yielding a GAM336489 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336489 RNA, hereby incorporated herein.

GAM336489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336489 target RNA, herein designated GAM TARGET RNA.

GAM336489 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336489 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336489 RNA, herein designated GAM RNA, to target binding sites on GAM336489 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336489 target RNA into GAM336489 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336489 target genes. The mRNA of each one of this plurality of GAM336489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336489 RNA, herein designated GAM RNA, and which when bound by GAM336489 RNA causes inhibition of translation of the GAM336489 target mRNA into a corresponding GAM336489 target protein.

The mechanism of the translational inhibition exerted by GAM336489 RNA, herein designated GAM RNA, on one or more GAM336489 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336489 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336489 RNA, herein designated GAM RNA, of GAM336489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336489 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336489 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336489 RNA correlate with, and may be deduced from, the identity of the GAM336489 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336490 6634 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336490 (GAM336490) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM336490 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336490 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336490 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336490 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336490 precursor RNA is designated SEQ ID:6634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6634 is located from position 21350021 to position 21350108 relative to chromosome 5 on the `-` strand.

GAM336490 precursor RNA folds onto itself, forming GAM336490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336490 precursor RNA, designated SEQ ID NO: 6634, and a schematic representation of a predicted secondary folding of GAM336490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336490 folded precursor RNA yielding a GAM336490 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336490 RNA, hereby incorporated herein. Expression of GAM336490 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336490 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336490 target RNA, herein designated GAM TARGET RNA.

GAM336490 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336490 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336490 RNA, herein designated GAM RNA, to target binding sites on GAM336490 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336490 target RNA into GAM336490 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336490 target genes. The mRNA of each one of this plurality of GAM336490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336490 RNA, herein designated GAM RNA, and which when bound by GAM336490 RNA causes inhibition of translation of the GAM336490 target mRNA into a corresponding GAM336490 target protein.

The mechanism of the translational inhibition exerted by GAM336490 RNA, herein designated GAM RNA, on one or more GAM336490 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336490 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336490 RNA, herein designated GAM RNA, of GAM336490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336490 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336490 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336490 RNA correlate with, and may be deduced from, the identity of the GAM336490 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336491 6562 GCTTGAACCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGATGTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTTGTAGTG Messenger 336491 (GAM336491) oligonucleotides modulates expression of respective target
AGCTGAGATT genes whose function and utility is known in the art.

GGGCCATTGC GAM336491 is a novel bioinformatically detectable regulatory, non protein
ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336491 was detected
GGGCAACAAG is described with additional reference to Figs. 9-15.

AGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336491 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336491 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336491 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336491 precursor RNA is designated SEQ ID:6562, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6562 is located from position 21374719 to position 21374791 relative to chromosome 21 on the `+` strand.

GAM336491 precursor RNA folds onto itself, forming GAM336491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336491 precursor RNA, designated SEQ ID NO: 6562, and a schematic representation of a predicted secondary folding of GAM336491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336491 folded precursor RNA yielding a GAM336491 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336491 RNA, hereby incorporated herein. Expression of GAM336491 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336491 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336491 target RNA, herein designated GAM TARGET RNA.

GAM336491 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336491 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336491 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336491 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336491 RNA, herein designated GAM RNA, to target binding sites on GAM336491 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336491 target RNA into GAM336491 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336491 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336491 target genes. The mRNA of each one of this plurality of GAM336491 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336491 RNA, herein designated GAM RNA, and which when bound by GAM336491 RNA causes inhibition of translation of the GAM336491 target mRNA into a corresponding GAM336491 target protein.

The mechanism of the translational inhibition exerted by GAM336491 RNA, herein designated GAM RNA, on one or more GAM336491 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336491 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336491 RNA, herein designated GAM RNA, of GAM336491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336491 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336491 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336491 RNA correlate with, and may be deduced from, the identity of the GAM336491 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336492 6593 GGACTACAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACATGCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CACGTCTGGC Messenger 336492 (GAM336492) oligonucleotides modulates expression of respective target

TAATTTTCTT genes whose function and utility is known in the art.

GAGTTTTAGT GAM336492 is a novel bioinformatically detectable regulatory, non protein

AGAGACTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336492 was detected

TCTCGTTATG is described with additional reference to Figs. 9-15.

TTGTCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCCCGAG encoded by the human genome.

CTCCTGAGTT GAM336492 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336492 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336492 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336492 precursor RNA is designated SEQ ID:6593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6593 is located from position 21380738 to position 21380838 relative to chromosome 16 on the `-` strand.

GAM336492 precursor RNA folds onto itself, forming GAM336492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336492 precursor RNA, designated SEQ ID NO: 6593, and a schematic representation of a predicted secondary folding of GAM336492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336492 folded precursor RNA yielding a GAM336492 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336492 RNA, hereby incorporated herein.

GAM336492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336492 target RNA, herein designated GAM TARGET RNA.

GAM336492 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336492 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336492 RNA, herein designated GAM RNA, to target binding sites on GAM336492 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336492 target RNA into GAM336492 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336492 target genes. The mRNA of each one of this plurality of GAM336492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336492 RNA, herein designated GAM RNA, and which when bound by GAM336492 RNA causes inhibition of translation of the GAM336492 target mRNA into a corresponding GAM336492 target protein.

The mechanism of the translational inhibition exerted by GAM336492 RNA, herein

designated GAM RNA, on one or more GAM336492 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336492 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336492 RNA, herein designated GAM RNA, of GAM336492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336492 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336492 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336492 RNA correlate with, and may be deduced from, the identity of the GAM336492 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336493 6741 GGCATGGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCTCTGATA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCTAGCTA Messenger 336493 (GAM336493) oligonucleotides modulates expression of respective target

CTCAGGAGGC genes whose function and utility is known in the art.

TGAGCCTAGT GAM336493 is a novel bioinformatically detectable regulatory, non protein

AGTTAGAGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336493 was detected

TGCAGTGAAC is described with additional reference to Figs. 9-15.

TATGATTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CC encoded by the human genome.

GAM336493 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336493 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336493 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336493 precursor RNA is designated SEQ ID:6741, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6741 is located from position 21401896 to position 21401977

relative to chromosome 14 on the `-` strand.

GAM336493 precursor RNA folds onto itself, forming GAM336493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336493 precursor RNA, designated SEQ ID NO: 6741, and a schematic representation of a predicted secondary folding of GAM336493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336493 folded precursor RNA yielding a GAM336493 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336493 RNA, hereby incorporated herein.

GAM336493 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336493 target RNA, herein designated GAM TARGET RNA.

GAM336493 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336493 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336493 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336493 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336493 RNA, herein designated GAM RNA, to target binding sites on GAM336493 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336493 target RNA into GAM336493 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336493 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336493 target genes. The mRNA of each one of this plurality of GAM336493 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336493 RNA, herein designated GAM RNA, and which when bound by GAM336493 RNA causes inhibition of translation of the GAM336493 target mRNA into a corresponding GAM336493 target protein.

The mechanism of the translational inhibition exerted by GAM336493 RNA, herein designated GAM RNA, on one or more GAM336493 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336493 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336493 RNA, herein designated GAM RNA, of GAM336493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336493 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336493 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336493 RNA correlate with, and may be deduced from, the identity of the GAM336493 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336494 7029 TCCCTATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGCAGCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGACGTCA Messenger 336494 (GAM336494) oligonucleotides modulates expression of respective target

TTGAGAGATA genes whose function and utility is known in the art.

AATTAGGTAC GAM336494 is a novel bioinformatically detectable regulatory, non protein

AAGTGGGCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336494 was detected

AGAATTGTAT is described with additional reference to Figs. 9-15.

GTGAGGTTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGA encoded by the human genome.

GAM336494 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336494 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336494 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336494 precursor RNA is designated SEQ ID:7029, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7029 is located from position 21775643 to position 21775725 relative to chromosome 21 on the `+` strand.

GAM336494 precursor RNA folds onto itself, forming GAM336494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336494 precursor RNA, designated SEQ ID NO: 7029, and a schematic representation of a predicted secondary folding of GAM336494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336494 folded precursor RNA yielding a GAM336494 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336494 RNA, hereby incorporated herein.

GAM336494 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336494 target RNA, herein designated GAM TARGET RNA.

GAM336494 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336494 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336494 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336494 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336494 RNA, herein designated GAM RNA, to target

binding sites on GAM336494 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336494 target RNA into GAM336494 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336494 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336494 target genes. The mRNA of each one of this plurality of GAM336494 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336494 RNA, herein designated GAM RNA, and which when bound by GAM336494 RNA causes inhibition of translation of the GAM336494 target mRNA into a corresponding GAM336494 target protein.

The mechanism of the translational inhibition exerted by GAM336494 RNA, herein designated GAM RNA, on one or more GAM336494 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336494 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336494 RNA, herein designated GAM RNA, of GAM336494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336494 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336494 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336494 RNA correlate with, and may be deduced from, the identity of the GAM336494 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336495 6594 GGACTACAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACATGCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CACGTCTGGC Messenger 336495 (GAM336495) oligonucleotides modulates expression of respective target

TAATTTTCTT genes whose function and utility is known in the art.

GAGTTTTAGT GAM336495 is a novel bioinformatically detectable regulatory, non protein

AGAGACTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336495 was detected

TCTCGTTATG is described with additional reference to Figs. 9-15.

TTGTCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCCCGAG encoded by the human genome.

CTCCTGAGTT GAM336495 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336495 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336495 precursor RNA is designated SEQ ID:6594, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6594 is located from position 21813001 to position 21813101 relative to chromosome 16 on the `-` strand.

GAM336495 precursor RNA folds onto itself, forming GAM336495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336495 precursor RNA, designated SEQ ID NO: 6594, and a schematic representation of a predicted secondary folding of GAM336495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336495 folded precursor RNA yielding a GAM336495 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336495 RNA, hereby incorporated herein.

GAM336495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336495 target RNA, herein designated GAM TARGET RNA.

GAM336495 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336495 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336495 RNA, herein designated GAM RNA, to target binding sites on GAM336495 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336495 target RNA into GAM336495 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336495 target genes. The mRNA of each one of this plurality of GAM336495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336495 RNA, herein designated GAM RNA, and which when bound by GAM336495 RNA causes inhibition of translation of the GAM336495 target mRNA into a corresponding GAM336495 target protein.

The mechanism of the translational inhibition exerted by GAM336495 RNA, herein designated GAM RNA, on one or more GAM336495 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336495 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336495 RNA, herein designated GAM RNA, of GAM336495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336495 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336495 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336495 RNA correlate with, and may be deduced from, the identity of the GAM336495 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336496 5845 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336496 (GAM336496) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336496 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336496 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336496 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336496 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336496 precursor RNA is designated SEQ ID:5845, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5845 is located from position 21821931 to position 21822012 relative to chromosome 18 on the `-` strand.

GAM336496 precursor RNA folds onto itself, forming GAM336496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336496 precursor RNA, designated SEQ ID NO: 5845, and a schematic representation of a predicted secondary folding of GAM336496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336496 folded precursor RNA yielding a GAM336496 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336496 RNA, hereby incorporated herein.

GAM336496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336496 target RNA, herein designated GAM TARGET RNA.

GAM336496 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336496 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336496 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336496 RNA, herein designated GAM RNA, to target binding sites on GAM336496 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336496 target RNA into GAM336496 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336496 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336496 target genes. The mRNA of each one of this plurality of GAM336496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336496 RNA, herein designated GAM RNA, and which when bound by GAM336496 RNA causes inhibition of translation of the GAM336496 target mRNA into a corresponding GAM336496 target protein.

The mechanism of the translational inhibition exerted by GAM336496 RNA, herein designated GAM RNA, on one or more GAM336496 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336496 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336496 RNA, herein designated GAM RNA, of GAM336496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336496 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336496 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336496

RNA correlate with, and may be deduced from, the identity of the GAM336496 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336497 7344 TTTGATAGAT TTTTCCCTCC AGAATGTTTG CATCTATTCA CATGTGCATC AGCAGTGCAT TTGTAGTTAA ATGTGTAGTT AACGTTCTGT TTTTAAAACT ATACAAA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336497 (GAM336497) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336497 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336497 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336497 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336497 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336497 precursor RNA is designated SEQ ID:7344, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7344 is located from position 21935927 to position 21936033 relative to chromosome 8 on the `+` strand.

GAM336497 precursor RNA folds onto itself, forming GAM336497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336497 precursor RNA, designated SEQ ID NO: 7344, and a schematic representation of a predicted secondary folding of GAM336497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336497 folded precursor RNA yielding a GAM336497 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336497 RNA, hereby incorporated herein.

GAM336497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336497 target RNA, herein designated GAM TARGET RNA.

GAM336497 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336497 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336497 RNA, herein designated GAM RNA, to target binding sites on GAM336497 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336497 target RNA into GAM336497 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336497 target genes. The mRNA of each one of this plurality of GAM336497 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336497 RNA, herein designated GAM RNA, and which when bound by GAM336497 RNA causes inhibition of translation of the GAM336497 target mRNA into a corresponding GAM336497 target protein.

The mechanism of the translational inhibition exerted by GAM336497 RNA, herein designated GAM RNA, on one or more GAM336497 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336497 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336497 RNA, herein designated GAM RNA, of GAM336497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336497 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336497 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336497 RNA correlate with, and may be deduced from, the identity of the GAM336497 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336498 6010 CAGAATGTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCATCTATTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ACATGTGCAT Messenger 336498 (GAM336498) oligonucleotides modulates expression of respective target
CAGCAGTGCA genes whose function and utility is known in the art.

TTTGTAGTTA GAM336498 is a novel bioinformatically detectable regulatory, non protein
AATGTGTAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336498 was detected
TAACGTTCTG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336498 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336498 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336498 precursor RNA is designated SEQ ID:6010, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6010 is located from position 21935946 to position 21936015 relative to chromosome 8 on the `+` strand.

GAM336498 precursor RNA folds onto itself, forming GAM336498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336498 precursor RNA, designated SEQ ID NO: 6010, and a schematic representation of a predicted secondary folding of GAM336498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336498 folded precursor RNA yielding a GAM336498 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336498 RNA, hereby incorporated herein.

GAM336498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336498 target RNA, herein designated GAM TARGET RNA.

GAM336498 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336498 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336498 RNA, herein designated GAM RNA, to target binding sites on GAM336498 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336498 target RNA into GAM336498 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336498 target genes. The mRNA of each one of this plurality of GAM336498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336498 RNA, herein designated GAM RNA, and which when bound by GAM336498 RNA causes inhibition of translation of the GAM336498 target mRNA into a corresponding GAM336498 target protein.

The mechanism of the translational inhibition exerted by GAM336498 RNA, herein designated GAM RNA, on one or more GAM336498 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336498 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336498 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336498 RNA, herein designated GAM RNA, of GAM336498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336498 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336498 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336498 RNA correlate with, and may be deduced from, the identity of the GAM336498 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336499 6916 GTGGGTATTC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAGAGAGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GATAATGAAT Messenger 336499 (GAM336499) oligonucleotides modulates expression of respective target

AGGGAGTGTC genes whose function and utility is known in the art.

AGAATGCCAG GAM336499 is a novel bioinformatically detectable regulatory, non protein

CATCATTTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336499 was detected

CTCAAATGCC is described with additional reference to Figs. 9-15.

ACTTGTTACG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCTTCCACT encoded by the human genome.

CTTTTATTCT GAM336499 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTCTGAGGAC GAM336499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AT GAM336499 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336499 precursor RNA is designated SEQ ID:6916, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6916 is located from position 21981294 to position 21981405 relative to chromosome 10 on the `+` strand.

GAM336499 precursor RNA folds onto itself, forming GAM336499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336499 precursor RNA, designated SEQ ID NO: 6916, and a schematic representation of a predicted secondary folding of GAM336499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336499 folded precursor RNA yielding a GAM336499 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336499 RNA, hereby incorporated herein.

GAM336499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336499 target RNA, herein designated GAM TARGET RNA.

GAM336499 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336499 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336499 RNA, herein designated GAM RNA, to target binding sites on GAM336499 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336499 target RNA into GAM336499 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336499 target genes. The mRNA of each one of this plurality of GAM336499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336499 RNA, herein designated GAM RNA, and which when bound by GAM336499 RNA causes inhibition of translation of the GAM336499 target mRNA into a corresponding GAM336499 target protein.

The mechanism of the translational inhibition exerted by GAM336499 RNA, herein designated GAM RNA, on one or more GAM336499 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336499 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336499 RNA, herein designated GAM RNA, of GAM336499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336499 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336499 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336499 RNA correlate with, and may be deduced from, the identity of the GAM336499 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336502 6050 CCAGAGAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTCCAGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

CGCCACACAG Messenger 336502 (GAM336502) oligonucleotides modulates expression of respective target

TCTTTGAGCT genes whose function and utility is known in the art.

GTGTCAGAGC GAM336502 is a novel bioinformatically detectable regulatory, non protein

TGGATTGTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336502 was detected

ACCTGGGGCT is described with additional reference to Figs. 9-15.

GGCTGTTTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336502 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336502 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336502 precursor RNA is designated SEQ ID:6050, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6050 is located from position 22350120 to position 22350199 relative to chromosome 22 on the `-` strand.

GAM336502 precursor RNA folds onto itself, forming GAM336502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336502 precursor RNA, designated SEQ ID NO: 6050, and a schematic representation of a predicted secondary folding of GAM336502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336502 folded precursor RNA yielding a GAM336502 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336502 RNA, hereby incorporated herein.

GAM336502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336502 target RNA, herein designated GAM TARGET RNA.

GAM336502 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336502 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336502 RNA, herein designated GAM RNA, to target binding sites on GAM336502 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336502 target RNA into GAM336502 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336502 target genes. The mRNA of each one of this plurality of GAM336502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336502 RNA, herein designated GAM RNA, and which when bound by GAM336502 RNA causes inhibition of translation of the GAM336502 target mRNA into a corresponding GAM336502 target protein.

The mechanism of the translational inhibition exerted by GAM336502 RNA, herein designated GAM RNA, on one or more GAM336502 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336502 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336502 RNA, herein designated GAM RNA, of GAM336502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336502 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336502 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336502 RNA correlate with, and may be deduced from, the identity of the GAM336502 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336503 6049 CCACGTGGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TACTGGGCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTCAGTGT Messenger 336503 (GAM336503) oligonucleotides modulates expression of respective target

GGAAGCTGAT genes whose function and utility is known in the art.

TTCCAACAAG GAM336503 is a novel bioinformatically detectable regulatory, non protein

GAGCATTCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336503 was detected

AGATTAGGAG is described with additional reference to Figs. 9-15.

TTCCCAGTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCATAAGTGG encoded by the human genome.

GAM336503 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336503 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336503 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336503 precursor RNA is designated SEQ ID:6049, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6049 is located from position 22360083 to position 22360172 relative to chromosome 13 on the `-` strand.

GAM336503 precursor RNA folds onto itself, forming GAM336503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336503 precursor RNA, designated SEQ ID NO: 6049, and a schematic representation of a predicted secondary folding of GAM336503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336503 folded precursor RNA yielding a GAM336503 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336503 RNA, hereby incorporated herein.

GAM336503 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336503 target RNA, herein designated GAM TARGET RNA.

GAM336503 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336503 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336503 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336503 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336503 RNA, herein designated GAM RNA, to target binding sites on GAM336503 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336503 target RNA into GAM336503 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336503 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336503 target genes. The mRNA of each one of this plurality of GAM336503 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336503 RNA, herein designated GAM RNA, and which when bound by GAM336503 RNA causes inhibition of translation of the GAM336503 target mRNA into a corresponding GAM336503 target protein.

The mechanism of the translational inhibition exerted by GAM336503 RNA, herein designated GAM RNA, on one or more GAM336503 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336503 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336503 RNA, herein designated GAM RNA, of GAM336503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336503 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336503 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336503 RNA correlate with, and may be deduced from, the identity of the GAM336503 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336504 6500 GCATCTTGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACATGTTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTCCAGGT Messenger 336504 (GAM336504) oligonucleotides modulates expression of respective target

CCCAGTAACT genes whose function and utility is known in the art.

GTGCCCATCC GAM336504 is a novel bioinformatically detectable regulatory, non protein

ATTGTTACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336504 was detected

CAGGTCACAG is described with additional reference to Figs. 9-15.

TGGCCCTGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGGGGCAT encoded by the human genome.

TATACTCTCT GAM336504 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTTGGTGT GAM336504 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336504 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336504 precursor RNA is designated SEQ ID:6500, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6500 is located from position 22376839 to position 22376946 relative to chromosome 13 on the `-` strand.

GAM336504 precursor RNA folds onto itself, forming GAM336504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336504 precursor RNA, designated SEQ ID NO: 6500, and a schematic representation of a predicted secondary folding of GAM336504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336504 folded precursor RNA yielding a GAM336504 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336504 RNA, hereby incorporated herein.

GAM336504 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336504 target RNA, herein designated GAM TARGET RNA.

GAM336504 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336504 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336504 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336504 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336504 RNA, herein designated GAM RNA, to target binding sites on GAM336504 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336504 target RNA into GAM336504 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336504 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336504 target genes. The mRNA of each one of this plurality of GAM336504 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336504 RNA, herein designated GAM RNA, and which when bound by GAM336504 RNA causes inhibition of translation of the GAM336504 target mRNA into a corresponding GAM336504 target protein.

The mechanism of the translational inhibition exerted by GAM336504 RNA, herein designated GAM RNA, on one or more GAM336504 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336504 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336504 RNA, herein designated GAM RNA, of GAM336504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336504 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336504 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336504 RNA correlate with, and may be deduced from, the identity of the GAM336504 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336505 6581 GGAAGTGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGGAAGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTCTCCCCA Messenger 336505 (GAM336505) oligonucleotides modulates expression of respective target
TCCCTCCTCT genes whose function and utility is known in the art.

CAGTTACCAT GAM336505 is a novel bioinformatically detectable regulatory, non protein
GAGGATGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336505 was detected
AGTTTCTTCC is described with additional reference to Figs. 9-15.

CTTTCCGTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCACTTTC encoded by the human genome.

GAM336505 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336505 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336505 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336505 precursor RNA is designated SEQ ID:6581, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6581 is located from position 22426100 to position 22426188 relative to chromosome 14 on the `+` strand.

GAM336505 precursor RNA folds onto itself, forming GAM336505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336505 precursor RNA, designated SEQ ID NO: 6581, and a schematic representation of a predicted secondary folding of GAM336505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336505 folded precursor RNA yielding a GAM336505 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336505 RNA, hereby incorporated herein.

GAM336505 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336505 target RNA, herein designated GAM TARGET RNA.

GAM336505 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336505 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336505 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336505 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336505 RNA, herein designated GAM RNA, to target binding sites on GAM336505 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336505 target RNA into GAM336505 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336505 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336505 target genes. The mRNA of each one of this plurality of GAM336505 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336505 RNA, herein designated GAM RNA, and which when bound by GAM336505 RNA causes inhibition of translation of the GAM336505 target mRNA into a corresponding GAM336505 target protein.

The mechanism of the translational inhibition exerted by GAM336505 RNA, herein designated GAM RNA, on one or more GAM336505 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336505 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336505 RNA, herein designated GAM RNA, of GAM336505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336505 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336505 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336505 RNA correlate with, and may be deduced from, the identity of the GAM336505 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336506 6595 GGACTACAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACATGCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CACGTCTGGC Messenger 336506 (GAM336506) oligonucleotides modulates expression of respective target
TAATTTTCTT genes whose function and utility is known in the art.

GAGTTTTAGT GAM336506 is a novel bioinformatically detectable regulatory, non protein
AGAGACTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336506 was detected
TCTCGTTATG is described with additional reference to Figs. 9-15.

TTGTCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGTCCCGAG encoded by the human genome.

CTCCTGAGTT GAM336506 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM336506 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336506 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336506 precursor RNA is designated SEQ ID:6595, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6595 is located from position 22435583 to position 22435683 relative to chromosome 16 on the `+` strand.

GAM336506 precursor RNA folds onto itself, forming GAM336506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336506 precursor RNA, designated SEQ ID NO: 6595, and a schematic representation of a predicted secondary folding of GAM336506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336506 folded precursor RNA yielding a GAM336506 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336506 RNA, hereby incorporated herein.

GAM336506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336506 target RNA, herein designated GAM TARGET RNA.

GAM336506 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336506 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336506 RNA, herein designated GAM RNA, to target binding sites on GAM336506 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336506 target RNA into GAM336506 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336506 target genes. The mRNA of each one of this plurality of GAM336506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336506 RNA, herein designated GAM RNA, and which when bound by GAM336506 RNA causes inhibition of translation of the GAM336506 target mRNA into a corresponding GAM336506 target protein.

The mechanism of the translational inhibition exerted by GAM336506 RNA, herein designated GAM RNA, on one or more GAM336506 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336506 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336506 RNA, herein designated GAM RNA, of GAM336506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336506 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336506 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336506 RNA correlate with, and may be deduced from, the identity of the GAM336506 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336507 6946 GTTTGGTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TATTGGATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAAGCATTGG Messenger 336507 (GAM336507) oligonucleotides modulates expression of respective target
GAGTTGACCT genes whose function and utility is known in the art.

TTATATAAAA GAM336507 is a novel bioinformatically detectable regulatory, non protein
CAAAACCCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336507 was detected
AAGCTTATAA is described with additional reference to Figs. 9-15.

TTCAGTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAAACAGAC encoded by the human genome.

AGTAAAC GAM336507 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336507 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336507 precursor RNA is designated SEQ ID:6946, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6946 is located from position 22440215 to position 22440311 relative to chromosome 10 on the `-` strand.

GAM336507 precursor RNA folds onto itself, forming GAM336507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336507 precursor RNA, designated SEQ ID NO: 6946, and a schematic representation of a predicted secondary folding of GAM336507 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336507 folded precursor RNA yielding a GAM336507 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336507 RNA, hereby incorporated herein.

GAM336507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336507 target RNA, herein designated GAM TARGET RNA.

GAM336507 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336507 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336507 RNA, herein designated GAM RNA, to target binding sites on GAM336507 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336507 target RNA into GAM336507 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336507 target genes. The mRNA of each one of this plurality of GAM336507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336507 RNA, herein designated GAM RNA, and which when bound by GAM336507 RNA causes inhibition of translation of the GAM336507 target mRNA into a corresponding GAM336507 target protein.

The mechanism of the translational inhibition exerted by GAM336507 RNA, herein designated GAM RNA, on one or more GAM336507 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336507 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336507 RNA, herein designated GAM RNA, of GAM336507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336507 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336507 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336507 RNA correlate with, and may be deduced from, the identity of the GAM336507 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336508 6945 GTTTGGTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TATTGGATTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TAAGCATTGG Messenger 336508 (GAM336508) oligonucleotides modulates expression of respective target

GAGTTGACCT genes whose function and utility is known in the art.

TTATATAAAA GAM336508 is a novel bioinformatically detectable regulatory, non protein

CAAAACCCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336508 was detected

AAGCTTATAA is described with additional reference to Figs. 9-15.

TTCAGTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAAACAGAC encoded by the human genome.

GAM336508 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336508 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336508 precursor RNA is designated SEQ ID:6945, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6945 is located from position 22440222 to position 22440311 relative to chromosome 10 on the `-` strand.

GAM336508 precursor RNA folds onto itself, forming GAM336508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336508 precursor RNA, designated SEQ ID NO: 6945, and a schematic representation of a predicted secondary folding of GAM336508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336508 folded precursor RNA yielding a GAM336508 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336508 RNA, hereby incorporated herein.

GAM336508 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336508 target RNA, herein designated GAM TARGET RNA.

GAM336508 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336508 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336508 RNA, herein designated GAM RNA, to target binding sites on GAM336508 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336508 target RNA into GAM336508 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336508 target genes. The mRNA of each one of this plurality of GAM336508 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336508 RNA, herein designated GAM RNA, and which when bound by GAM336508 RNA causes inhibition of translation of the GAM336508 target mRNA into a corresponding GAM336508 target protein.

The mechanism of the translational inhibition exerted by GAM336508 RNA, herein designated GAM RNA, on one or more GAM336508 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336508 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336508 RNA, herein designated GAM RNA, of GAM336508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336508 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336508 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336508 RNA correlate with, and may be deduced from, the identity of the GAM336508 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336509 7321 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGTAG Messenger 336509 (GAM336509) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TCGCGCCACT GAM336509 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336509 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

G GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336509 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336509 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336509 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336509 precursor RNA is designated SEQ

ID:7321, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7321 is located from position 22444388 to position 22444458 relative to chromosome 22 on the `+` strand.

GAM336509 precursor RNA folds onto itself, forming GAM336509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336509 precursor RNA, designated SEQ ID NO: 7321, and a schematic representation of a predicted secondary folding of GAM336509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336509 folded precursor RNA yielding a GAM336509 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336509 RNA, hereby incorporated herein. Expression of GAM336509 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336509 target RNA, herein designated GAM TARGET RNA.

GAM336509 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336509 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336509 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336509 RNA, herein designated GAM RNA, to target binding sites on GAM336509 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336509 target RNA

into GAM336509 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336509 target genes. The mRNA of each one of this plurality of GAM336509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336509 RNA, herein designated GAM RNA, and which when bound by GAM336509 RNA causes inhibition of translation of the GAM336509 target mRNA into a corresponding GAM336509 target protein.

The mechanism of the translational inhibition exerted by GAM336509 RNA, herein designated GAM RNA, on one or more GAM336509 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336509 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336509 RNA, herein designated GAM RNA, of GAM336509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336509 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336509 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336509 RNA correlate with, and may be deduced from, the identity of the GAM336509 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336510 6596 GGACTACAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACATGCAAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CACGTCTGGC Messenger 336510 (GAM336510) oligonucleotides modulates expression of respective target
TAATTTTCTT genes whose function and utility is known in the art.

GAGTTTTAGT GAM336510 is a novel bioinformatically detectable regulatory, non protein
AGAGACTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336510 was detected
TCTCGTTATG is described with additional reference to Figs. 9-15.

TTGTCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCCCGAG encoded by the human genome.

CTCCTGAGTT GAM336510 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336510 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336510 precursor RNA is designated SEQ ID:6596, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6596 is located from position 22480967 to position 22481067 relative to chromosome 16 on the `+` strand.

GAM336510 precursor RNA folds onto itself, forming GAM336510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336510 precursor RNA, designated SEQ ID NO: 6596, and a schematic representation of a predicted secondary folding of GAM336510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336510 folded precursor RNA yielding a GAM336510 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336510 RNA, hereby incorporated herein.

GAM336510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336510 target RNA, herein designated GAM TARGET RNA.

GAM336510 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336510 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336510 RNA, herein designated GAM RNA, to target binding sites on GAM336510 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336510 target RNA into GAM336510 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336510 target genes. The mRNA of each one of this plurality of GAM336510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336510 RNA, herein designated GAM RNA, and which when bound by GAM336510 RNA causes inhibition of translation of the GAM336510 target mRNA into a corresponding GAM336510 target protein.

The mechanism of the translational inhibition exerted by GAM336510 RNA, herein designated GAM RNA, on one or more GAM336510 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336510 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336510 RNA, herein designated GAM RNA, of GAM336510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336510 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336510 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336510 RNA correlate with, and may be deduced from, the identity of the GAM336510 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336511 5846 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336511 (GAM336511) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336511 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336511 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336511 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336511 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336511 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336511 precursor RNA is designated SEQ ID:5846, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5846 is located from position 22524532 to position 22524613 relative to chromosome 5 on the `+` strand.

GAM336511 precursor RNA folds onto itself, forming GAM336511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336511 precursor RNA, designated SEQ ID NO: 5846, and a schematic representation of a predicted secondary folding of GAM336511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336511 folded precursor RNA yielding a GAM336511 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336511 RNA, hereby incorporated herein.

GAM336511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336511 target RNA, herein designated GAM TARGET RNA.

GAM336511 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336511 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336511 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336511 RNA, herein designated GAM RNA, to target binding sites on GAM336511 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336511 target RNA into GAM336511 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336511 target genes. The mRNA of each one of this plurality of GAM336511 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336511 RNA, herein designated GAM RNA, and which when bound by GAM336511 RNA causes inhibition of translation of the GAM336511 target mRNA into a corresponding GAM336511 target protein.

The mechanism of the translational inhibition exerted by GAM336511 RNA, herein designated GAM RNA, on one or more GAM336511 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336511 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336511 RNA, herein designated GAM RNA, of GAM336511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336511 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336511 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336511 RNA correlate with, and may be deduced from, the identity of the GAM336511 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336512 6987 TATTGGTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTCTTGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGAAATCAT Messenger 336512 (GAM336512) oligonucleotides modulates expression of respective target

AAAAGTCCAG genes whose function and utility is known in the art.

GACAGAAAGT GAM336512 is a novel bioinformatically detectable regulatory, non protein

GACCTATAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336512 was detected

GATGACCTGG is described with additional reference to Figs. 9-15.

CCTCTTGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTCTTTGC encoded by the human genome.

TTCTGGAAAG GAM336512 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAGTA GAM336512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336512 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336512 precursor RNA is designated SEQ ID:6987, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6987 is located from position 22572448 to position 22572552 relative to chromosome 18 on the `+` strand.

GAM336512 precursor RNA folds onto itself, forming GAM336512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336512 precursor RNA, designated SEQ ID NO: 6987, and a schematic representation of a predicted secondary folding of GAM336512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336512 folded precursor RNA yielding a GAM336512 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336512 RNA, hereby incorporated herein.

GAM336512 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336512 target RNA, herein designated GAM TARGET RNA.

GAM336512 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336512 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336512 RNA, herein designated GAM RNA, to target binding sites on GAM336512 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336512 target RNA into GAM336512 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336512 target genes. The mRNA of each one of this plurality of GAM336512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336512 RNA, herein designated GAM RNA, and which when bound by GAM336512 RNA causes inhibition of translation of the GAM336512 target mRNA into a corresponding GAM336512 target protein.

The mechanism of the translational inhibition exerted by GAM336512 RNA, herein designated GAM RNA, on one or more GAM336512 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336512 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336512 RNA, herein designated GAM RNA, of GAM336512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336512 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336512 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336512 RNA correlate with, and may be deduced from, the identity of the GAM336512 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336513 5976 ATGTTATGAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTTTCATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTGGAAATA Messenger 336513 (GAM336513) oligonucleotides modulates expression of respective target
AGGAAAACTT genes whose function and utility is known in the art.

GCATGGTTTG GAM336513 is a novel bioinformatically detectable regulatory, non protein
AATTGTGGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336513 was detected
CAATAGGTGG is described with additional reference to Figs. 9-15.

TGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336513 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336513 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336513 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336513 precursor RNA is designated SEQ ID:5976, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5976 is located from position 22650373 to position 22650445 relative to chromosome 15 on the `+` strand.

GAM336513 precursor RNA folds onto itself, forming GAM336513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336513 precursor RNA, designated SEQ ID NO: 5976, and a schematic representation of a predicted secondary folding of GAM336513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336513 folded precursor RNA yielding a GAM336513 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336513 RNA, hereby incorporated herein.

GAM336513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336513 target RNA, herein designated GAM TARGET RNA.

GAM336513 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336513 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336513 RNA, herein designated GAM RNA, to target binding sites on GAM336513 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336513 target RNA into GAM336513 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336513 target genes. The mRNA of each one of this plurality of GAM336513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336513 RNA, herein designated GAM RNA, and which when bound by GAM336513 RNA causes inhibition of translation of the GAM336513 target mRNA into a corresponding GAM336513 target protein.

The mechanism of the translational inhibition exerted by GAM336513 RNA, herein designated GAM RNA, on one or more GAM336513 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336513 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336513 RNA, herein designated GAM RNA, of GAM336513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336513 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336513 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336513 RNA correlate with, and may be deduced from, the identity of the GAM336513 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336514 6332 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGGAGGT Messenger 336514 (GAM336514) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CGAGATTGCA GAM336514 is a novel bioinformatically detectable regulatory, non protein

CCATTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336514 was detected

CCACCCTAGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAACTC encoded by the human genome.

GAM336514 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336514 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336514 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336514 precursor RNA is designated SEQ ID:6332, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6332 is located from position 22660392 to position 22660478 relative to chromosome 15 on the `+` strand.

GAM336514 precursor RNA folds onto itself, forming GAM336514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336514 precursor RNA, designated SEQ ID NO: 6332, and a schematic representation of a predicted secondary folding of GAM336514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336514 folded precursor RNA yielding a GAM336514 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336514 RNA, hereby incorporated herein.

GAM336514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336514 target RNA, herein designated GAM TARGET RNA.

GAM336514 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336514 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336514 RNA, herein designated GAM RNA, to target binding sites on GAM336514 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336514 target RNA into GAM336514 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336514 target genes. The mRNA of each one of this plurality of GAM336514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336514 RNA, herein designated GAM RNA, and which when bound by GAM336514 RNA causes inhibition of translation of the GAM336514 target mRNA into a corresponding GAM336514 target protein.

The mechanism of the translational inhibition exerted by GAM336514 RNA, herein designated GAM RNA, on one or more GAM336514 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336514 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336514 RNA, herein designated GAM RNA, of GAM336514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336514 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336514 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336514 RNA correlate with, and may be deduced from, the identity of the GAM336514 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336516 5755 AGGAAGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGAGTCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAATTGGAG Messenger 336516 (GAM336516) oligonucleotides modulates expression of respective target
GCTGCAGTGA genes whose function and utility is known in the art.

GCTATAATTG GAM336516 is a novel bioinformatically detectable regulatory, non protein
TGCCAACTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336516 was detected
ACTCCAGCCT is described with additional reference to Figs. 9-15.

GGGCAACAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGACCCT encoded by the human genome.

GAM336516 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336516 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336516 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336516 precursor RNA is designated SEQ ID:5755, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5755 is located from position 22796154 to position 22796241 relative to chromosome 22 on the `+` strand.

GAM336516 precursor RNA folds onto itself, forming GAM336516 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336516 precursor RNA, designated SEQ ID NO: 5755, and a schematic representation of a predicted secondary folding of GAM336516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336516 folded precursor RNA yielding a GAM336516 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336516 RNA, hereby incorporated herein.

GAM336516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336516 target RNA, herein designated GAM TARGET RNA.

GAM336516 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336516 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336516 RNA, herein designated GAM RNA, to target binding sites on GAM336516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336516 target RNA into GAM336516 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336516 target genes. The mRNA of each one of this plurality of GAM336516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336516 RNA,

herein designated GAM RNA, and which when bound by GAM336516 RNA causes inhibition of translation of the GAM336516 target mRNA into a corresponding GAM336516 target protein.

The mechanism of the translational inhibition exerted by GAM336516 RNA, herein designated GAM RNA, on one or more GAM336516 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336516 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336516 RNA, herein designated GAM RNA, of GAM336516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336516 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336516 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336516 RNA correlate with, and may be deduced from, the identity of the GAM336516 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336518 6504 GCCCCTGCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGAGATCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTTATTTTC Messenger 336518 (GAM336518) oligonucleotides modulates expression of respective target

ATCTCACCCA genes whose function and utility is known in the art.

GAATATTGAG GAM336518 is a novel bioinformatically detectable regulatory, non protein

GTGATCAGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336518 was detected

AGGTGGAGTG is described with additional reference to Figs. 9-15.

GTTGGGAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGT encoded by the human genome.

GAM336518 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336518 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336518 precursor RNA is designated SEQ ID:6504, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6504 is located from position 22950966 to position 22951048 relative to chromosome 15 on the `+` strand.

GAM336518 precursor RNA folds onto itself, forming GAM336518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336518 precursor RNA, designated SEQ ID NO: 6504, and a schematic representation of a predicted secondary folding of GAM336518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336518 folded precursor RNA yielding a GAM336518 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336518 RNA, hereby incorporated herein.

GAM336518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336518 target RNA, herein designated GAM TARGET RNA.

GAM336518 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336518 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336518 RNA, herein designated GAM RNA, to target binding sites on GAM336518 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336518 target RNA

into GAM336518 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336518 target genes. The mRNA of each one of this plurality of GAM336518 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336518 RNA, herein designated GAM RNA, and which when bound by GAM336518 RNA causes inhibition of translation of the GAM336518 target mRNA into a corresponding GAM336518 target protein.

The mechanism of the translational inhibition exerted by GAM336518 RNA, herein designated GAM RNA, on one or more GAM336518 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336518 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336518 RNA, herein designated GAM RNA, of GAM336518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336518 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336518 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336518 RNA correlate with, and may be deduced from, the identity of the GAM336518 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336519 5847 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336519 (GAM336519) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336519 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336519 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336519 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336519 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336519 precursor RNA is designated SEQ ID:5847, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5847 is located from position 23259601 to position 23259682 relative to chromosome 18 on the `-` strand.

GAM336519 precursor RNA folds onto itself, forming GAM336519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336519 precursor RNA, designated SEQ ID NO: 5847, and a schematic representation of a predicted secondary folding of GAM336519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336519 folded precursor RNA yielding a GAM336519 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336519 RNA, hereby incorporated herein.

GAM336519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336519 target RNA, herein designated GAM TARGET RNA.

GAM336519 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336519 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336519 RNA, herein designated GAM RNA, to target binding sites on GAM336519 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336519 target RNA into GAM336519 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336519 target genes. The mRNA of each one of this plurality of GAM336519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336519 RNA, herein designated GAM RNA, and which when bound by GAM336519 RNA causes inhibition of translation of the GAM336519 target mRNA into a corresponding GAM336519 target protein.

The mechanism of the translational inhibition exerted by GAM336519 RNA, herein designated GAM RNA, on one or more GAM336519 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336519 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336519 RNA, herein designated GAM RNA, of GAM336519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336519 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336519 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336519 RNA correlate with, and may be deduced from, the identity of the GAM336519 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336520 6555 GCTTCACTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGGGCAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTTGGGAAA Messenger 336520 (GAM336520) oligonucleotides modulates expression of respective target

TAAGCTGATA genes whose function and utility is known in the art.

GTAAAGTCAT GAM336520 is a novel bioinformatically detectable regulatory, non protein
GTAACACTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336520 was detected
CTGTGCAGGT is described with additional reference to Figs. 9-15.

TAACATTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGACCTTGCT encoded by the human genome.

TTCCTTCTCA GAM336520 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTGTATGC GAM336520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336520 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336520 precursor RNA is designated SEQ ID:6555, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6555 is located from position 23264637 to position 23264744 relative to chromosome 19 on the `-` strand.

GAM336520 precursor RNA folds onto itself, forming GAM336520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336520 precursor RNA, designated SEQ ID NO: 6555, and a schematic representation of a predicted secondary folding of GAM336520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336520 folded precursor RNA yielding a GAM336520 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336520 RNA, hereby incorporated herein.

GAM336520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336520 target RNA, herein designated GAM TARGET RNA.

GAM336520 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336520 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336520 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336520 RNA, herein designated GAM RNA, to target binding sites on GAM336520 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336520 target RNA into GAM336520 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336520 target genes. The mRNA of each one of this plurality of GAM336520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336520 RNA, herein designated GAM RNA, and which when bound by GAM336520 RNA causes inhibition of translation of the GAM336520 target mRNA into a corresponding GAM336520 target protein.

The mechanism of the translational inhibition exerted by GAM336520 RNA, herein designated GAM RNA, on one or more GAM336520 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336520 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336520 RNA, herein designated GAM RNA, of GAM336520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336520 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336520 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336520 RNA correlate with, and may be deduced from, the identity of the GAM336520 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336522 5790 AGGGTGCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCTTCTAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTTTGAGA Messenger 336522 (GAM336522) oligonucleotides modulates expression of respective target

GCATAGAGCC genes whose function and utility is known in the art.

AGGAAGCATA GAM336522 is a novel bioinformatically detectable regulatory, non protein

CACACATTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336522 was detected

TGGCTCCTGA is described with additional reference to Figs. 9-15.

CTTTTTGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTCCCAGGT encoded by the human genome.

TATTGAGTTT GAM336522 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GCCCCT GAM336522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336522 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336522 precursor RNA is designated SEQ ID:5790, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5790 is located from position 23295481 to position 23295586 relative to chromosome X on the `+` strand.

GAM336522 precursor RNA folds onto itself, forming GAM336522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336522 precursor RNA, designated SEQ ID NO: 5790, and a schematic representation of a predicted secondary folding of GAM336522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336522 folded precursor RNA yielding a GAM336522 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336522 RNA, hereby incorporated herein.

GAM336522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336522 target RNA, herein designated GAM TARGET RNA.

GAM336522 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336522 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336522 RNA, herein designated GAM RNA, to target binding sites on GAM336522 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336522 target RNA into GAM336522 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336522 target genes. The mRNA of each one of this plurality of GAM336522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336522 RNA, herein designated GAM RNA, and which when bound by GAM336522 RNA causes inhibition of translation of the GAM336522 target mRNA into a corresponding GAM336522 target protein.

The mechanism of the translational inhibition exerted by GAM336522 RNA, herein designated GAM RNA, on one or more GAM336522 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336522 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336522 RNA, herein designated GAM RNA, of GAM336522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336522 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336522 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336522 RNA correlate with, and may be deduced from, the identity of the GAM336522 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336523 5848 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336523 (GAM336523) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336523 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336523 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336523 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336523 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336523 precursor RNA is designated SEQ ID:5848, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5848 is located from position 23320241 to position 23320322 relative to chromosome 12 on the `-` strand.

GAM336523 precursor RNA folds onto itself, forming GAM336523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336523 precursor RNA, designated SEQ ID NO: 5848, and a schematic representation of a predicted secondary folding of GAM336523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336523 folded precursor

RNA yielding a GAM336523 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336523 RNA, hereby incorporated herein.

GAM336523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336523 target RNA, herein designated GAM TARGET RNA.

GAM336523 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336523 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336523 RNA, herein designated GAM RNA, to target binding sites on GAM336523 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336523 target RNA into GAM336523 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336523 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336523 target genes. The mRNA of each one of this plurality of GAM336523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336523 RNA, herein designated GAM RNA, and which when bound by GAM336523 RNA causes inhibition of translation of the GAM336523 target mRNA into a corresponding GAM336523 target protein.

The mechanism of the translational inhibition exerted by GAM336523 RNA, herein designated GAM RNA, on one or more GAM336523 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336523 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336523 RNA, herein designated GAM RNA, of GAM336523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336523 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336523 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336523 RNA correlate with, and may be deduced from, the identity of the GAM336523 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336524 6134 CGAACCAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAAGTAATG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTGCCAGGA Messenger 336524 (GAM336524) oligonucleotides modulates expression of respective target

CAAGAGACGC genes whose function and utility is known in the art.

ACCCAGAGCC GAM336524 is a novel bioinformatically detectable regulatory, non protein

TCTGGCCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336524 was detected

GTCTCCTATC is described with additional reference to Figs. 9-15.

CTGGCTCACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCACACTCC encoded by the human genome.

AAGTTTG GAM336524 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336524 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336524 precursor RNA is designated SEQ ID:6134, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6134 is located from position 23523635 to position 23523731 relative to chromosome 16 on the `-` strand.

GAM336524 precursor RNA folds onto itself, forming GAM336524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336524 precursor RNA, designated SEQ ID NO: 6134, and a schematic representation of a predicted secondary folding of GAM336524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336524 folded precursor RNA yielding a GAM336524 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336524 RNA, hereby incorporated herein.

GAM336524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336524 target RNA, herein designated GAM TARGET RNA.

GAM336524 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336524 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336524 RNA, herein designated GAM RNA, to target binding sites on GAM336524 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336524 target RNA into GAM336524 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336524 target genes. The mRNA of each one of this plurality of GAM336524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336524 RNA, herein designated GAM RNA, and which when bound by GAM336524 RNA causes inhibition of translation of the GAM336524 target mRNA into a corresponding GAM336524 target protein.

The mechanism of the translational inhibition exerted by GAM336524 RNA, herein designated GAM RNA, on one or more GAM336524 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336524 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336524 RNA, herein designated GAM RNA, of GAM336524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336524 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336524 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336524 RNA correlate with, and may be deduced from, the identity of the GAM336524 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336526 6984 TATGTCACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTTGGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTTTCTCCT Messenger 336526 (GAM336526) oligonucleotides modulates expression of respective target

TTGCCTGCTG genes whose function and utility is known in the art.

CTTCTTTCAA GAM336526 is a novel bioinformatically detectable regulatory, non protein

GTAGGACATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336526 was detected

GAGACAACAG is described with additional reference to Figs. 9-15.

CCAAATTTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTTCAGTGA encoded by the human genome.

TGTG GAM336526 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336526 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336526 precursor RNA is designated SEQ ID:6984, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6984 is located from position 23528432 to position 23528525

relative to chromosome X on the `-` strand.

GAM336526 precursor RNA folds onto itself, forming GAM336526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336526 precursor RNA, designated SEQ ID NO: 6984, and a schematic representation of a predicted secondary folding of GAM336526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336526 folded precursor RNA yielding a GAM336526 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336526 RNA, hereby incorporated herein.

GAM336526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336526 target RNA, herein designated GAM TARGET RNA.

GAM336526 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336526 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336526 RNA, herein designated GAM RNA, to target binding sites on GAM336526 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336526 target RNA into GAM336526 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336526 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336526 target genes. The mRNA of each one of this plurality of GAM336526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336526 RNA, herein designated GAM RNA, and which when bound by GAM336526 RNA causes inhibition of translation of the GAM336526 target mRNA into a corresponding GAM336526 target protein.

The mechanism of the translational inhibition exerted by GAM336526 RNA, herein designated GAM RNA, on one or more GAM336526 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336526 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336526 RNA, herein designated GAM RNA, of GAM336526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336526 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336526 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336526 RNA correlate with, and may be deduced from, the identity of the GAM336526 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336527 5985 CAAATTTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGCTTTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTTGCCTGC Messenger 336527 (GAM336527) oligonucleotides modulates expression of respective target

TGCTTCTTTC genes whose function and utility is known in the art.

AAGTAGGACA GAM336527 is a novel bioinformatically detectable regulatory, non protein

TGGAGACAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336527 was detected

AGCCAAATTT is described with additional reference to Figs. 9-15.

G GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336527 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336527 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336527 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336527 precursor RNA is designated SEQ ID:5985, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5985 is located from position 23528447 to position 23528517 relative to chromosome X on the `-` strand.

GAM336527 precursor RNA folds onto itself, forming GAM336527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336527 precursor RNA, designated SEQ ID NO: 5985, and a schematic representation of a predicted secondary folding of GAM336527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336527 folded precursor RNA yielding a GAM336527 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336527 RNA, hereby incorporated herein.

GAM336527 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336527 target RNA, herein designated GAM TARGET RNA.

GAM336527 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336527 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336527 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336527 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336527 RNA, herein designated GAM RNA, to target

binding sites on GAM336527 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336527 target RNA into GAM336527 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336527 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336527 target genes. The mRNA of each one of this plurality of GAM336527 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336527 RNA, herein designated GAM RNA, and which when bound by GAM336527 RNA causes inhibition of translation of the GAM336527 target mRNA into a corresponding GAM336527 target protein.

The mechanism of the translational inhibition exerted by GAM336527 RNA, herein designated GAM RNA, on one or more GAM336527 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336527 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336527 RNA, herein designated GAM RNA, of GAM336527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336527 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336527 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336527 RNA correlate with, and may be deduced from, the identity of the GAM336527 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336528 6169 CTCCTTAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTATCAATC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGTGCCCT Messenger 336528 (GAM336528) oligonucleotides modulates expression of respective target

TCCATTGTAT genes whose function and utility is known in the art.

CACATCCTTG GAM336528 is a novel bioinformatically detectable regulatory, non protein

GATCACAGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336528 was detected

ATGGGTTCAG is described with additional reference to Figs. 9-15.

GAATAGACAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGACCCAAG encoded by the human genome.

GGAG GAM336528 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336528 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336528 precursor RNA is designated SEQ ID:6169, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6169 is located from position 24199772 to position 24199865 relative to chromosome 22 on the `+` strand.

GAM336528 precursor RNA folds onto itself, forming GAM336528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336528 precursor RNA, designated SEQ ID NO: 6169, and a schematic representation of a predicted secondary folding of GAM336528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336528 folded precursor RNA yielding a GAM336528 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336528 RNA, hereby incorporated herein.

GAM336528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336528 target RNA, herein designated GAM TARGET RNA.

GAM336528 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336528 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336528 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336528 RNA, herein designated GAM RNA, to target binding sites on GAM336528 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336528 target RNA into GAM336528 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336528 target genes. The mRNA of each one of this plurality of GAM336528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336528 RNA, herein designated GAM RNA, and which when bound by GAM336528 RNA causes inhibition of translation of the GAM336528 target mRNA into a corresponding GAM336528 target protein.

The mechanism of the translational inhibition exerted by GAM336528 RNA, herein designated GAM RNA, on one or more GAM336528 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336528 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336528 RNA, herein designated GAM RNA, of GAM336528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336528 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336528 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336528 RNA correlate with, and may be deduced from, the identity of the GAM336528 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336529 6125 CCTTAGGTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TATCAATCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTGCCCTTC Messenger 336529 (GAM336529) oligonucleotides modulates expression of respective target
CATTGTATCA genes whose function and utility is known in the art.

CATCCTTGGA GAM336529 is a novel bioinformatically detectable regulatory, non protein
TCACAGTGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336529 was detected
GGGTTCAGGA is described with additional reference to Figs. 9-15.

ATAGACACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GACCCAAGG encoded by the human genome.

GAM336529 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336529 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336529 precursor RNA is designated SEQ ID:6125, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6125 is located from position 24199774 to position 24199862 relative to chromosome 22 on the `+` strand.

GAM336529 precursor RNA folds onto itself, forming GAM336529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336529 precursor RNA, designated SEQ ID NO: 6125, and a schematic representation of a predicted secondary folding of GAM336529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336529 folded precursor RNA yielding a GAM336529 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336529 RNA, hereby incorporated herein.

GAM336529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336529 target RNA, herein designated GAM TARGET RNA.

GAM336529 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336529 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336529 RNA, herein designated GAM RNA, to target binding sites on GAM336529 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336529 target RNA into GAM336529 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336529 target genes. The mRNA of each one of this plurality of GAM336529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336529 RNA, herein designated GAM RNA, and which when bound by GAM336529 RNA causes inhibition of translation of the GAM336529 target mRNA into a corresponding GAM336529 target protein.

The mechanism of the translational inhibition exerted by GAM336529 RNA, herein designated GAM RNA, on one or more GAM336529 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336529 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336529 RNA, herein designated GAM RNA, of GAM336529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336529 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336529 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336529

RNA correlate with, and may be deduced from, the identity of the GAM336529 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336532 6365 GAGCTGTCCG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGACGTAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGTACGTCA Messenger 336532 (GAM336532) oligonucleotides modulates expression of respective target
ACTCAGCCTT genes whose function and utility is known in the art.

ATTCTGGGAA GAM336532 is a novel bioinformatically detectable regulatory, non protein
ATCATTAATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336532 was detected
CTTAACTCTG is described with additional reference to Figs. 9-15.

ATGACTGTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAAAGTAGTC encoded by the human genome.

ACTGACCACT GAM336532 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM336532 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336532 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336532 precursor RNA is designated SEQ ID:6365, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6365 is located from position 24278760 to position 24278860 relative to chromosome 15 on the `-` strand.

GAM336532 precursor RNA folds onto itself, forming GAM336532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336532 precursor RNA, designated SEQ ID NO: 6365, and a schematic representation of a predicted secondary folding of GAM336532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336532 folded precursor RNA yielding a GAM336532 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336532 RNA, hereby incorporated herein.

GAM336532 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336532 target RNA, herein designated GAM TARGET RNA.

GAM336532 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336532 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336532 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336532 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336532 RNA, herein designated GAM RNA, to target binding sites on GAM336532 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336532 target RNA into GAM336532 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336532 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336532 target genes. The mRNA of each one of this plurality of GAM336532 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336532 RNA, herein designated GAM RNA, and which when bound by GAM336532 RNA causes inhibition of translation of the GAM336532 target mRNA into a corresponding GAM336532 target protein.

The mechanism of the translational inhibition exerted by GAM336532 RNA, herein designated GAM RNA, on one or more GAM336532 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336532 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336532 RNA, herein designated GAM RNA, of GAM336532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336532 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336532 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336532 RNA correlate with, and may be deduced from, the identity of the GAM336532 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336533 6894 GTGACGTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTGTACGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCAGCCT Messenger 336533 (GAM336533) oligonucleotides modulates expression of respective target
TATTCTGGGA genes whose function and utility is known in the art.

AATCATTAAT GAM336533 is a novel bioinformatically detectable regulatory, non protein
CCTTAACTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336533 was detected
GATGACTGTG is described with additional reference to Figs. 9-15.

CAAAAGTAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAC encoded by the human genome.

GAM336533 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336533 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336533 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336533 precursor RNA is designated SEQ ID:6894, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6894 is located from position 24278769 to position 24278851 relative to chromosome 15 on the `-` strand.

GAM336533 precursor RNA folds onto itself, forming GAM336533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336533 precursor RNA, designated SEQ ID NO: 6894, and a schematic representation of a predicted secondary folding of GAM336533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336533 folded precursor RNA yielding a GAM336533 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336533 RNA, hereby incorporated herein.

GAM336533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336533 target RNA, herein designated GAM TARGET RNA.

GAM336533 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336533 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336533 RNA, herein designated GAM RNA, to target binding sites on GAM336533 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336533 target RNA into GAM336533 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336533 target genes. The mRNA of each one of this plurality of GAM336533 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336533 RNA, herein designated GAM RNA, and which when bound by GAM336533 RNA causes inhibition of translation of the GAM336533 target mRNA into a corresponding GAM336533 target protein.

The mechanism of the translational inhibition exerted by GAM336533 RNA, herein designated GAM RNA, on one or more GAM336533 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336533 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336533 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336533 RNA, herein designated GAM RNA, of GAM336533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336533 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336533 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336533 RNA correlate with, and may be deduced from, the identity of the GAM336533 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336534 6698 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGAAG Messenger 336534 (GAM336534) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCGC GAM336534 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336534 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336534 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336534 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336534 precursor RNA is designated SEQ ID:6698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6698 is located from position 24437886 to position 24437973 relative to chromosome 13 on the `-` strand.

GAM336534 precursor RNA folds onto itself, forming GAM336534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336534 precursor RNA, designated SEQ ID NO: 6698, and a schematic representation of a predicted secondary folding of GAM336534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336534 folded precursor RNA yielding a GAM336534 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336534 RNA, hereby incorporated herein. Expression of GAM336534 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336534 target RNA, herein designated GAM TARGET RNA.

GAM336534 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336534 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336534 RNA, herein designated GAM RNA, to target binding sites on GAM336534 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336534 target RNA into GAM336534 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336534 target genes. The mRNA of each one of this plurality of GAM336534 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336534 RNA, herein designated GAM RNA, and which when bound by GAM336534 RNA causes inhibition of translation of the GAM336534 target mRNA into a corresponding GAM336534 target protein.

The mechanism of the translational inhibition exerted by GAM336534 RNA, herein designated GAM RNA, on one or more GAM336534 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336534 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336534 RNA, herein designated GAM RNA, of GAM336534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336534 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336534 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336534 RNA correlate with, and may be deduced from, the identity of the GAM336534 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336535 6590 GGACCATTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGTGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGCAGCAGG Messenger 336535 (GAM336535) oligonucleotides modulates expression of respective target

ACCCCCAGAA genes whose function and utility is known in the art.

CCGAAGCCTG GAM336535 is a novel bioinformatically detectable regulatory, non protein

TGTCTCTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336535 was detected

GTCTCATCCC is described with additional reference to Figs. 9-15.

TTCATTCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

C encoded by the human genome.

GAM336535 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336535 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336535 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336535 precursor RNA is designated SEQ ID:6590, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6590 is located from position 24538340 to position 24538420 relative to chromosome 13 on the `+` strand.

GAM336535 precursor RNA folds onto itself, forming GAM336535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336535 precursor RNA, designated SEQ ID NO: 6590, and a schematic representation of a predicted secondary folding of GAM336535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336535 folded precursor RNA yielding a GAM336535 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336535 RNA, hereby incorporated herein.

GAM336535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336535 target RNA, herein designated GAM TARGET RNA.

GAM336535 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336535 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336535 RNA, herein designated GAM RNA, to target binding sites on GAM336535 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336535 target RNA into GAM336535 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336535 target genes. The mRNA of each one of this plurality of GAM336535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336535 RNA, herein designated GAM RNA, and which when bound by GAM336535 RNA causes inhibition of translation of the GAM336535 target mRNA into a corresponding GAM336535 target protein.

The mechanism of the translational inhibition exerted by GAM336535 RNA, herein designated GAM RNA, on one or more GAM336535 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336535 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336535 RNA, herein designated GAM RNA, of GAM336535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336535 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336535 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336535 RNA correlate with, and may be deduced from, the identity of the GAM336535 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336536 5849 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336536 (GAM336536) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336536 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336536 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336536 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336536 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336536 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336536 precursor RNA is designated SEQ ID:5849, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5849 is located from position 24634603 to position 24634684 relative to chromosome 11 on the `+` strand.

GAM336536 precursor RNA folds onto itself, forming GAM336536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336536 precursor RNA, designated SEQ ID NO: 5849, and a schematic representation of a predicted secondary folding of GAM336536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336536 folded precursor RNA yielding a GAM336536 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336536 RNA, hereby incorporated herein.

GAM336536 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336536 target RNA, herein designated GAM TARGET RNA.

GAM336536 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336536 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336536 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336536 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336536 RNA, herein designated GAM RNA, to target binding sites on GAM336536 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336536 target RNA into GAM336536 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336536 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336536 target genes. The mRNA of each one of this plurality of GAM336536 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336536 RNA, herein designated GAM RNA, and which when bound by GAM336536 RNA causes inhibition of translation of the GAM336536 target mRNA into a corresponding GAM336536 target protein.

The mechanism of the translational inhibition exerted by GAM336536 RNA, herein designated GAM RNA, on one or more GAM336536 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336536 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336536 RNA, herein designated GAM RNA, of GAM336536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336536 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336536 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336536 RNA correlate with, and may be deduced from, the identity of the GAM336536 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336537 5827 AGTTTAAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCTCATGT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTACCCAGC Messenger 336537 (GAM336537) oligonucleotides modulates expression of respective target

TACTCTGGGC genes whose function and utility is known in the art.

GACTGAGCCC GAM336537 is a novel bioinformatically detectable regulatory, non protein
AGGGTACTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336537 was detected
GGGATCACTT is described with additional reference to Figs. 9-15.

GAGCCCAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCT encoded by the human genome.

GAM336537 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336537 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336537 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336537 precursor RNA is designated SEQ ID:5827, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5827 is located from position 24755757 to position 24755839 relative to chromosome 16 on the `+` strand.

GAM336537 precursor RNA folds onto itself, forming GAM336537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336537 precursor RNA, designated SEQ ID NO: 5827, and a schematic representation of a predicted secondary folding of GAM336537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336537 folded precursor RNA yielding a GAM336537 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336537 RNA, hereby incorporated herein.

GAM336537 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336537 target RNA, herein designated GAM TARGET RNA.

GAM336537 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336537 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336537 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336537 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336537 RNA, herein designated GAM RNA, to target binding sites on GAM336537 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336537 target RNA into GAM336537 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336537 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336537 target genes. The mRNA of each one of this plurality of GAM336537 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336537 RNA, herein designated GAM RNA, and which when bound by GAM336537 RNA causes inhibition of translation of the GAM336537 target mRNA into a corresponding GAM336537 target protein.

The mechanism of the translational inhibition exerted by GAM336537 RNA, herein designated GAM RNA, on one or more GAM336537 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336537 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336537 RNA, herein designated GAM RNA, of GAM336537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336537 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336537 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336537 RNA correlate with, and may be deduced from, the identity of the GAM336537 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336538 6942 GTTTAAGAAT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTCATGTA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTACCCAGCT Messenger 336538 (GAM336538) oligonucleotides modulates expression of respective target
ACTCTGGGCG genes whose function and utility is known in the art.

ACTGAGCCCA GAM336538 is a novel bioinformatically detectable regulatory, non protein
GGGTACTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336538 was detected
GGATCACTTG is described with additional reference to Figs. 9-15.

AGCCCAGGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
C encoded by the human genome.

GAM336538 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336538 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336538 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336538 precursor RNA is designated SEQ ID:6942, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6942 is located from position 24755758 to position 24755838 relative to chromosome 16 on the `+` strand.

GAM336538 precursor RNA folds onto itself, forming GAM336538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336538 precursor RNA, designated SEQ ID NO: 6942, and a schematic representation of a predicted secondary folding of GAM336538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336538 folded precursor RNA yielding a GAM336538 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336538 RNA, hereby incorporated herein.

GAM336538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336538 target RNA, herein designated GAM TARGET RNA.

GAM336538 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336538 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336538 RNA, herein designated GAM RNA, to target binding sites on GAM336538 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336538 target RNA into GAM336538 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336538 target genes. The mRNA of each one of this plurality of GAM336538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336538 RNA, herein designated GAM RNA, and which when bound by GAM336538 RNA causes inhibition of translation of the GAM336538 target mRNA into a corresponding GAM336538 target protein.

The mechanism of the translational inhibition exerted by GAM336538 RNA, herein designated GAM RNA, on one or more GAM336538 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336538 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336538 RNA, herein designated GAM RNA, of GAM336538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336538 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336538 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336538 RNA correlate with, and may be deduced from, the identity of the GAM336538 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336539 6905 GTGCCTAGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGCAGATGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGAGGTAGA Messenger 336539 (GAM336539) oligonucleotides modulates expression of respective target
ACAGTCTTGT genes whose function and utility is known in the art.

TCATACATTG GAM336539 is a novel bioinformatically detectable regulatory, non protein
CCATTATATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336539 was detected
TAGTGCAGTT is described with additional reference to Figs. 9-15.

GAATGAACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCTGTGTC encoded by the human genome.

TGGGCTTAGG GAM336539 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGC GAM336539 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336539 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336539 precursor RNA is designated SEQ ID:6905, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6905 is located from position 24906581 to position 24906683 relative to chromosome 10 on the `+` strand.

GAM336539 precursor RNA folds onto itself, forming GAM336539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336539 precursor RNA, designated SEQ ID NO: 6905, and a schematic representation of a predicted secondary folding of GAM336539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336539 folded precursor RNA yielding a GAM336539 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336539 RNA, hereby incorporated herein.

GAM336539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336539 target RNA, herein designated GAM TARGET RNA.

GAM336539 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336539 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336539 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336539 RNA, herein designated GAM RNA, to target binding sites on GAM336539 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336539 target RNA into GAM336539 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336539 target genes. The mRNA of each one of this plurality of GAM336539 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336539 RNA, herein designated GAM RNA, and which when bound by GAM336539 RNA causes inhibition of translation of the GAM336539 target mRNA into a corresponding GAM336539 target protein.

The mechanism of the translational inhibition exerted by GAM336539 RNA, herein designated GAM RNA, on one or more GAM336539 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336539 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336539 RNA, herein designated GAM RNA, of GAM336539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336539 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336539 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336539 RNA correlate with, and may be deduced from, the identity of the GAM336539 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336540 5760 AGGATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGCCCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTGGAGGCT Messenger 336540 (GAM336540) oligonucleotides modulates expression of respective target
GCAGTGAGCT genes whose function and utility is known in the art.

ATGATTGCAC GAM336540 is a novel bioinformatically detectable regulatory, non protein
TACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336540 was detected
CAGCCTGGGC is described with additional reference to Figs. 9-15.

AACAGAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATCCT encoded by the human genome.

GAM336540 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336540 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336540 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336540 precursor RNA is designated SEQ ID:5760, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5760 is located from position 24922097 to position 24922182 relative to chromosome 10 on the `+` strand.

GAM336540 precursor RNA folds onto itself, forming GAM336540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336540 precursor RNA, designated SEQ ID NO: 5760, and a schematic representation of a predicted secondary folding of GAM336540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336540 folded precursor RNA yielding a GAM336540 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336540 RNA, hereby incorporated herein. Expression of GAM336540 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336540 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336540 target RNA, herein designated GAM TARGET RNA.

GAM336540 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336540 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336540 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336540 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336540 RNA, herein designated GAM RNA, to target binding sites on GAM336540 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336540 target RNA into GAM336540 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336540 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336540 target genes. The mRNA of each one of this plurality of GAM336540 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336540 RNA, herein designated GAM RNA, and which when bound by GAM336540 RNA causes inhibition of translation of the GAM336540 target mRNA into a corresponding GAM336540 target protein.

The mechanism of the translational inhibition exerted by GAM336540 RNA, herein designated GAM RNA, on one or more GAM336540 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336540 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336540 RNA, herein designated GAM RNA, of GAM336540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336540 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336540 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336540 RNA correlate with, and may be deduced from, the identity of the GAM336540 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336541 6182 CTCTTGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGAAGTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTTGCAGT Messenger 336541 (GAM336541) oligonucleotides modulates expression of respective target

GAGCTGAGAT genes whose function and utility is known in the art.

AGCAACACTG GAM336541 is a novel bioinformatically detectable regulatory, non protein

CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336541 was detected

TGGGCAACAA is described with additional reference to Figs. 9-15.

GAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336541 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336541 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336541 precursor RNA is designated SEQ ID:6182, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6182 is located from position 25258227 to position 25258300 relative to chromosome 14 on the `-` strand.

GAM336541 precursor RNA folds onto itself, forming GAM336541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336541 precursor RNA, designated SEQ ID NO: 6182, and a schematic representation of a predicted secondary folding of GAM336541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336541 folded precursor RNA yielding a GAM336541 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336541 RNA, hereby incorporated herein. Expression of GAM336541 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336541 target RNA, herein designated GAM TARGET RNA.

GAM336541 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336541 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336541 RNA, herein designated GAM RNA, to target binding sites on GAM336541 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336541 target RNA into GAM336541 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336541 target genes. The mRNA of each one of this plurality of GAM336541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336541 RNA,

herein designated GAM RNA, and which when bound by GAM336541 RNA causes inhibition of translation of the GAM336541 target mRNA into a corresponding GAM336541 target protein.

The mechanism of the translational inhibition exerted by GAM336541 RNA, herein designated GAM RNA, on one or more GAM336541 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336541 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336541 RNA, herein designated GAM RNA, of GAM336541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336541 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336541 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336541 RNA correlate with, and may be deduced from, the identity of the GAM336541 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336545 6652 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGTGGAGG Messenger 336545 (GAM336545) oligonucleotides modulates expression of respective target

TAGTGGTGAG genes whose function and utility is known in the art.

CCGAGCTTGC GAM336545 is a novel bioinformatically detectable regulatory, non protein

ACACCATTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336545 was detected

ACTCCAGCCT is described with additional reference to Figs. 9-15.

GGGCAACAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGAAACTC encoded by the human genome.

C GAM336545 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336545 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336545 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336545 precursor RNA is designated SEQ ID:6652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6652 is located from position 25807898 to position 25807988 relative to chromosome 2 on the `+` strand.

GAM336545 precursor RNA folds onto itself, forming GAM336545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336545 precursor RNA, designated SEQ ID NO: 6652, and a schematic representation of a predicted secondary folding of GAM336545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336545 folded precursor RNA yielding a GAM336545 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336545 RNA, hereby incorporated herein. Expression of GAM336545 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336545 target RNA, herein designated GAM TARGET RNA.

GAM336545 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336545 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336545 RNA, herein designated GAM RNA, to target binding sites on GAM336545 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336545 target RNA into GAM336545 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336545 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336545 target genes. The mRNA of each one of this plurality of GAM336545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336545 RNA, herein designated GAM RNA, and which when bound by GAM336545 RNA causes inhibition of translation of the GAM336545 target mRNA into a corresponding GAM336545 target protein.

The mechanism of the translational inhibition exerted by GAM336545 RNA, herein designated GAM RNA, on one or more GAM336545 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336545 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336545 RNA, herein designated GAM RNA, of GAM336545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336545 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336545 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336545 RNA correlate with, and may be deduced from, the identity of the GAM336545 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336546 5850 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336546 (GAM336546) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336546 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336546 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336546 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336546 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336546 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336546 precursor RNA is designated SEQ ID:5850, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5850 is located from position 25943926 to position 25944007 relative to chromosome 11 on the `+` strand.

GAM336546 precursor RNA folds onto itself, forming GAM336546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336546 precursor RNA, designated SEQ ID NO: 5850, and a schematic representation of a predicted secondary folding of GAM336546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336546 folded precursor RNA yielding a GAM336546 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336546 RNA, hereby incorporated herein.

GAM336546 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336546 target RNA, herein designated GAM TARGET RNA.

GAM336546 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336546 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336546 RNA, herein designated GAM RNA, to target binding sites on GAM336546 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336546 target RNA into GAM336546 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336546 target genes. The mRNA of each one of this plurality of GAM336546 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336546 RNA, herein designated GAM RNA, and which when bound by GAM336546 RNA causes inhibition of translation of the GAM336546 target mRNA into a corresponding GAM336546 target protein.

The mechanism of the translational inhibition exerted by GAM336546 RNA, herein designated GAM RNA, on one or more GAM336546 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336546 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336546 RNA, herein designated GAM RNA, of GAM336546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336546 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336546 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336546 RNA correlate with, and may be deduced from, the identity of the GAM336546 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336548 6980 TATCTCATCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTTTTAATC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGAAGGCAT Messenger 336548 (GAM336548) oligonucleotides modulates expression of respective target

ATATGTATGA genes whose function and utility is known in the art.

CATTATCTGT GAM336548 is a novel bioinformatically detectable regulatory, non protein
CTTTAGGGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336548 was detected
GAGACCCAAC is described with additional reference to Figs. 9-15.

AGAGGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336548 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336548 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336548 precursor RNA is designated SEQ ID:6980, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6980 is located from position 26121979 to position 26122055 relative to chromosome 12 on the `+` strand.

GAM336548 precursor RNA folds onto itself, forming GAM336548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336548 precursor RNA, designated SEQ ID NO: 6980, and a schematic representation of a predicted secondary folding of GAM336548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336548 folded precursor RNA yielding a GAM336548 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336548 RNA, hereby incorporated herein.

GAM336548 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336548 target RNA, herein designated GAM TARGET RNA.

GAM336548 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336548 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336548 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336548 RNA, herein designated GAM RNA, to target binding sites on GAM336548 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336548 target RNA into GAM336548 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336548 target genes. The mRNA of each one of this plurality of GAM336548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336548 RNA, herein designated GAM RNA, and which when bound by GAM336548 RNA causes inhibition of translation of the GAM336548 target mRNA into a corresponding GAM336548 target protein.

The mechanism of the translational inhibition exerted by GAM336548 RNA, herein designated GAM RNA, on one or more GAM336548 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336548 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336548 RNA, herein designated GAM RNA, of GAM336548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336548 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336548 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336548 RNA correlate with, and may be deduced from, the identity of the GAM336548 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336549 5851 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336549 (GAM336549) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336549 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336549 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336549 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336549 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336549 precursor RNA is designated SEQ ID:5851, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5851 is located from position 26362757 to position 26362838 relative to chromosome 14 on the `+` strand.

GAM336549 precursor RNA folds onto itself, forming GAM336549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336549 precursor RNA, designated SEQ ID NO: 5851, and a schematic representation of a predicted secondary folding of GAM336549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336549 folded precursor RNA yielding a GAM336549 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336549 RNA, hereby incorporated herein.

GAM336549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336549 target RNA, herein designated GAM TARGET RNA.

GAM336549 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336549 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336549 RNA, herein designated GAM RNA, to target binding sites on GAM336549 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336549 target RNA into GAM336549 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336549 target genes. The mRNA of each one of this plurality of GAM336549 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336549 RNA, herein designated GAM RNA, and which when bound by GAM336549 RNA causes inhibition of translation of the GAM336549 target mRNA into a corresponding GAM336549 target protein.

The mechanism of the translational inhibition exerted by GAM336549 RNA, herein designated GAM RNA, on one or more GAM336549 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336549 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336549 RNA, herein designated GAM RNA, of GAM336549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336549 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336549 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336549 RNA correlate with, and may be deduced from, the identity of the GAM336549 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336550 5688 ACAGCTCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCAAGGCTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAACTCTGC Messenger 336550 (GAM336550) oligonucleotides modulates expression of respective target
TGACCTTCAG genes whose function and utility is known in the art.

AGTGTCAGAG GAM336550 is a novel bioinformatically detectable regulatory, non protein
CAGTGCCGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336550 was detected
GCCCAGGACA is described with additional reference to Figs. 9-15.

TGGCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336550 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336550 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336550 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336550 precursor RNA is designated SEQ ID:5688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5688 is located from position 26370649 to position 26370725 relative to chromosome 12 on the `+` strand.

GAM336550 precursor RNA folds onto itself, forming GAM336550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336550 precursor RNA, designated SEQ ID NO: 5688, and a schematic representation of a predicted secondary folding of GAM336550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336550 folded precursor RNA yielding a GAM336550 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336550 RNA, hereby incorporated herein.

GAM336550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336550 target RNA, herein designated GAM TARGET RNA.

GAM336550 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336550 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336550 RNA, herein designated GAM RNA, to target binding sites on GAM336550 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336550 target RNA into GAM336550 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336550 target genes. The mRNA of each one of this plurality of GAM336550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336550 RNA, herein designated GAM RNA, and which when bound by GAM336550 RNA causes inhibition of translation of the GAM336550 target mRNA into a corresponding GAM336550 target protein.

The mechanism of the translational inhibition exerted by GAM336550 RNA, herein designated GAM RNA, on one or more GAM336550 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336550 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336550 RNA, herein designated GAM RNA, of GAM336550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336550 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336550 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336550 RNA correlate with, and may be deduced from, the identity of the GAM336550 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336551 6751 GGCCTTCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGAGTTAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAAAGAGAGG Messenger 336551 (GAM336551) oligonucleotides modulates expression of respective target
AAGAATGGCA genes whose function and utility is known in the art.

AATAGTTTGA GAM336551 is a novel bioinformatically detectable regulatory, non protein
GTCTTCCCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336551 was detected
ATCTTTTTAG is described with additional reference to Figs. 9-15.

CATTTGAGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGCT encoded by the human genome.

GAM336551 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336551 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336551 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336551 precursor RNA is designated SEQ ID:6751, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6751 is located from position 26442598 to position 26442683 relative to chromosome 7 on the `+` strand.

GAM336551 precursor RNA folds onto itself, forming GAM336551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336551 precursor RNA, designated SEQ ID NO: 6751, and a schematic representation of a predicted secondary folding of GAM336551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336551 folded precursor RNA yielding a GAM336551 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336551 RNA, hereby incorporated herein.

GAM336551 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336551 target RNA, herein designated GAM TARGET RNA.

GAM336551 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336551 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336551 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336551 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336551 RNA, herein designated GAM RNA, to target binding sites on GAM336551 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336551 target RNA into GAM336551 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336551 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336551 target genes. The mRNA of each one of this plurality of GAM336551 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336551 RNA, herein designated GAM RNA, and which when bound by GAM336551 RNA causes inhibition of translation of the GAM336551 target mRNA into a corresponding GAM336551 target protein.

The mechanism of the translational inhibition exerted by GAM336551 RNA, herein designated GAM RNA, on one or more GAM336551 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336551 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336551 RNA, herein designated GAM RNA, of GAM336551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336551 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336551 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336551 RNA correlate with, and may be deduced from, the identity of the GAM336551 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336552 5708 ACTGAAGCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTGCCAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTCACATGAG Messenger 336552 (GAM336552) oligonucleotides modulates expression of respective target
TGAGTCTGGA genes whose function and utility is known in the art.

AGTGAATCTT GAM336552 is a novel bioinformatically detectable regulatory, non protein
TCAGCACCAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336552 was detected
CAGATGACTG is described with additional reference to Figs. 9-15.

TATCACTGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTACAGT encoded by the human genome.

GAM336552 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336552 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336552 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336552 precursor RNA is designated SEQ ID:5708, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5708 is located from position 26468156 to position 26468242 relative to chromosome 9 on the `+` strand.

GAM336552 precursor RNA folds onto itself, forming GAM336552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336552 precursor RNA, designated SEQ ID NO: 5708, and a schematic representation of a predicted secondary folding of GAM336552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336552 folded precursor RNA yielding a GAM336552 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336552 RNA, hereby incorporated herein.

GAM336552 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336552 target RNA, herein designated GAM TARGET RNA.

GAM336552 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336552 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336552 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336552 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336552 RNA, herein designated GAM RNA, to target binding sites on GAM336552 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336552 target RNA into GAM336552 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336552 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336552 target genes. The mRNA of each one of this plurality of GAM336552 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336552 RNA, herein designated GAM RNA, and which when bound by GAM336552 RNA causes inhibition of translation of the GAM336552 target mRNA into a corresponding GAM336552 target protein.

The mechanism of the translational inhibition exerted by GAM336552 RNA, herein designated GAM RNA, on one or more GAM336552 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336552 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336552 RNA, herein designated GAM RNA, of GAM336552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336552 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336552 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336552 RNA correlate with, and may be deduced from, the identity of the GAM336552 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336553 6986 TATTCCAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCTTAGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTCAGCAG Messenger 336553 (GAM336553) oligonucleotides modulates expression of respective target

GATGGTTGGA genes whose function and utility is known in the art.

CTGAAGGGGG GAM336553 is a novel bioinformatically detectable regulatory, non protein

CTGGTTTACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336553 was detected

TCTTCAGTGG is described with additional reference to Figs. 9-15.

AAGTGTTCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTGCAAAT encoded by the human genome.

ACTAGTTACT GAM336553 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGAATA GAM336553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336553 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336553 precursor RNA is designated SEQ

ID:6986, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6986 is located from position 26541313 to position 26541418 relative to chromosome X on the `-` strand.

GAM336553 precursor RNA folds onto itself, forming GAM336553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336553 precursor RNA, designated SEQ ID NO: 6986, and a schematic representation of a predicted secondary folding of GAM336553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336553 folded precursor RNA yielding a GAM336553 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336553 RNA, hereby incorporated herein.

GAM336553 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336553 target RNA, herein designated GAM TARGET RNA.

GAM336553 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336553 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336553 RNA, herein designated GAM RNA, to target binding sites on GAM336553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336553 target RNA into GAM336553 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336553 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336553 target genes. The mRNA of each one of this plurality of GAM336553 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336553 RNA, herein designated GAM RNA, and which when bound by GAM336553 RNA causes inhibition of translation of the GAM336553 target mRNA into a corresponding GAM336553 target protein.

The mechanism of the translational inhibition exerted by GAM336553 RNA, herein designated GAM RNA, on one or more GAM336553 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336553 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336553 RNA, herein designated GAM RNA, of GAM336553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336553 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336553 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336553 RNA correlate with, and may be deduced from, the identity of the GAM336553 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336556 6052 CCAGCTGCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCTTCTACC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACCCCATC Messenger 336556 (GAM336556) oligonucleotides modulates expression of respective target

TCATAGAACT genes whose function and utility is known in the art.

CACAACAACC GAM336556 is a novel bioinformatically detectable regulatory, non protein

TTGTTGGGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336556 was detected

AAAAGGAGGG is described with additional reference to Figs. 9-15.

GATACAGGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTAAAGAGG encoded by the human genome.

GGGAAATAAC GAM336556 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CATATAGCTG GAM336556 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

G GAM336556 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336556 precursor RNA is designated SEQ ID:6052, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6052 is located from position 26895579 to position 26895689 relative to chromosome 17 on the `+` strand.

GAM336556 precursor RNA folds onto itself, forming GAM336556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336556 precursor RNA, designated SEQ ID NO: 6052, and a schematic representation of a predicted secondary folding of GAM336556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336556 folded precursor RNA yielding a GAM336556 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336556 RNA, hereby incorporated herein.

GAM336556 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336556 target RNA, herein designated GAM TARGET RNA.

GAM336556 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336556 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336556 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336556 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336556 RNA, herein designated GAM RNA, to target binding sites on GAM336556 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336556 target RNA into GAM336556 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336556 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336556 target genes. The mRNA of each one of this plurality of GAM336556 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336556 RNA, herein designated GAM RNA, and which when bound by GAM336556 RNA causes inhibition of translation of the GAM336556 target mRNA into a corresponding GAM336556 target protein.

The mechanism of the translational inhibition exerted by GAM336556 RNA, herein designated GAM RNA, on one or more GAM336556 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336556 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336556 RNA, herein designated GAM RNA, of GAM336556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336556 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336556 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336556 RNA correlate with, and may be deduced from, the identity of the GAM336556 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336557 5852 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336557 (GAM336557) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336557 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336557 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336557 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336557 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336557 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336557 precursor RNA is designated SEQ ID:5852, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5852 is located from position 26976985 to position 26977066 relative to chromosome 18 on the `+` strand.

GAM336557 precursor RNA folds onto itself, forming GAM336557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336557 precursor RNA, designated SEQ ID NO: 5852, and a schematic representation of a predicted secondary folding of GAM336557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336557 folded precursor RNA yielding a GAM336557 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336557 RNA, hereby incorporated herein.

GAM336557 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336557 target RNA, herein designated GAM TARGET RNA.

GAM336557 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336557 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336557 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336557 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336557 RNA, herein designated GAM RNA, to target binding sites on GAM336557 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336557 target RNA into GAM336557 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336557 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336557 target genes. The mRNA of each one of this plurality of GAM336557 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336557 RNA, herein designated GAM RNA, and which when bound by GAM336557 RNA causes inhibition of translation of the GAM336557 target mRNA into a corresponding GAM336557 target protein.

The mechanism of the translational inhibition exerted by GAM336557 RNA, herein designated GAM RNA, on one or more GAM336557 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336557 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336557 RNA, herein designated GAM RNA, of GAM336557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336557 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336557 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336557 RNA correlate with, and may be deduced from, the identity of the GAM336557 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336558 6635 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336558 (GAM336558) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM336558 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336558 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336558 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336558 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336558 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336558 precursor RNA is designated SEQ ID:6635, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6635 is located from position 26978328 to position 26978415 relative to chromosome 6 on the `+` strand.

GAM336558 precursor RNA folds onto itself, forming GAM336558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336558 precursor RNA, designated SEQ ID NO: 6635, and a schematic representation of a predicted secondary folding of GAM336558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336558 folded precursor RNA yielding a GAM336558 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336558 RNA, hereby incorporated herein. Expression of GAM336558 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336558 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336558 target RNA, herein designated GAM TARGET RNA.

GAM336558 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336558 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336558 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336558 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336558 RNA, herein designated GAM RNA, to target binding sites on GAM336558 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336558 target RNA into GAM336558 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336558 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336558 target genes. The mRNA of each one of this plurality of GAM336558 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336558 RNA, herein designated GAM RNA, and which when bound by GAM336558 RNA causes inhibition of translation of the GAM336558 target mRNA into a corresponding GAM336558 target protein.

The mechanism of the translational inhibition exerted by GAM336558 RNA, herein designated GAM RNA, on one or more GAM336558 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336558 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336558 RNA, herein designated GAM RNA, of GAM336558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336558 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336558 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336558 RNA correlate with, and may be deduced from, the identity of the GAM336558 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336559 5695 ACCCACATTC TTAGCTTGGC TTCAGTTTCT TTCCGGGTCT TACTGAGAGG TGAAGCCAGG CTTCTGGGTG GGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336559 (GAM336559) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336559 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336559 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336559 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336559 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336559 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336559 precursor RNA is designated SEQ ID:5695, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5695 is located from position 27187756 to position 27187828 relative to chromosome Y on the `+` strand.

GAM336559 precursor RNA folds onto itself, forming GAM336559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336559 precursor RNA, designated SEQ ID NO: 5695, and a schematic representation of a predicted secondary folding of GAM336559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336559 folded precursor RNA yielding a GAM336559 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336559 RNA, hereby incorporated herein.

GAM336559 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336559 target RNA, herein designated GAM TARGET RNA.

GAM336559 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336559 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336559 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336559 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336559 RNA, herein designated GAM RNA, to target binding sites on GAM336559 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336559 target RNA into GAM336559 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336559 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336559 target genes. The mRNA of each one of this plurality of GAM336559 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336559 RNA, herein designated GAM RNA, and which when bound by GAM336559 RNA causes inhibition of translation of the GAM336559 target mRNA into a corresponding GAM336559 target protein.

The mechanism of the translational inhibition exerted by GAM336559 RNA, herein designated GAM RNA, on one or more GAM336559 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336559 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336559 RNA, herein designated GAM RNA, of GAM336559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336559 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336559 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336559 RNA correlate with, and may be deduced from, the identity of the GAM336559 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336560 7289 TTCACCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGCCAGGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTCTTGAAC Messenger 336560 (GAM336560) oligonucleotides modulates expression of respective target

TCCTGACTTT genes whose function and utility is known in the art.

GTGATCCACC GAM336560 is a novel bioinformatically detectable regulatory, non protein

TGCCTTGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336560 was detected

ACCCAAAGTG is described with additional reference to Figs. 9-15.

CTGGTATTAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGTGTGAGC encoded by the human genome.

CACCGCGCCT GAM336560 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGCCGGTGAA GAM336560 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336560 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336560 precursor RNA is designated SEQ ID:7289, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7289 is located from position 27457170 to position 27457279 relative to chromosome 8 on the `+` strand.

GAM336560 precursor RNA folds onto itself, forming GAM336560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336560 precursor RNA, designated SEQ ID NO: 7289, and a schematic representation of a predicted secondary folding of GAM336560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336560 folded precursor RNA yielding a GAM336560 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336560 RNA, hereby incorporated herein.

GAM336560 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336560 target RNA, herein designated GAM TARGET RNA.

GAM336560 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336560 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336560 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336560 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336560 RNA, herein designated GAM RNA, to target binding sites on GAM336560 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336560 target RNA into GAM336560 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336560 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336560 target genes. The mRNA of each one of this plurality of GAM336560 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336560 RNA, herein designated GAM RNA, and which when bound by GAM336560 RNA causes inhibition of translation of the GAM336560 target mRNA into a corresponding GAM336560 target protein.

The mechanism of the translational inhibition exerted by GAM336560 RNA, herein designated GAM RNA, on one or more GAM336560 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336560 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336560 RNA, herein designated GAM RNA, of GAM336560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336560 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336560 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336560 RNA correlate with, and may be deduced from, the identity of the GAM336560 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336561 6537 GCTCTGTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGAATCGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAATATGGGG Messenger 336561 (GAM336561) oligonucleotides modulates expression of respective target

CTCTTTTCTG genes whose function and utility is known in the art.

TCTTTGCGAT GAM336561 is a novel bioinformatically detectable regulatory, non protein

TTTGGCTATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336561 was detected

AATTTGTAGC is described with additional reference to Figs. 9-15.

AGAACACTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCCAGTTTC encoded by the human genome.

TTCATTATCT GAM336561 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTTTACTGAG GAM336561 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

C GAM336561 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336561 precursor RNA is designated SEQ ID:6537, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6537 is located from position 27480931 to position 27481041 relative to chromosome 11 on the `+` strand.

GAM336561 precursor RNA folds onto itself, forming GAM336561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336561 precursor RNA, designated SEQ ID NO: 6537, and a schematic representation of a predicted secondary folding of GAM336561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336561 folded precursor RNA yielding a GAM336561 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336561 RNA, hereby incorporated herein.

GAM336561 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336561 target RNA, herein designated GAM TARGET RNA.

GAM336561 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336561 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336561 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336561 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336561 RNA, herein designated GAM RNA, to target binding sites on GAM336561 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336561 target RNA into GAM336561 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336561 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336561 target genes. The mRNA of each one of this

plurality of GAM336561 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336561 RNA, herein designated GAM RNA, and which when bound by GAM336561 RNA causes inhibition of translation of the GAM336561 target mRNA into a corresponding GAM336561 target protein.

The mechanism of the translational inhibition exerted by GAM336561 RNA, herein designated GAM RNA, on one or more GAM336561 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336561 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336561 RNA, herein designated GAM RNA, of GAM336561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336561 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336561 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336561 RNA correlate with, and may be deduced from, the identity of the GAM336561 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336563 5759 AGGATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGCCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTTCGAGGC Messenger 336563 (GAM336563) oligonucleotides modulates expression of respective target
TGTAGTGAGC genes whose function and utility is known in the art.

TATGACTGTG GAM336563 is a novel bioinformatically detectable regulatory, non protein
TCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336563 was detected
TCAGCCTGGG is described with additional reference to Figs. 9-15.

CAATGGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGATCCT encoded by the human genome.

GAM336563 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336563 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336563 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336563 precursor RNA is designated SEQ ID:5759, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5759 is located from position 27711245 to position 27711331 relative to chromosome 12 on the `+` strand.

GAM336563 precursor RNA folds onto itself, forming GAM336563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336563 precursor RNA, designated SEQ ID NO: 5759, and a schematic representation of a predicted secondary folding of GAM336563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336563 folded precursor RNA yielding a GAM336563 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336563 RNA, hereby incorporated herein.

GAM336563 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336563 target RNA, herein designated GAM TARGET RNA.

GAM336563 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336563 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336563 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336563 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336563 RNA, herein designated GAM RNA, to target binding sites on GAM336563 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336563 target RNA into GAM336563 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336563 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336563 target genes. The mRNA of each one of this plurality of GAM336563 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336563 RNA, herein designated GAM RNA, and which when bound by GAM336563 RNA causes inhibition of translation of the GAM336563 target mRNA into a corresponding GAM336563 target protein.

The mechanism of the translational inhibition exerted by GAM336563 RNA, herein designated GAM RNA, on one or more GAM336563 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336563 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336563 RNA, herein designated GAM RNA, of GAM336563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336563 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336563 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336563 RNA correlate with, and may be deduced from, the identity of the GAM336563 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336564 6601 GGAGAATAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 336564 (GAM336564) oligonucleotides modulates expression of respective target

TTACAGTGAG genes whose function and utility is known in the art.

CCACCGAGAT GAM336564 is a novel bioinformatically detectable regulatory, non protein

TGTGTCATTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336564 was detected

CACTCCAGCC is described with additional reference to Figs. 9-15.

TGGGCAACAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCAAATCT encoded by the human genome.

CC GAM336564 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336564 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336564 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336564 precursor RNA is designated SEQ ID:6601, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6601 is located from position 27748402 to position 27748493 relative to chromosome 6 on the `+` strand.

GAM336564 precursor RNA folds onto itself, forming GAM336564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336564 precursor RNA, designated SEQ ID NO: 6601, and a schematic representation of a predicted secondary folding of GAM336564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336564 folded precursor RNA yielding a GAM336564 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336564 RNA, hereby incorporated herein. Expression of GAM336564 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336564 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336564 target RNA, herein designated GAM TARGET RNA.

GAM336564 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336564 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336564 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336564 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336564 RNA, herein designated GAM RNA, to target binding sites on GAM336564 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336564 target RNA into GAM336564 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336564 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336564 target genes. The mRNA of each one of this plurality of GAM336564 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336564 RNA, herein designated GAM RNA, and which when bound by GAM336564 RNA causes inhibition of translation of the GAM336564 target mRNA into a corresponding GAM336564 target protein.

The mechanism of the translational inhibition exerted by GAM336564 RNA, herein designated GAM RNA, on one or more GAM336564 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336564 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336564 RNA, herein designated GAM RNA, of GAM336564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336564 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336564 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336564 RNA correlate with, and may be deduced from, the identity of the GAM336564 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336565 5997 CACCTGTCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCAGTTACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGGGGGCTA Messenger 336565 (GAM336565) oligonucleotides modulates expression of respective target
AGGTGGGAGG genes whose function and utility is known in the art.

ATTAGTGAGC GAM336565 is a novel bioinformatically detectable regulatory, non protein
TGTGATTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336565 was detected
CCACTGCATT is described with additional reference to Figs. 9-15.

CCAGCCTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGACAGAGTG encoded by the human genome.

GAM336565 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336565 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336565 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336565 precursor RNA is designated SEQ ID:5997, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5997 is located from position 27947083 to position 27947172 relative to chromosome 10 on the `+` strand.

GAM336565 precursor RNA folds onto itself, forming GAM336565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336565 precursor RNA, designated SEQ ID NO: 5997, and a schematic representation of a predicted secondary folding of GAM336565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336565 folded precursor RNA yielding a GAM336565 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336565 RNA, hereby incorporated herein.

GAM336565 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336565 target RNA, herein designated GAM TARGET RNA.

GAM336565 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336565 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336565 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336565 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336565 RNA, herein designated GAM RNA, to target binding sites on GAM336565 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336565 target RNA into GAM336565 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336565 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336565 target genes. The mRNA of each one of this plurality of GAM336565 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336565 RNA, herein designated GAM RNA, and which when bound by GAM336565 RNA causes inhibition of translation of the GAM336565 target mRNA into a corresponding GAM336565 target protein.

The mechanism of the translational inhibition exerted by GAM336565 RNA, herein designated GAM RNA, on one or more GAM336565 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336565 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336565 RNA, herein designated GAM RNA, of GAM336565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336565 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336565 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336565

RNA correlate with, and may be deduced from, the identity of the GAM336565 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336567 6966 TAGAAGCATC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTAGTTTTA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGAAGTGTC Messenger 336567 (GAM336567) oligonucleotides modulates expression of respective target
TCTTGGCTGG genes whose function and utility is known in the art.

CCCCTAGATA GAM336567 is a novel bioinformatically detectable regulatory, non protein
GCTTTAGGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336567 was detected
GGGAGCTAGT is described with additional reference to Figs. 9-15.

CACCAGAAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACCAATCCTT encoded by the human genome.

GATTAGAAGC GAM336567 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTGTA GAM336567 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336567 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336567 precursor RNA is designated SEQ ID:6966, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6966 is located from position 28064331 to position 28064435 relative to chromosome 17 on the `+` strand.

GAM336567 precursor RNA folds onto itself, forming GAM336567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336567 precursor RNA, designated SEQ ID NO: 6966, and a schematic representation of a predicted secondary folding of GAM336567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336567 folded precursor RNA yielding a GAM336567 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336567 RNA, hereby incorporated herein.

GAM336567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336567 target RNA, herein designated GAM TARGET RNA.

GAM336567 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336567 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336567 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336567 RNA, herein designated GAM RNA, to target binding sites on GAM336567 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336567 target RNA into GAM336567 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336567 target genes. The mRNA of each one of this plurality of GAM336567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336567 RNA, herein designated GAM RNA, and which when bound by GAM336567 RNA causes inhibition of translation of the GAM336567 target mRNA into a corresponding GAM336567 target protein.

The mechanism of the translational inhibition exerted by GAM336567 RNA, herein designated GAM RNA, on one or more GAM336567 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336567 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336567 RNA, herein designated GAM RNA, of GAM336567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336567 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336567 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336567 RNA correlate with, and may be deduced from, the identity of the GAM336567 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336568 6270 CTTTAGTTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGAAGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCTTGGCTG Messenger 336568 (GAM336568) oligonucleotides modulates expression of respective target
GCCCCTAGAT genes whose function and utility is known in the art.

AGCTTTAGGA GAM336568 is a novel bioinformatically detectable regulatory, non protein
TGGGAGCTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336568 was detected
TCACCAGAAA is described with additional reference to Figs. 9-15.

CACCAATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGATTAGAAG encoded by the human genome.

GAM336568 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336568 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336568 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336568 precursor RNA is designated SEQ ID:6270, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6270 is located from position 28064340 to position 28064429 relative to chromosome 17 on the `+` strand.

GAM336568 precursor RNA folds onto itself, forming GAM336568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336568 precursor RNA, designated SEQ ID NO: 6270, and a schematic representation of a predicted secondary folding of GAM336568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336568 folded precursor RNA yielding a GAM336568 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336568 RNA, hereby incorporated herein.

GAM336568 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336568 target RNA, herein designated GAM TARGET RNA.

GAM336568 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336568 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336568 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336568 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336568 RNA, herein designated GAM RNA, to target binding sites on GAM336568 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336568 target RNA into GAM336568 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336568 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336568 target genes. The mRNA of each one of this plurality of GAM336568 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336568 RNA, herein designated GAM RNA, and which when bound by GAM336568 RNA causes inhibition of translation of the GAM336568 target mRNA into a corresponding GAM336568 target protein.

The mechanism of the translational inhibition exerted by GAM336568 RNA, herein designated GAM RNA, on one or more GAM336568 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336568 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336568 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336568 RNA, herein designated GAM RNA, of GAM336568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336568 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336568 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336568 RNA correlate with, and may be deduced from, the identity of the GAM336568 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336569 7342 TTTAGTTTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGAAGTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTGGCTGG Messenger 336569 (GAM336569) oligonucleotides modulates expression of respective target

CCCCTAGATA genes whose function and utility is known in the art.

GCTTTAGGAT GAM336569 is a novel bioinformatically detectable regulatory, non protein

GGGAGCTAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336569 was detected

CACCAGAAAC is described with additional reference to Figs. 9-15.

ACCAATCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATTAGA encoded by the human genome.

GAM336569 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336569 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336569 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336569 precursor RNA is designated SEQ ID:7342, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7342 is located from position 28064341 to position 28064427 relative to chromosome 17 on the `+` strand.

GAM336569 precursor RNA folds onto itself, forming GAM336569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336569 precursor RNA, designated SEQ ID NO: 7342, and a schematic representation of a predicted secondary folding of GAM336569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336569 folded precursor RNA yielding a GAM336569 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336569 RNA, hereby incorporated herein.

GAM336569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336569 target RNA, herein designated GAM TARGET RNA.

GAM336569 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336569 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336569 RNA, herein designated GAM RNA, to target binding sites on GAM336569 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336569 target RNA into GAM336569 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336569 target genes. The mRNA of each one of this plurality of GAM336569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336569 RNA, herein designated GAM RNA, and which when bound by GAM336569 RNA causes inhibition of translation of the GAM336569 target mRNA into a corresponding GAM336569 target protein.

The mechanism of the translational inhibition exerted by GAM336569 RNA, herein

designated GAM RNA, on one or more GAM336569 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336569 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336569 RNA, herein designated GAM RNA, of GAM336569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336569 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336569 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336569 RNA correlate with, and may be deduced from, the identity of the GAM336569 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336570 6577 GGAACAGTAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCACGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCTGGAGAG Messenger 336570 (GAM336570) oligonucleotides modulates expression of respective target

GAGCGGTCAC genes whose function and utility is known in the art.

TGGTTGCTGA GAM336570 is a novel bioinformatically detectable regulatory, non protein

GTGAATTAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336570 was detected

CGAATGTTTG is described with additional reference to Figs. 9-15.

CTGCTTTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGCAACAG encoded by the human genome.

TTCATTATTC GAM336570 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336570 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336570 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336570 precursor RNA is designated SEQ ID:6577, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6577 is located from position 28404293 to position 28404393 relative to chromosome 22 on the `+` strand.

GAM336570 precursor RNA folds onto itself, forming GAM336570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336570 precursor RNA, designated SEQ ID NO: 6577, and a schematic representation of a predicted secondary folding of GAM336570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336570 folded precursor RNA yielding a GAM336570 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336570 RNA, hereby incorporated herein.

GAM336570 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336570 target RNA, herein designated GAM TARGET RNA.

GAM336570 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336570 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336570 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336570 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336570 RNA, herein designated GAM RNA, to target binding sites on GAM336570 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336570 target RNA into GAM336570 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336570 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336570 target genes. The mRNA of each one of this plurality of GAM336570 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336570 RNA, herein designated GAM RNA, and which when bound by GAM336570 RNA causes inhibition of translation of the GAM336570 target mRNA into a corresponding GAM336570 target protein.

The mechanism of the translational inhibition exerted by GAM336570 RNA, herein designated GAM RNA, on one or more GAM336570 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336570 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336570 RNA, herein designated GAM RNA, of GAM336570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336570 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336570 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336570 RNA correlate with, and may be deduced from, the identity of the GAM336570 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336571 6556 GCTTCATCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGGTTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGTGTTTC Messenger 336571 (GAM336571) oligonucleotides modulates expression of respective target

TTCTCTATCA genes whose function and utility is known in the art.

GGCCTGGTGG GAM336571 is a novel bioinformatically detectable regulatory, non protein

CTGTTGTTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336571 was detected

GGGCTCCCCA is described with additional reference to Figs. 9-15.

AGGCGAGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGGCCCTGGA encoded by the human genome.

CAAGTGGGTT GAM336571 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGAAGACACG GAM336571 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GTGACCAGAG GAM336571 precursor RNA does not encode a protein. A nucleotide sequence identical or

AAGAGGGAAG highly similar to the nucleotide sequence of GAM336571 precursor RNA is designated SEQ

C ID:6556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6556 is located from position 28441207 to position 28441337 relative to chromosome 15 on the `-` strand.

GAM336571 precursor RNA folds onto itself, forming GAM336571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336571 precursor RNA, designated SEQ ID NO: 6556, and a schematic representation of a predicted secondary folding of GAM336571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336571 folded precursor RNA yielding a GAM336571 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336571 RNA, hereby incorporated herein.

GAM336571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336571 target RNA, herein designated GAM TARGET RNA.

GAM336571 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336571 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336571 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336571 RNA, herein designated GAM RNA, to target binding sites on GAM336571 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336571 target RNA into GAM336571 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336571 target genes. The mRNA of each one of this plurality of GAM336571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336571 RNA, herein designated GAM RNA, and which when bound by GAM336571 RNA causes inhibition of translation of the GAM336571 target mRNA into a corresponding GAM336571 target protein.

The mechanism of the translational inhibition exerted by GAM336571 RNA, herein designated GAM RNA, on one or more GAM336571 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336571 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336571 RNA, herein designated GAM RNA, of GAM336571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336571 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336571 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336571 RNA correlate with, and may be deduced from, the identity of the GAM336571 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336572 6465 GAGTGACCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTCTACAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAGTTTTTT Messenger 336572 (GAM336572) oligonucleotides modulates expression of respective target

TAAATTAGCT genes whose function and utility is known in the art.

AGGCATGGTG GAM336572 is a novel bioinformatically detectable regulatory, non protein
GTATACACTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336572 was detected
GTAGTCCTAG is described with additional reference to Figs. 9-15.

CTACTTAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCTGAGGCA encoded by the human genome.

GGAGGGTCAC GAM336572 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TT GAM336572 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336572 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336572 precursor RNA is designated SEQ ID:6465, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6465 is located from position 28604728 to position 28604829 relative to chromosome 8 on the `-` strand.

GAM336572 precursor RNA folds onto itself, forming GAM336572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336572 precursor RNA, designated SEQ ID NO: 6465, and a schematic representation of a predicted secondary folding of GAM336572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336572 folded precursor RNA yielding a GAM336572 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336572 RNA, hereby incorporated herein.

GAM336572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336572 target RNA, herein designated GAM TARGET RNA.

GAM336572 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336572 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336572 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336572 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336572 RNA, herein designated GAM RNA, to target binding sites on GAM336572 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336572 target RNA into GAM336572 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336572 target genes. The mRNA of each one of this plurality of GAM336572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336572 RNA, herein designated GAM RNA, and which when bound by GAM336572 RNA causes inhibition of translation of the GAM336572 target mRNA into a corresponding GAM336572 target protein.

The mechanism of the translational inhibition exerted by GAM336572 RNA, herein designated GAM RNA, on one or more GAM336572 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336572 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336572 RNA, herein designated GAM RNA, of GAM336572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336572 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336572 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336572 RNA correlate with, and may be deduced from, the identity of the GAM336572 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336573 6678 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336573 (GAM336573) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCACGATTGT GAM336573 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336573 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336573 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336573 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336573 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336573 precursor RNA is designated SEQ ID:6678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6678 is located from position 28680032 to position 28680119 relative to chromosome 16 on the `+` strand.

GAM336573 precursor RNA folds onto itself, forming GAM336573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336573 precursor RNA, designated SEQ ID NO: 6678, and a schematic representation of a predicted secondary folding of GAM336573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336573 folded precursor RNA yielding a GAM336573 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336573 RNA, hereby incorporated herein.

GAM336573 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336573 target RNA, herein designated GAM TARGET RNA.

GAM336573 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336573 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336573 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336573 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336573 RNA, herein designated GAM RNA, to target binding sites on GAM336573 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336573 target RNA into GAM336573 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336573 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336573 target genes. The mRNA of each one of this plurality of GAM336573 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336573 RNA, herein designated GAM RNA, and which when bound by GAM336573 RNA causes inhibition of translation of the GAM336573 target mRNA into a corresponding GAM336573 target protein.

The mechanism of the translational inhibition exerted by GAM336573 RNA, herein designated GAM RNA, on one or more GAM336573 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336573 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336573 RNA, herein designated GAM RNA, of GAM336573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336573 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336573 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336573 RNA correlate with, and may be deduced from, the identity of the GAM336573 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336574 7308 TTCTGTGATG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGTGTACGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATTATTTT Messenger 336574 (GAM336574) oligonucleotides modulates expression of respective target
GTGACTGCAG genes whose function and utility is known in the art.

TCTGTTCAAA GAM336574 is a novel bioinformatically detectable regulatory, non protein
TCACATCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336574 was detected
AAGCAGCGCT is described with additional reference to Figs. 9-15.

GAGATGATTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTGGTGCAT encoded by the human genome.

TAAAAGGTTT GAM336574 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGCATCATGG GAM336574 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
AA GAM336574 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336574 precursor RNA is designated SEQ ID:7308, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7308 is located from position 28740486 to position 28740597 relative to chromosome 8 on the `+` strand.

GAM336574 precursor RNA folds onto itself, forming GAM336574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336574 precursor RNA, designated SEQ ID NO: 7308, and a schematic representation of a predicted secondary folding of GAM336574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336574 folded precursor

RNA yielding a GAM336574 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336574 RNA, hereby incorporated herein.

GAM336574 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336574 target RNA, herein designated GAM TARGET RNA.

GAM336574 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336574 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336574 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336574 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336574 RNA, herein designated GAM RNA, to target binding sites on GAM336574 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336574 target RNA into GAM336574 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336574 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336574 target genes. The mRNA of each one of this plurality of GAM336574 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336574 RNA, herein designated GAM RNA, and which when bound by GAM336574 RNA causes inhibition of translation of the GAM336574 target mRNA into a corresponding GAM336574 target protein.

The mechanism of the translational inhibition exerted by GAM336574 RNA, herein designated GAM RNA, on one or more GAM336574 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336574 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336574 RNA, herein designated GAM RNA, of GAM336574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336574 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336574 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336574 RNA correlate with, and may be deduced from, the identity of the GAM336574 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336575 6679 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 336575 (GAM336575) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCACGATTGT GAM336575 is a novel bioinformatically detectable regulatory, non protein

GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336575 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336575 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336575 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336575 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336575 precursor RNA is designated SEQ ID:6679, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6679 is located from position 28794191 to position 28794278 relative to chromosome 16 on the `+` strand.

GAM336575 precursor RNA folds onto itself, forming GAM336575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336575 precursor RNA, designated SEQ ID NO: 6679, and a schematic representation of a predicted secondary folding of GAM336575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336575 folded precursor RNA yielding a GAM336575 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336575 RNA, hereby incorporated herein.

GAM336575 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336575 target RNA, herein designated GAM TARGET RNA.

GAM336575 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336575 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336575 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336575 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336575 RNA, herein designated GAM RNA, to target binding sites on GAM336575 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336575 target RNA into GAM336575 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336575 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336575 target genes. The mRNA of each one of this plurality of GAM336575 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336575 RNA, herein designated GAM RNA, and which when bound by GAM336575 RNA causes inhibition of translation of the GAM336575 target mRNA into a corresponding GAM336575 target protein.

The mechanism of the translational inhibition exerted by GAM336575 RNA, herein designated GAM RNA, on one or more GAM336575 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336575 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336575 RNA, herein designated GAM RNA, of GAM336575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336575 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336575 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336575 RNA correlate with, and may be deduced from, the identity of the GAM336575 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336578 7166 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTTGAAAG Messenger 336578 (GAM336578) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336578 is a novel bioinformatically detectable regulatory, non protein

AAATTGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336578 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAGA encoded by the human genome.

CTCCATCTCA GAM336578 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336578 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336578 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336578 precursor RNA is designated SEQ ID:7166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7166 is located from position 28958697 to position 28958796 relative to chromosome 17 on the `-` strand.

GAM336578 precursor RNA folds onto itself, forming GAM336578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336578 precursor RNA, designated SEQ ID NO: 7166, and a schematic representation of a predicted secondary folding of GAM336578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336578 folded precursor RNA yielding a GAM336578 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336578 RNA, hereby incorporated herein.

GAM336578 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336578 target RNA, herein designated GAM TARGET RNA.

GAM336578 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336578 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336578 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336578 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336578 RNA, herein designated GAM RNA, to target binding sites on GAM336578 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336578 target RNA into GAM336578 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336578 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336578 target genes. The mRNA of each one of this

plurality of GAM336578 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336578 RNA, herein designated GAM RNA, and which when bound by GAM336578 RNA causes inhibition of translation of the GAM336578 target mRNA into a corresponding GAM336578 target protein.

The mechanism of the translational inhibition exerted by GAM336578 RNA, herein designated GAM RNA, on one or more GAM336578 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336578 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336578 RNA, herein designated GAM RNA, of GAM336578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336578 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336578 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336578 RNA correlate with, and may be deduced from, the identity of the GAM336578 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336579 6427 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTTGAAAGG Messenger 336579 (GAM336579) oligonucleotides modulates expression of respective target
CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336579 is a novel bioinformatically detectable regulatory, non protein
AATTGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336579 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGCGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGCAAGAC encoded by the human genome.

TCCATCTC GAM336579 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336579 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336579 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336579 precursor RNA is designated SEQ ID:6427, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6427 is located from position 28958698 to position 28958795 relative to chromosome 17 on the `-` strand.

GAM336579 precursor RNA folds onto itself, forming GAM336579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336579 precursor RNA, designated SEQ ID NO: 6427, and a schematic representation of a predicted secondary folding of GAM336579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336579 folded precursor RNA yielding a GAM336579 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336579 RNA, hereby incorporated herein.

GAM336579 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336579 target RNA, herein designated GAM TARGET RNA.

GAM336579 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336579 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336579 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336579 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336579 RNA, herein designated GAM RNA, to target binding sites on GAM336579 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336579 target RNA into GAM336579 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336579 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336579 target genes. The mRNA of each one of this plurality of GAM336579 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336579 RNA, herein designated GAM RNA, and which when bound by GAM336579 RNA causes inhibition of translation of the GAM336579 target mRNA into a corresponding GAM336579 target protein.

The mechanism of the translational inhibition exerted by GAM336579 RNA, herein designated GAM RNA, on one or more GAM336579 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336579 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336579 RNA, herein designated GAM RNA, of GAM336579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336579 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336579 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336579 RNA correlate with, and may be deduced from, the identity of the GAM336579 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336580 6621 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAGCCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAAG Messenger 336580 (GAM336580) oligonucleotides modulates expression of respective target
ATGCAGTGAG genes whose function and utility is known in the art.

CCTGGGTCAT GAM336580 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336580 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACTCC encoded by the human genome.

GAM336580 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336580 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336580 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336580 precursor RNA is designated SEQ ID:6621, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6621 is located from position 28986610 to position 28986698 relative to chromosome 10 on the `+` strand.

GAM336580 precursor RNA folds onto itself, forming GAM336580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336580 precursor RNA, designated SEQ ID NO: 6621, and a schematic representation of a predicted secondary folding of GAM336580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336580 folded precursor RNA yielding a GAM336580 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336580 RNA, hereby incorporated herein. Expression of GAM336580 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336580 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336580 target RNA, herein designated GAM TARGET RNA.

GAM336580 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336580 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336580 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336580 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336580 RNA, herein designated GAM RNA, to target binding sites on GAM336580 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336580 target RNA into GAM336580 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336580 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336580 target genes. The mRNA of each one of this plurality of GAM336580 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336580 RNA, herein designated GAM RNA, and which when bound by GAM336580 RNA causes inhibition of translation of the GAM336580 target mRNA into a corresponding GAM336580 target protein.

The mechanism of the translational inhibition exerted by GAM336580 RNA, herein designated GAM RNA, on one or more GAM336580 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336580 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336580 RNA, herein designated GAM RNA, of GAM336580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336580 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336580 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336580 RNA correlate with, and may be deduced from, the identity of the GAM336580 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336581 6551 GCTGTCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCTGTTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAATGGGGA Messenger 336581 (GAM336581) oligonucleotides modulates expression of respective target
AGATCATCTA genes whose function and utility is known in the art.

GATATTCCAG GAM336581 is a novel bioinformatically detectable regulatory, non protein
TTTCTCCTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336581 was detected
CACTCACCCT is described with additional reference to Figs. 9-15.

ATAGTACCGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAGC encoded by the human genome.

GAM336581 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336581 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336581 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336581 precursor RNA is designated SEQ ID:6551, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6551 is located from position 29024288 to position 29024372 relative to chromosome 8 on the `-` strand.

GAM336581 precursor RNA folds onto itself, forming GAM336581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336581 precursor RNA, designated SEQ ID NO: 6551, and a schematic representation of a predicted secondary folding of GAM336581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336581 folded precursor RNA yielding a GAM336581 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336581 RNA, hereby incorporated herein.

GAM336581 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336581 target RNA, herein designated GAM TARGET RNA.

GAM336581 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336581 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336581 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336581 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336581 RNA, herein designated GAM RNA, to target binding sites on GAM336581 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336581 target RNA into GAM336581 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336581 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336581 target genes. The mRNA of each one of this plurality of GAM336581 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336581 RNA, herein designated GAM RNA, and which when bound by GAM336581 RNA causes inhibition of translation of the GAM336581 target mRNA into a corresponding GAM336581 target protein.

The mechanism of the translational inhibition exerted by GAM336581 RNA, herein designated GAM RNA, on one or more GAM336581 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336581 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336581 RNA, herein designated GAM RNA, of GAM336581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336581 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336581 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336581

RNA correlate with, and may be deduced from, the identity of the GAM336581 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336582 6680 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336582 (GAM336582) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCACGATTGT GAM336582 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336582 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336582 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336582 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336582 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336582 precursor RNA is designated SEQ ID:6680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6680 is located from position 29073962 to position 29074049 relative to chromosome 16 on the `+` strand.

GAM336582 precursor RNA folds onto itself, forming GAM336582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336582 precursor RNA, designated SEQ ID NO: 6680, and a schematic representation of a predicted secondary folding of GAM336582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336582 folded precursor RNA yielding a GAM336582 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336582 RNA, hereby incorporated herein.

GAM336582 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336582 target RNA, herein designated GAM TARGET RNA.

GAM336582 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336582 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336582 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336582 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336582 RNA, herein designated GAM RNA, to target binding sites on GAM336582 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336582 target RNA into GAM336582 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336582 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336582 target genes. The mRNA of each one of this plurality of GAM336582 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336582 RNA, herein designated GAM RNA, and which when bound by GAM336582 RNA causes inhibition of translation of the GAM336582 target mRNA into a corresponding GAM336582 target protein.

The mechanism of the translational inhibition exerted by GAM336582 RNA, herein designated GAM RNA, on one or more GAM336582 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336582 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336582 RNA, herein designated GAM RNA, of GAM336582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336582 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336582 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336582 RNA correlate with, and may be deduced from, the identity of the GAM336582 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336583 6825 GGGTGTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGCACGCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTATCCCAG Messenger 336583 (GAM336583) oligonucleotides modulates expression of respective target
CTACTCAGGA genes whose function and utility is known in the art.

GGCTGAGGTG GAM336583 is a novel bioinformatically detectable regulatory, non protein
GGAGAATCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336583 was detected
CTGAGCCCGG is described with additional reference to Figs. 9-15.

GAGGTAGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGCAGTGAG encoded by the human genome.

TGGAGATCGT GAM336583 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTCACCACAC GAM336583 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TC GAM336583 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336583 precursor RNA is designated SEQ ID:6825, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6825 is located from position 29086596 to position 29086707 relative to chromosome 17 on the `+` strand.

GAM336583 precursor RNA folds onto itself, forming GAM336583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336583 precursor RNA, designated SEQ ID NO: 6825, and a schematic representation of a predicted secondary folding of GAM336583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336583 folded precursor RNA yielding a GAM336583 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336583 RNA, hereby incorporated herein.

GAM336583 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336583 target RNA, herein designated GAM TARGET RNA.

GAM336583 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336583 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336583 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336583 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336583 RNA, herein designated GAM RNA, to target binding sites on GAM336583 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336583 target RNA into GAM336583 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336583 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336583 target genes. The mRNA of each one of this plurality of GAM336583 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336583 RNA, herein designated GAM RNA, and which when bound by GAM336583 RNA causes inhibition of translation of the GAM336583 target mRNA into a corresponding GAM336583 target protein.

The mechanism of the translational inhibition exerted by GAM336583 RNA, herein designated GAM RNA, on one or more GAM336583 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336583 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336583 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336583 RNA, herein designated GAM RNA, of GAM336583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336583 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336583 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336583 RNA correlate with, and may be deduced from, the identity of the GAM336583 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336584 6928 GTGTGGTGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCACGCCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TATCCCAGCT Messenger 336584 (GAM336584) oligonucleotides modulates expression of respective target

ACTCAGGAGG genes whose function and utility is known in the art.

CTGAGGTGGG GAM336584 is a novel bioinformatically detectable regulatory, non protein

AGAATCACCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336584 was detected

GAGCCCGGGA is described with additional reference to Figs. 9-15.

GGTAGAGGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCAGTGAGTG encoded by the human genome.

GAGATCGTGT GAM336584 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CACCACAC GAM336584 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336584 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336584 precursor RNA is designated SEQ ID:6928, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6928 is located from position 29086598 to position 29086705 relative to chromosome 17 on the `+` strand.

GAM336584 precursor RNA folds onto itself, forming GAM336584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336584 precursor RNA, designated SEQ ID NO: 6928, and a schematic representation of a predicted secondary folding of GAM336584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336584 folded precursor RNA yielding a GAM336584 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336584 RNA, hereby incorporated herein.

GAM336584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336584 target RNA, herein designated GAM TARGET RNA.

GAM336584 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336584 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336584 RNA, herein designated GAM RNA, to target binding sites on GAM336584 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336584 target RNA into GAM336584 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336584 target genes. The mRNA of each one of this plurality of GAM336584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336584 RNA, herein designated GAM RNA, and which when bound by GAM336584 RNA causes inhibition of translation of the GAM336584 target mRNA into a corresponding GAM336584 target protein.

The mechanism of the translational inhibition exerted by GAM336584 RNA, herein designated GAM RNA, on one or more GAM336584 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336584 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336584 RNA, herein designated GAM RNA, of GAM336584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336584 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336584 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336584 RNA correlate with, and may be deduced from, the identity of the GAM336584 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336585 7339 TTGTGGTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGATTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAATGGAGC Messenger 336585 (GAM336585) oligonucleotides modulates expression of respective target

CCCAGACCTT genes whose function and utility is known in the art.

CCTGGTGTTA GAM336585 is a novel bioinformatically detectable regulatory, non protein

CAGCTCTCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336585 was detected

AGAAGACAAG is described with additional reference to Figs. 9-15.

GACCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336585 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336585 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336585 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336585 precursor RNA is designated SEQ ID:7339, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:7339 is located from position 29098204 to position 29098280 relative to chromosome 15 on the `+` strand.

GAM336585 precursor RNA folds onto itself, forming GAM336585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336585 precursor RNA, designated SEQ ID NO: 7339, and a schematic representation of a predicted secondary folding of GAM336585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336585 folded precursor RNA yielding a GAM336585 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336585 RNA, hereby incorporated herein.

GAM336585 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336585 target RNA, herein designated GAM TARGET RNA.

GAM336585 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336585 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336585 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336585 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336585 RNA, herein designated GAM RNA, to target binding sites on GAM336585 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336585 target RNA into GAM336585 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336585 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336585 target genes. The mRNA of each one of this plurality of GAM336585 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336585 RNA, herein designated GAM RNA, and which when bound by GAM336585 RNA causes inhibition of translation of the GAM336585 target mRNA into a corresponding GAM336585 target protein.

The mechanism of the translational inhibition exerted by GAM336585 RNA, herein designated GAM RNA, on one or more GAM336585 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336585 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336585 RNA, herein designated GAM RNA, of GAM336585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336585 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336585 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336585 RNA correlate with, and may be deduced from, the identity of the GAM336585 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336586 6692 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCGGAGGT Messenger 336586 (GAM336586) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CGAGATTGTG GAM336586 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336586 was detected

CCAGCCCGGC is described with additional reference to Figs. 9-15.

AACAGAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACTCC encoded by the human genome.

GAM336586 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336586 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336586 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336586 precursor RNA is designated SEQ ID:6692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6692 is located from position 29424019 to position 29424104 relative to chromosome 17 on the `+` strand.

GAM336586 precursor RNA folds onto itself, forming GAM336586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336586 precursor RNA, designated SEQ ID NO: 6692, and a schematic representation of a predicted secondary folding of GAM336586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336586 folded precursor RNA yielding a GAM336586 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336586 RNA, hereby incorporated herein.

GAM336586 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336586 target RNA, herein designated GAM TARGET RNA.

GAM336586 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336586 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336586 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336586 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336586 RNA, herein designated GAM RNA, to target binding sites on GAM336586 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336586 target RNA into GAM336586 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336586 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336586 target genes. The mRNA of each one of this plurality of GAM336586 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336586 RNA, herein designated GAM RNA, and which when bound by GAM336586 RNA causes inhibition of translation of the GAM336586 target mRNA into a corresponding GAM336586 target protein.

The mechanism of the translational inhibition exerted by GAM336586 RNA, herein designated GAM RNA, on one or more GAM336586 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336586 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336586 RNA, herein designated GAM RNA, of GAM336586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336586 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336586 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336586 RNA correlate with, and may be deduced from, the identity of the GAM336586 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336587 6717 GGATACATAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGTCACTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTTAAGAT Messenger 336587 (GAM336587) oligonucleotides modulates expression of respective target

GTTTGCATTT genes whose function and utility is known in the art.

CAGCACTTTT GAM336587 is a novel bioinformatically detectable regulatory, non protein

ATAATTCAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336587 was detected

TATGGTGCTG is described with additional reference to Figs. 9-15.

TCCCTTGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTCTTGTTGA encoded by the human genome.

GAGCCACATG GAM336587 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TATCT GAM336587 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336587 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336587 precursor RNA is designated SEQ ID:6717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6717 is located from position 29435833 to position 29435937 relative to chromosome 7 on the `+` strand.

GAM336587 precursor RNA folds onto itself, forming GAM336587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336587 precursor RNA, designated SEQ ID NO: 6717, and a schematic representation of a predicted secondary folding of GAM336587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336587 folded precursor RNA yielding a GAM336587 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336587 RNA, hereby incorporated herein.

GAM336587 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336587 target RNA, herein designated GAM TARGET RNA.

GAM336587 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336587 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336587 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336587 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336587 RNA, herein designated GAM RNA, to target binding sites on GAM336587 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336587 target RNA into GAM336587 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336587 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336587 target genes. The mRNA of each one of this plurality of GAM336587 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336587 RNA, herein designated GAM RNA, and which when bound by GAM336587 RNA causes inhibition of translation of the GAM336587 target mRNA into a corresponding GAM336587 target protein.

The mechanism of the translational inhibition exerted by GAM336587 RNA, herein designated GAM RNA, on one or more GAM336587 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336587 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336587 RNA, herein designated GAM RNA, of GAM336587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336587 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336587 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336587 RNA correlate with, and may be deduced from, the identity of the GAM336587 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336588 6467 GATACATAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGTCACTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTAAGATG Messenger 336588 (GAM336588) oligonucleotides modulates expression of respective target
TTTGCATTTC genes whose function and utility is known in the art.

AGCACTTTTA GAM336588 is a novel bioinformatically detectable regulatory, non protein
TAATTCAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336588 was detected
ATGGTGCTGT is described with additional reference to Figs. 9-15.

CCCTTGAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTGTTGAG encoded by the human genome.

AGCCACATGT GAM336588 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ATC GAM336588 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336588 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336588 precursor RNA is designated SEQ ID:6467, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6467 is located from position 29435834 to position 29435936 relative to chromosome 7 on the `+` strand.

GAM336588 precursor RNA folds onto itself, forming GAM336588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336588 precursor RNA, designated SEQ ID NO: 6467, and a schematic representation of a predicted secondary folding of GAM336588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336588 folded precursor RNA yielding a GAM336588 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336588 RNA, hereby incorporated herein.

GAM336588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336588 target RNA, herein designated GAM TARGET RNA.

GAM336588 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336588 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336588 RNA, herein designated GAM RNA, to target binding sites on GAM336588 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336588 target RNA into GAM336588 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336588 target genes. The mRNA of each one of this plurality of GAM336588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336588 RNA, herein designated GAM RNA, and which when bound by GAM336588 RNA causes inhibition of translation of the GAM336588 target mRNA into a corresponding GAM336588 target protein.

The mechanism of the translational inhibition exerted by GAM336588 RNA, herein designated GAM RNA, on one or more GAM336588 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336588 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336588 RNA, herein designated GAM RNA, of GAM336588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336588 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336588 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336588 RNA correlate with, and may be deduced from, the identity of the GAM336588 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336589 6817 GGGGGCCACA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCTCTGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTCAGAAGC Messenger 336589 (GAM336589) oligonucleotides modulates expression of respective target
CAGGATTTCA genes whose function and utility is known in the art.

TAGGCCATGA GAM336589 is a novel bioinformatically detectable regulatory, non protein
AATCTGCTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336589 was detected
CTTTTAGAAG is described with additional reference to Figs. 9-15.

TGGGCTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336589 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336589 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336589 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336589 precursor RNA is designated SEQ ID:6817, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6817 is located from position 29509893 to position 29509970 relative to chromosome 22 on the `+` strand.

GAM336589 precursor RNA folds onto itself, forming GAM336589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336589 precursor RNA, designated SEQ ID NO: 6817, and a schematic representation of a predicted secondary folding of GAM336589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336589 folded precursor RNA yielding a GAM336589 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336589 RNA, hereby incorporated herein.

GAM336589 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336589 target RNA, herein designated GAM TARGET RNA.

GAM336589 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336589 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336589 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336589 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336589 RNA, herein designated GAM RNA, to target binding sites on GAM336589 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336589 target RNA into GAM336589 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336589 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336589 target genes. The mRNA of each one of this plurality of GAM336589 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336589 RNA, herein designated GAM RNA, and which when bound by GAM336589 RNA causes inhibition of translation of the GAM336589 target mRNA into a corresponding GAM336589 target protein.

The mechanism of the translational inhibition exerted by GAM336589 RNA, herein designated GAM RNA, on one or more GAM336589 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336589 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336589 RNA, herein designated GAM RNA, of GAM336589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336589 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336589 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336589 RNA correlate with, and may be deduced from, the identity of the GAM336589 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336590 6083 CCCTAAAAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GACTGAATTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCAAGTGCT Messenger 336590 (GAM336590) oligonucleotides modulates expression of respective target
TGAACATGGC genes whose function and utility is known in the art.

AGAGGTAGTT GAM336590 is a novel bioinformatically detectable regulatory, non protein
ACTCCTATTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336590 was detected
TGCAGTTTGT is described with additional reference to Figs. 9-15.

GCACTTAAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTCCTACAG encoded by the human genome.

TGATTGTTAC GAM336590 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTTACTGGGG GAM336590 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336590 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336590 precursor RNA is designated SEQ ID:6083, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6083 is located from position 29554384 to position 29554493 relative to chromosome 12 on the `-` strand.

GAM336590 precursor RNA folds onto itself, forming GAM336590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336590 precursor RNA, designated SEQ ID NO: 6083, and a schematic representation of a predicted secondary folding of GAM336590 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336590 folded precursor RNA yielding a GAM336590 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336590 RNA, hereby incorporated herein.

GAM336590 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336590 target RNA, herein designated GAM TARGET RNA.

GAM336590 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336590 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336590 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336590 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336590 RNA, herein designated GAM RNA, to target binding sites on GAM336590 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336590 target RNA into GAM336590 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336590 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336590 target genes. The mRNA of each one of this plurality of GAM336590 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336590 RNA, herein designated GAM RNA, and which when bound by GAM336590 RNA causes inhibition of translation of the GAM336590 target mRNA into a corresponding GAM336590 target protein.

The mechanism of the translational inhibition exerted by GAM336590 RNA, herein designated GAM RNA, on one or more GAM336590 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336590 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336590 RNA, herein designated GAM RNA, of GAM336590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336590 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336590 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336590 RNA correlate with, and may be deduced from, the identity of the GAM336590 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336591 5853 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336591 (GAM336591) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336591 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336591 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336591 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336591 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336591 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336591 precursor RNA is designated SEQ ID:5853, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5853 is located from position 29889968 to position 29890049 relative to chromosome 18 on the `+` strand.

GAM336591 precursor RNA folds onto itself, forming GAM336591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336591 precursor RNA, designated SEQ ID NO: 5853, and a schematic representation of a predicted secondary folding of GAM336591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336591 folded precursor RNA yielding a GAM336591 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336591 RNA, hereby incorporated herein.

GAM336591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336591 target RNA, herein designated GAM TARGET RNA.

GAM336591 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336591 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336591 RNA, herein designated GAM RNA, to target binding sites on GAM336591 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336591 target RNA into GAM336591 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336591 target genes. The mRNA of each one of this plurality of GAM336591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336591 RNA, herein designated GAM RNA, and which when bound by GAM336591 RNA causes inhibition of translation of the GAM336591 target mRNA into a corresponding GAM336591 target protein.

The mechanism of the translational inhibition exerted by GAM336591 RNA, herein designated GAM RNA, on one or more GAM336591 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336591 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336591 RNA, herein designated GAM RNA, of GAM336591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336591 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336591 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336591 RNA correlate with, and may be deduced from, the identity of the GAM336591 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336592 6777 GGGACAAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATGAGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAAGGCCGT Messenger 336592 (GAM336592) oligonucleotides modulates expression of respective target

AGGGAAGGGC genes whose function and utility is known in the art.

TTCTCTCCTA GAM336592 is a novel bioinformatically detectable regulatory, non protein

CCTCCCACGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336592 was detected

CTTTATCTGT is described with additional reference to Figs. 9-15.

CCAAATCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTATTTCCC encoded by the human genome.

GAM336592 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336592 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336592 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336592 precursor RNA is designated SEQ

ID:6777, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6777 is located from position 30010422 to position 30010511 relative to chromosome 22 on the `+` strand.

GAM336592 precursor RNA folds onto itself, forming GAM336592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336592 precursor RNA, designated SEQ ID NO: 6777, and a schematic representation of a predicted secondary folding of GAM336592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336592 folded precursor RNA yielding a GAM336592 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336592 RNA, hereby incorporated herein.

GAM336592 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336592 target RNA, herein designated GAM TARGET RNA.

GAM336592 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336592 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336592 RNA, herein designated GAM RNA, to target binding sites on GAM336592 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336592 target RNA into GAM336592 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336592 target genes. The mRNA of each one of this plurality of GAM336592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336592 RNA, herein designated GAM RNA, and which when bound by GAM336592 RNA causes inhibition of translation of the GAM336592 target mRNA into a corresponding GAM336592 target protein.

The mechanism of the translational inhibition exerted by GAM336592 RNA, herein designated GAM RNA, on one or more GAM336592 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336592 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336592 RNA, herein designated GAM RNA, of GAM336592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336592 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336592 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336592 RNA correlate with, and may be deduced from, the identity of the GAM336592 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336593 6953 TAAATCTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGAGGGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCATGTCCAC Messenger 336593 (GAM336593) oligonucleotides modulates expression of respective target

ACCAGGTGCC genes whose function and utility is known in the art.

CAGACATCTG GAM336593 is a novel bioinformatically detectable regulatory, non protein

GTTGGCTTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336593 was detected

GCTGATTTGT is described with additional reference to Figs. 9-15.

CCTGCAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGCCTTGT encoded by the human genome.

CTGGATTTGC GAM336593 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

ACACTTTCCA GAM336593 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AGTTGCCCAT GAM336593 precursor RNA does not encode a protein. A nucleotide sequence identical or

TA highly similar to the nucleotide sequence of GAM336593 precursor RNA is designated SEQ ID:6953, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6953 is located from position 30068447 to position 30068568 relative to chromosome 15 on the `+` strand.

GAM336593 precursor RNA folds onto itself, forming GAM336593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336593 precursor RNA, designated SEQ ID NO: 6953, and a schematic representation of a predicted secondary folding of GAM336593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336593 folded precursor RNA yielding a GAM336593 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336593 RNA, hereby incorporated herein.

GAM336593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336593 target RNA, herein designated GAM TARGET RNA.

GAM336593 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336593 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336593 RNA, herein designated GAM RNA, to target binding sites on GAM336593 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336593 target RNA into GAM336593 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336593 target genes. The mRNA of each one of this plurality of GAM336593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336593 RNA, herein designated GAM RNA, and which when bound by GAM336593 RNA causes inhibition of translation of the GAM336593 target mRNA into a corresponding GAM336593 target protein.

The mechanism of the translational inhibition exerted by GAM336593 RNA, herein designated GAM RNA, on one or more GAM336593 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336593 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336593 RNA, herein designated GAM RNA, of GAM336593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336593 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336593 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336593 RNA correlate with, and may be deduced from, the identity of the GAM336593 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336594 7238 TGGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAAGCATGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCACACCAGG Messenger 336594 (GAM336594) oligonucleotides modulates expression of respective target

TGCCCAGACA genes whose function and utility is known in the art.

TCTGGTTGGC GAM336594 is a novel bioinformatically detectable regulatory, non protein
TTTGGCTGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336594 was detected
TTGTCCTGCA is described with additional reference to Figs. 9-15.

GGCACCTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGTCTGGAT encoded by the human genome.

TTGCACACTT GAM336594 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCCAAGTTGC GAM336594 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CCA GAM336594 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336594 precursor RNA is designated SEQ ID:7238, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7238 is located from position 30068453 to position 30068565 relative to chromosome 15 on the `+` strand.

GAM336594 precursor RNA folds onto itself, forming GAM336594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336594 precursor RNA, designated SEQ ID NO: 7238, and a schematic representation of a predicted secondary folding of GAM336594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336594 folded precursor RNA yielding a GAM336594 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336594 RNA, hereby incorporated herein.

GAM336594 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336594 target RNA, herein designated GAM TARGET RNA.

GAM336594 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336594 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336594 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336594 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336594 RNA, herein designated GAM RNA, to target binding sites on GAM336594 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336594 target RNA into GAM336594 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336594 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336594 target genes. The mRNA of each one of this plurality of GAM336594 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336594 RNA, herein designated GAM RNA, and which when bound by GAM336594 RNA causes inhibition of translation of the GAM336594 target mRNA into a corresponding GAM336594 target protein.

The mechanism of the translational inhibition exerted by GAM336594 RNA, herein designated GAM RNA, on one or more GAM336594 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336594 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336594 RNA, herein designated GAM RNA, of GAM336594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336594 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336594 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336594 RNA correlate with, and may be deduced from, the identity of the GAM336594 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336595 6787 GGGAGCTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCAAAACA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAGATGTCT Messenger 336595 (GAM336595) oligonucleotides modulates expression of respective target

TCTTTTCCCT genes whose function and utility is known in the art.

TAGCCCTTGG GAM336595 is a novel bioinformatically detectable regulatory, non protein

TTTTGTTTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336595 was detected

CAGATGGTGT is described with additional reference to Figs. 9-15.

AGGTGAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACATTAGTT encoded by the human genome.

GTGGAAGAGG GAM336595 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TATGTATGAC GAM336595 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TCCC GAM336595 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336595 precursor RNA is designated SEQ ID:6787, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6787 is located from position 30119301 to position 30119414 relative to chromosome 8 on the `+` strand.

GAM336595 precursor RNA folds onto itself, forming GAM336595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336595 precursor RNA, designated SEQ ID NO: 6787, and a schematic representation of a predicted secondary folding of GAM336595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336595 folded precursor RNA yielding a GAM336595 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336595 RNA, hereby incorporated herein.

GAM336595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336595 target RNA, herein designated GAM TARGET RNA.

GAM336595 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336595 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336595 RNA, herein designated GAM RNA, to target binding sites on GAM336595 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336595 target RNA into GAM336595 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336595 target genes. The mRNA of each one of this plurality of GAM336595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336595 RNA, herein designated GAM RNA, and which when bound by GAM336595 RNA causes inhibition of translation of the GAM336595 target mRNA into a corresponding GAM336595 target protein.

The mechanism of the translational inhibition exerted by GAM336595 RNA, herein designated GAM RNA, on one or more GAM336595 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336595 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336595 RNA, herein designated GAM RNA, of GAM336595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336595 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336595 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336595 RNA correlate with, and may be deduced from, the identity of the GAM336595 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336596 6190 CTCTTTTGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAACAAAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTCTTCTTT Messenger 336596 (GAM336596) oligonucleotides modulates expression of respective target
TCCCTTAGCC genes whose function and utility is known in the art.

CTTGGTTTTG GAM336596 is a novel bioinformatically detectable regulatory, non protein
TTTGGCAGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336596 was detected
GGTGTAGGTG is described with additional reference to Figs. 9-15.

AAGAGAACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGTTGTGGA encoded by the human genome.

AGAG GAM336596 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336596 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336596 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336596 precursor RNA is designated SEQ ID:6190, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6190 is located from position 30119306 to position 30119399 relative to chromosome 8 on the `+` strand.

GAM336596 precursor RNA folds onto itself, forming GAM336596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336596 precursor RNA, designated SEQ ID NO: 6190, and a schematic representation of a predicted secondary folding of GAM336596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336596 folded precursor RNA yielding a GAM336596 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336596 RNA, hereby incorporated herein.

GAM336596 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336596 target RNA, herein designated GAM TARGET RNA.

GAM336596 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336596 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336596 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336596 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336596 RNA, herein designated GAM RNA, to target binding sites on GAM336596 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336596 target RNA into GAM336596 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336596 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336596 target genes. The mRNA of each one of this plurality of GAM336596 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336596 RNA, herein designated GAM RNA, and which when bound by GAM336596 RNA causes inhibition of translation of the GAM336596 target mRNA into a corresponding GAM336596 target protein.

The mechanism of the translational inhibition exerted by GAM336596 RNA, herein designated GAM RNA, on one or more GAM336596 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336596 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336596 RNA, herein designated GAM RNA, of GAM336596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336596 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336596 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336596 RNA correlate with, and may be deduced from, the identity of the GAM336596 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336597 6147 CGGTGAGATG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTGAAAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGACATCGAG Messenger 336597 (GAM336597) oligonucleotides modulates expression of respective target
AAGTTTTAAT genes whose function and utility is known in the art.

ATTCAGAATC GAM336597 is a novel bioinformatically detectable regulatory, non protein
TTTTCTTCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336597 was detected
AAGACGCTGA is described with additional reference to Figs. 9-15.

ATGTAATCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTTGTAAAT encoded by the human genome.

ACCCATCACC GAM336597 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGCCAGTCAC GAM336597 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CG GAM336597 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336597 precursor RNA is designated SEQ ID:6147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6147 is located from position 30195269 to position 30195380 relative to chromosome 7 on the `-` strand.

GAM336597 precursor RNA folds onto itself, forming GAM336597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336597 precursor RNA, designated SEQ ID NO: 6147, and a schematic representation of a predicted secondary folding of GAM336597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336597 folded precursor RNA yielding a GAM336597 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336597 RNA, hereby incorporated herein.

GAM336597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336597 target RNA, herein designated GAM TARGET RNA.

GAM336597 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336597 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336597 RNA, herein designated GAM RNA, to target binding sites on GAM336597 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336597 target RNA into GAM336597 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336597 target genes. The mRNA of each one of this plurality of GAM336597 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336597 RNA, herein designated GAM RNA, and which when bound by GAM336597 RNA causes inhibition of translation of the GAM336597 target mRNA into a corresponding GAM336597 target protein.

The mechanism of the translational inhibition exerted by GAM336597 RNA, herein

designated GAM RNA, on one or more GAM336597 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336597 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336597 RNA, herein designated GAM RNA, of GAM336597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336597 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336597 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336597 RNA correlate with, and may be deduced from, the identity of the GAM336597 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336598 5854 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336598 (GAM336598) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336598 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336598 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336598 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336598 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336598 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336598 precursor RNA is designated SEQ ID:5854, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5854 is located from position 30200618 to position 30200699

relative to chromosome 11 on the `+` strand.

GAM336598 precursor RNA folds onto itself, forming GAM336598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336598 precursor RNA, designated SEQ ID NO: 5854, and a schematic representation of a predicted secondary folding of GAM336598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336598 folded precursor RNA yielding a GAM336598 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336598 RNA, hereby incorporated herein.

GAM336598 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336598 target RNA, herein designated GAM TARGET RNA.

GAM336598 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336598 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336598 RNA, herein designated GAM RNA, to target binding sites on GAM336598 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336598 target RNA into GAM336598 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336598 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336598 target genes. The mRNA of each one of this plurality of GAM336598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336598 RNA, herein designated GAM RNA, and which when bound by GAM336598 RNA causes inhibition of translation of the GAM336598 target mRNA into a corresponding GAM336598 target protein.

The mechanism of the translational inhibition exerted by GAM336598 RNA, herein designated GAM RNA, on one or more GAM336598 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336598 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336598 RNA, herein designated GAM RNA, of GAM336598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336598 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336598 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336598 RNA correlate with, and may be deduced from, the identity of the GAM336598 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336599 7150 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGGAG Messenger 336599 (GAM336599) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCCG GAM336599 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336599 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGG encoded by the human genome.

AATTCTGTCT GAM336599 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336599 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336599 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336599 precursor RNA is designated SEQ ID:7150, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7150 is located from position 30643328 to position 30643429 relative to chromosome 16 on the `+` strand.

GAM336599 precursor RNA folds onto itself, forming GAM336599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336599 precursor RNA, designated SEQ ID NO: 7150, and a schematic representation of a predicted secondary folding of GAM336599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336599 folded precursor RNA yielding a GAM336599 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336599 RNA, hereby incorporated herein. Expression of GAM336599 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336599 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336599 target RNA, herein designated GAM TARGET RNA.

GAM336599 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336599 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336599 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336599 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336599 RNA, herein designated GAM RNA, to target binding sites on GAM336599 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336599 target RNA into GAM336599 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336599 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336599 target genes. The mRNA of each one of this plurality of GAM336599 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336599 RNA, herein designated GAM RNA, and which when bound by GAM336599 RNA causes inhibition of translation of the GAM336599 target mRNA into a corresponding GAM336599 target protein.

The mechanism of the translational inhibition exerted by GAM336599 RNA, herein designated GAM RNA, on one or more GAM336599 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336599 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336599 RNA, herein designated GAM RNA, of GAM336599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336599 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336599 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336599 RNA correlate with, and may be deduced from, the identity of the GAM336599 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336600 6404 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTTA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 336600 (GAM336600) oligonucleotides modulates expression of respective target

CAGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCGA GAM336600 is a novel bioinformatically detectable regulatory, non protein
GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336600 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCGGA encoded by the human genome.

ATTCTGTCTC GAM336600 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336600 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336600 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336600 precursor RNA is designated SEQ ID:6404, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6404 is located from position 30643329 to position 30643428 relative to chromosome 16 on the `+` strand.

GAM336600 precursor RNA folds onto itself, forming GAM336600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336600 precursor RNA, designated SEQ ID NO: 6404, and a schematic representation of a predicted secondary folding of GAM336600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336600 folded precursor RNA yielding a GAM336600 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336600 RNA, hereby incorporated herein. Expression of GAM336600 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336600 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336600 target RNA, herein designated GAM TARGET RNA.

GAM336600 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336600 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336600 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336600 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336600 RNA, herein designated GAM RNA, to target binding sites on GAM336600 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336600 target RNA into GAM336600 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336600 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336600 target genes. The mRNA of each one of this plurality of GAM336600 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336600 RNA, herein designated GAM RNA, and which when bound by GAM336600 RNA causes inhibition of translation of the GAM336600 target mRNA into a corresponding GAM336600 target protein.

The mechanism of the translational inhibition exerted by GAM336600 RNA, herein designated GAM RNA, on one or more GAM336600 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336600 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336600 RNA, herein designated GAM RNA, of GAM336600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336600 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336600 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336600 RNA correlate with, and may be deduced from, the identity of the GAM336600 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336601 6024 CAGGCAGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATGATCTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGGAGTAA Messenger 336601 (GAM336601) oligonucleotides modulates expression of respective target
AATGTCAGGT genes whose function and utility is known in the art.

GTTTTTTTTT GAM336601 is a novel bioinformatically detectable regulatory, non protein
TTAAGAAATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336601 was detected
GATTTTTAGT is described with additional reference to Figs. 9-15.

TGTGACGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTGGCAGGC encoded by the human genome.

TGTCCACGGT GAM336601 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ATCACTTTCT GAM336601 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GCTTATTTTT GAM336601 precursor RNA does not encode a protein. A nucleotide sequence identical or

AAAAGGTCTG highly similar to the nucleotide sequence of GAM336601 precursor RNA is designated SEQ
ID:6024, and is provided hereinbelow with reference to the sequence listing part.
Nucleotide sequence SEQ ID:6024 is located from position 30673441 to position 30673570 relative to chromosome 13 on the `+` strand.

GAM336601 precursor RNA folds onto itself, forming GAM336601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336601 precursor RNA, designated SEQ ID NO: 6024, and a schematic representation of a predicted secondary folding of GAM336601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336601 folded precursor RNA yielding a GAM336601 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336601 RNA, hereby incorporated herein.

GAM336601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336601 target RNA, herein designated GAM TARGET RNA.

GAM336601 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336601 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336601 RNA, herein designated GAM RNA, to target binding sites on GAM336601 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336601 target RNA into GAM336601 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336601 target genes. The mRNA of each one of this plurality of GAM336601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336601 RNA, herein designated GAM RNA, and which when bound by GAM336601 RNA causes inhibition of translation of the GAM336601 target mRNA into a corresponding GAM336601 target protein.

The mechanism of the translational inhibition exerted by GAM336601 RNA, herein designated GAM RNA, on one or more GAM336601 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336601 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336601 RNA, herein designated GAM RNA, of GAM336601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336601 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336601 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336601 RNA correlate with, and may be deduced from, the identity of the GAM336601 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336602 7171 TGAGGCCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336602 (GAM336602) oligonucleotides modulates expression of respective target
GTAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM336602 is a novel bioinformatically detectable regulatory, non protein
AGATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336602 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCTAG encoded by the human genome.

ACTCTGCCTC GAM336602 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336602 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336602 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336602 precursor RNA is designated SEQ ID:7171, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7171 is located from position 30748368 to position 30748468 relative to chromosome 10 on the `+` strand.

GAM336602 precursor RNA folds onto itself, forming GAM336602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336602 precursor RNA, designated SEQ ID NO: 7171, and a schematic representation of a predicted secondary folding of GAM336602 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336602 folded precursor RNA yielding a GAM336602 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336602 RNA, hereby incorporated herein. Expression of GAM336602 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336602 target RNA, herein designated GAM TARGET RNA.

GAM336602 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336602 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336602 RNA, herein designated GAM RNA, to target binding sites on GAM336602 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336602 target RNA into GAM336602 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336602 target genes. The mRNA of each one of this plurality of GAM336602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336602 RNA, herein designated GAM RNA, and which when bound by GAM336602 RNA causes inhibition of translation of the GAM336602 target mRNA into a corresponding GAM336602 target protein.

The mechanism of the translational inhibition exerted by GAM336602 RNA, herein designated GAM RNA, on one or more GAM336602 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336602 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336602 RNA, herein designated GAM RNA, of GAM336602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336602 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336602 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336602 RNA correlate with, and may be deduced from, the identity of the GAM336602 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336605 7202 TGCTAAAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAGGGGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTTGTCAGA Messenger 336605 (GAM336605) oligonucleotides modulates expression of respective target

CTATTTTGTC genes whose function and utility is known in the art.

TATAACTAGG GAM336605 is a novel bioinformatically detectable regulatory, non protein

GTAGCCATAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336605 was detected

ATGCCAATTT is described with additional reference to Figs. 9-15.

CCCCAAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCTTGATTA encoded by the human genome.

GCTTCTATTT GAM336605 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTTGGCA GAM336605 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336605 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336605 precursor RNA is designated SEQ ID:7202, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7202 is located from position 31058191 to position 31058297 relative to chromosome 8 on the `+` strand.

GAM336605 precursor RNA folds onto itself, forming GAM336605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336605 precursor RNA, designated SEQ ID NO: 7202, and a schematic representation of a predicted secondary folding of GAM336605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336605 folded precursor RNA yielding a GAM336605 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336605 RNA, hereby incorporated herein.

GAM336605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336605 target RNA, herein designated GAM TARGET RNA.

GAM336605 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336605 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336605 RNA, herein designated GAM RNA, to target binding sites on GAM336605 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336605 target RNA into GAM336605 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336605 target genes. The mRNA of each one of this plurality of GAM336605 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336605 RNA, herein designated GAM RNA, and which when bound by GAM336605 RNA causes inhibition of translation of the GAM336605 target mRNA into a corresponding GAM336605 target protein.

The mechanism of the translational inhibition exerted by GAM336605 RNA, herein designated GAM RNA, on one or more GAM336605 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336605 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336605 RNA, herein designated GAM RNA, of GAM336605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336605 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336605 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336605 RNA correlate with, and may be deduced from, the identity of the GAM336605 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336606 6732 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCACTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGAGGCA Messenger 336606 (GAM336606) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TGAGCCAAGA GAM336606 is a novel bioinformatically detectable regulatory, non protein

TCATGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336606 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAATGAAAC encoded by the human genome.

TCTGTC GAM336606 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336606 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336606 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336606 precursor RNA is designated SEQ ID:6732, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6732 is located from position 31418591 to position 31418686 relative to chromosome 1 on the `+` strand.

GAM336606 precursor RNA folds onto itself, forming GAM336606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336606 precursor RNA, designated SEQ ID NO: 6732, and a schematic representation of a predicted secondary folding of GAM336606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336606 folded precursor RNA yielding a GAM336606 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336606 RNA, hereby incorporated herein. Expression of GAM336606 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336606 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336606 target RNA, herein designated GAM TARGET RNA.

GAM336606 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336606 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336606 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336606 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336606 RNA, herein designated GAM RNA, to target binding sites on GAM336606 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336606 target RNA into GAM336606 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336606 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336606 target genes. The mRNA of each one of this plurality of GAM336606 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336606 RNA, herein designated GAM RNA, and which when bound by GAM336606 RNA causes inhibition of translation of the GAM336606 target mRNA into a corresponding GAM336606 target protein.

The mechanism of the translational inhibition exerted by GAM336606 RNA, herein designated GAM RNA, on one or more GAM336606 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336606 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336606 RNA, herein designated GAM RNA, of GAM336606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336606 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336606 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336606 RNA correlate with, and may be deduced from, the identity of the GAM336606 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336607 7155 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336607 (GAM336607) oligonucleotides modulates expression of respective target

GCAGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCC GAM336607 is a novel bioinformatically detectable regulatory, non protein

AGATTGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336607 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCGAG encoded by the human genome.

ACTCCGTCTC GAM336607 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336607 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336607 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336607 precursor RNA is designated SEQ ID:7155, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7155 is located from position 31554609 to position 31554709 relative to chromosome 6 on the `+` strand.

GAM336607 precursor RNA folds onto itself, forming GAM336607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336607 precursor RNA, designated SEQ ID NO: 7155, and a schematic representation of a predicted secondary folding of GAM336607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336607 folded precursor RNA yielding a GAM336607 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336607 RNA, hereby incorporated herein. Expression of GAM336607 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336607 target RNA, herein designated GAM TARGET RNA.

GAM336607 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336607 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336607 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336607 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336607 RNA, herein designated GAM RNA, to target binding sites on GAM336607 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336607 target RNA into GAM336607 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336607 target genes. The mRNA of each one of this plurality of GAM336607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336607 RNA, herein designated GAM RNA, and which when bound by GAM336607 RNA causes inhibition of translation of the GAM336607 target mRNA into a corresponding GAM336607 target protein.

The mechanism of the translational inhibition exerted by GAM336607 RNA, herein designated GAM RNA, on one or more GAM336607 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336607 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336607 RNA, herein designated GAM RNA, of GAM336607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336607 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336607 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336607 RNA correlate with, and may be deduced from, the identity of the GAM336607 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336608 6411 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATGGCGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGAGG Messenger 336608 (GAM336608) oligonucleotides modulates expression of respective target
CAGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCCCA GAM336608 is a novel bioinformatically detectable regulatory, non protein
GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336608 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCCGTCTC GAM336608 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336608 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336608 precursor RNA is designated SEQ ID:6411, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6411 is located from position 31554610 to position 31554708 relative to chromosome 6 on the `+` strand.

GAM336608 precursor RNA folds onto itself, forming GAM336608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336608 precursor RNA, designated SEQ ID NO: 6411, and a schematic representation of a predicted secondary folding of GAM336608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336608 folded precursor RNA yielding a GAM336608 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336608 RNA, hereby incorporated herein. Expression of GAM336608 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336608 target RNA, herein designated GAM TARGET RNA.

GAM336608 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336608 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336608 RNA, herein designated GAM RNA, to target binding sites on GAM336608 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336608 target RNA into GAM336608 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336608 target genes. The mRNA of each one of this plurality of GAM336608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336608 RNA, herein designated GAM RNA, and which when bound by GAM336608 RNA causes inhibition of translation of the GAM336608 target mRNA into a corresponding GAM336608 target protein.

The mechanism of the translational inhibition exerted by GAM336608 RNA, herein designated GAM RNA, on one or more GAM336608 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336608 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336608 RNA, herein designated GAM RNA, of GAM336608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336608 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336608 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336608 RNA correlate with, and may be deduced from, the identity of the GAM336608 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336609 6469 GATCATAAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCCTGAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CACGTTGCAT Messenger 336609 (GAM336609) oligonucleotides modulates expression of respective target
CTGTGTCTCT genes whose function and utility is known in the art.

AGCAACTTCC GAM336609 is a novel bioinformatically detectable regulatory, non protein
ACAAATGTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336609 was detected
GGAGAATAAA is described with additional reference to Figs. 9-15.

TTAATGTGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAGGGCGCG encoded by the human genome.

GTC GAM336609 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336609 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336609 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336609 precursor RNA is designated SEQ ID:6469, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6469 is located from position 31572572 to position 31572664 relative to chromosome 10 on the `-` strand.

GAM336609 precursor RNA folds onto itself, forming GAM336609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336609 precursor RNA, designated SEQ ID NO: 6469, and a schematic representation of a predicted secondary folding of GAM336609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336609 folded precursor RNA yielding a GAM336609 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336609 RNA, hereby incorporated herein.

GAM336609 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336609 target RNA, herein designated GAM TARGET RNA.

GAM336609 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336609 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336609 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336609 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336609 RNA, herein designated GAM RNA, to target binding sites on GAM336609 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336609 target RNA into GAM336609 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336609 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336609 target genes. The mRNA of each one of this plurality of GAM336609 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336609 RNA, herein designated GAM RNA, and which when bound by GAM336609 RNA causes inhibition of translation of the GAM336609 target mRNA into a corresponding GAM336609 target protein.

The mechanism of the translational inhibition exerted by GAM336609 RNA, herein designated GAM RNA, on one or more GAM336609 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336609 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336609 RNA, herein designated GAM RNA, of GAM336609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336609 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336609 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336609 RNA correlate with, and may be deduced from, the identity of the GAM336609 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336610 6205 CTGAGGCAGG AGAATGGCAT GAACCCAGGA GGTGGAGCTT GCAGTGAGCC GAGATCACGC CACTGCACTC CAGCCTGGGC AACACAGCGA GACTCCGTCT CAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336610 (GAM336610) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336610 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336610 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336610 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336610 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336610 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336610 precursor RNA is designated SEQ ID:6205, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6205 is located from position 31820024 to position 31820126 relative to chromosome 6 on the `+` strand.

GAM336610 precursor RNA folds onto itself, forming GAM336610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336610 precursor RNA, designated SEQ ID NO: 6205, and a schematic representation of a predicted secondary folding of GAM336610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336610 folded precursor RNA yielding a GAM336610 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336610 RNA, hereby incorporated herein. Expression of GAM336610 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336610 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336610 target RNA, herein designated GAM TARGET RNA.

GAM336610 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336610 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336610 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336610 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336610 RNA, herein designated GAM RNA, to target binding sites on GAM336610 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336610 target RNA into GAM336610 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336610 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336610 target genes. The mRNA of each one of this plurality of GAM336610 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336610 RNA, herein designated GAM RNA, and which when bound by GAM336610 RNA causes inhibition of translation of the GAM336610 target mRNA into a corresponding GAM336610 target protein.

The mechanism of the translational inhibition exerted by GAM336610 RNA, herein designated GAM RNA, on one or more GAM336610 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336610 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336610 RNA, herein designated GAM RNA, of GAM336610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336610 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336610 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336610 RNA correlate with, and may be deduced from, the identity of the GAM336610 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336611 6838 GGTCGTTTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTTCAGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGTTCTT Messenger 336611 (GAM336611) oligonucleotides modulates expression of respective target

CATACACATG genes whose function and utility is known in the art.

GATGTCTCAC GAM336611 is a novel bioinformatically detectable regulatory, non protein

AGATCAGCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336611 was detected

AGGCCTGTGT is described with additional reference to Figs. 9-15.

TTGAACACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCACCCC encoded by the human genome.

TGCAAGGAGC GAM336611 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336611 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336611 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336611 precursor RNA is designated SEQ ID:6838, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6838 is located from position 32058440 to position 32058540 relative to chromosome 18 on the `+` strand.

GAM336611 precursor RNA folds onto itself, forming GAM336611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336611 precursor RNA, designated SEQ ID NO: 6838, and a schematic representation of a predicted secondary folding of GAM336611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336611 folded precursor RNA yielding a GAM336611 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336611 RNA, hereby incorporated herein.

GAM336611 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336611 target RNA, herein designated GAM TARGET RNA.

GAM336611 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336611 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336611 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336611 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336611 RNA, herein designated GAM RNA, to target binding sites on GAM336611 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336611 target RNA into GAM336611 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336611 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336611 target genes. The mRNA of each one of this plurality of GAM336611 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336611 RNA, herein designated GAM RNA, and which when bound by GAM336611 RNA causes inhibition of translation of the GAM336611 target mRNA into a corresponding GAM336611 target protein.

The mechanism of the translational inhibition exerted by GAM336611 RNA, herein designated GAM RNA, on one or more GAM336611 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336611 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336611 RNA, herein designated GAM RNA, of GAM336611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336611 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336611 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336611 RNA correlate with, and may be deduced from, the identity of the GAM336611 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336614 5855 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336614 (GAM336614) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336614 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336614 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336614 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336614 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336614 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336614 precursor RNA is designated SEQ ID:5855, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5855 is located from position 32152882 to position 32152963 relative to chromosome 10 on the `+` strand.

GAM336614 precursor RNA folds onto itself, forming GAM336614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336614 precursor RNA, designated SEQ ID NO: 5855, and a schematic representation of a predicted secondary folding of GAM336614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336614 folded precursor RNA yielding a GAM336614 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336614 RNA, hereby incorporated herein.

GAM336614 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336614 target RNA, herein designated GAM TARGET RNA.

GAM336614 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336614 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336614 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336614 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336614 RNA, herein designated GAM RNA, to target binding sites on GAM336614 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336614 target RNA into GAM336614 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336614 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336614 target genes. The mRNA of each one of this plurality of GAM336614 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336614 RNA, herein designated GAM RNA, and which when bound by GAM336614 RNA causes inhibition of translation of the GAM336614 target mRNA into a corresponding GAM336614 target protein.

The mechanism of the translational inhibition exerted by GAM336614 RNA, herein designated GAM RNA, on one or more GAM336614 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336614 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336614 RNA, herein designated GAM RNA, of GAM336614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336614 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336614 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336614 RNA correlate with, and may be deduced from, the identity of the GAM336614 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336615 6023 CAGGCAAAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCTTAATG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGAGCAAGG Messenger 336615 (GAM336615) oligonucleotides modulates expression of respective target

GGTTTTTAGA genes whose function and utility is known in the art.

TGACATGGTG GAM336615 is a novel bioinformatically detectable regulatory, non protein
GTAGTGTTAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336615 was detected
TAATAAACTC is described with additional reference to Figs. 9-15.

TTTTTCCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTATGCAGCT encoded by the human genome.

GGTTCCTG GAM336615 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336615 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336615 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336615 precursor RNA is designated SEQ ID:6023, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6023 is located from position 32235142 to position 32235239 relative to chromosome 7 on the `-` strand.

GAM336615 precursor RNA folds onto itself, forming GAM336615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336615 precursor RNA, designated SEQ ID NO: 6023, and a schematic representation of a predicted secondary folding of GAM336615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336615 folded precursor RNA yielding a GAM336615 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336615 RNA, hereby incorporated herein.

GAM336615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336615 target RNA, herein designated GAM TARGET RNA.

GAM336615 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336615 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336615 RNA, herein designated GAM RNA, to target binding sites on GAM336615 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336615 target RNA into GAM336615 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336615 target genes. The mRNA of each one of this plurality of GAM336615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336615 RNA, herein designated GAM RNA, and which when bound by GAM336615 RNA causes inhibition of translation of the GAM336615 target mRNA into a corresponding GAM336615 target protein.

The mechanism of the translational inhibition exerted by GAM336615 RNA, herein designated GAM RNA, on one or more GAM336615 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336615 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336615 RNA, herein designated GAM RNA, of GAM336615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336615 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336615 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336615 RNA correlate with, and may be deduced from, the identity of the GAM336615 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336617 6347 GAGACAGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCTGCAAGG Messenger 336617 (GAM336617) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336617 is a novel bioinformatically detectable regulatory, non protein

GATTGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336617 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAATGAGAC encoded by the human genome.

TCTATCTC GAM336617 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336617 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336617 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336617 precursor RNA is designated SEQ ID:6347, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6347 is located from position 32403384 to position 32403481 relative to chromosome 9 on the `+` strand.

GAM336617 precursor RNA folds onto itself, forming GAM336617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336617 precursor RNA, designated SEQ ID NO: 6347, and a schematic representation of a predicted secondary folding of GAM336617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336617 folded precursor RNA yielding a GAM336617 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336617 RNA, hereby incorporated herein.

GAM336617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336617 target RNA, herein designated GAM TARGET RNA.

GAM336617 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336617 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336617 RNA, herein designated GAM RNA, to target binding sites on GAM336617 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336617 target RNA into GAM336617 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336617 target genes. The mRNA of each one of this plurality of GAM336617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336617 RNA, herein designated GAM RNA, and which when bound by GAM336617 RNA causes inhibition of translation of the GAM336617 target mRNA into a corresponding GAM336617 target protein.

The mechanism of the translational inhibition exerted by GAM336617 RNA, herein designated GAM RNA, on one or more GAM336617 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336617 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336617 RNA, herein designated GAM RNA, of GAM336617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336617 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336617 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336617 RNA correlate with, and may be deduced from, the identity of the GAM336617 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336618 6235 CTGGTCTGGC AGCACTAAGA GGCAGGCATT CTGGGTATCA GACATAAATC CCCTCCCAGG AACTTTTGTG TCCTGACCCA GAGGACTGGC TCTTGAGAAT GAGAACAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336618 (GAM336618) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336618 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336618 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336618 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336618 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336618 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336618 precursor RNA is designated SEQ ID:6235, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6235 is located from position 32615342 to position 32615449 relative to chromosome 21 on the `+` strand.

GAM336618 precursor RNA folds onto itself, forming GAM336618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336618 precursor RNA, designated SEQ ID NO: 6235, and a schematic representation of a predicted secondary folding of GAM336618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336618 folded precursor RNA yielding a GAM336618 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336618 RNA, hereby incorporated herein.

GAM336618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336618 target RNA, herein designated GAM TARGET RNA.

GAM336618 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336618 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336618 RNA, herein designated GAM RNA, to target binding sites on GAM336618 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336618 target RNA into GAM336618 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336618 target genes. The mRNA of each one of this plurality of GAM336618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336618 RNA, herein designated GAM RNA, and which when bound by GAM336618 RNA causes inhibition of translation of the GAM336618 target mRNA into a corresponding GAM336618 target protein.

The mechanism of the translational inhibition exerted by GAM336618 RNA, herein designated GAM RNA, on one or more GAM336618 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336618 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336618 RNA, herein designated GAM RNA, of

GAM336618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336618 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336618 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336618 RNA correlate with, and may be deduced from, the identity of the GAM336618 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336619 6956 TAAGAGGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCATTCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TATCAGACAT Messenger 336619 (GAM336619) oligonucleotides modulates expression of respective target

AAATCCCCTC genes whose function and utility is known in the art.

CCAGGAACTT GAM336619 is a novel bioinformatically detectable regulatory, non protein

TTGTGTCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336619 was detected

ACCCAGAGGA is described with additional reference to Figs. 9-15.

CTGGCTCTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336619 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336619 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336619 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336619 precursor RNA is designated SEQ ID:6956, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6956 is located from position 32615357 to position 32615436 relative to chromosome 21 on the `+` strand.

GAM336619 precursor RNA folds onto itself, forming GAM336619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336619 precursor RNA, designated SEQ ID NO: 6956, and

a schematic representation of a predicted secondary folding of GAM336619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336619 folded precursor RNA yielding a GAM336619 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336619 RNA, hereby incorporated herein.

GAM336619 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336619 target RNA, herein designated GAM TARGET RNA.

GAM336619 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336619 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336619 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336619 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336619 RNA, herein designated GAM RNA, to target binding sites on GAM336619 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336619 target RNA into GAM336619 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336619 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336619 target genes. The mRNA of each one of this plurality of GAM336619 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336619 RNA, herein designated GAM RNA, and which when bound by GAM336619 RNA causes inhibition of translation of the GAM336619 target mRNA into a corresponding GAM336619 target protein.

The mechanism of the translational inhibition exerted by GAM336619 RNA, herein designated GAM RNA, on one or more GAM336619 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336619 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336619 RNA, herein designated GAM RNA, of GAM336619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336619 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336619 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336619 RNA correlate with, and may be deduced from, the identity of the GAM336619 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336620 5662 AAGAGGCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CATTCTGGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCAGACATA Messenger 336620 (GAM336620) oligonucleotides modulates expression of respective target

AATCCCCTCC genes whose function and utility is known in the art.

CAGGAACTTT GAM336620 is a novel bioinformatically detectable regulatory, non protein

TGTGTCCTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336620 was detected

CCCAGAGGAC is described with additional reference to Figs. 9-15.

TGGCTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336620 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336620 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336620 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336620 precursor RNA is designated SEQ ID:5662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5662 is located from position 32615358 to position 32615435 relative to chromosome 21 on the `+` strand.

GAM336620 precursor RNA folds onto itself, forming GAM336620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336620 precursor RNA, designated SEQ ID NO: 5662, and a schematic representation of a predicted secondary folding of GAM336620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336620 folded precursor RNA yielding a GAM336620 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336620 RNA, hereby incorporated herein.

GAM336620 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336620 target RNA, herein designated GAM TARGET RNA.

GAM336620 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336620 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336620 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336620 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336620 RNA, herein designated GAM RNA, to target binding sites on GAM336620 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336620 target RNA into GAM336620 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336620 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336620 target genes. The mRNA of each one of this plurality of GAM336620 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336620 RNA, herein designated GAM RNA, and which when bound by GAM336620 RNA causes inhibition of translation of the GAM336620 target mRNA into a corresponding GAM336620 target protein.

The mechanism of the translational inhibition exerted by GAM336620 RNA, herein designated GAM RNA, on one or more GAM336620 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336620 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336620 RNA, herein designated GAM RNA, of GAM336620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336620 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336620 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336620 RNA correlate with, and may be deduced from, the identity of the GAM336620 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336621 6722 GGATTAGATG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGTGACAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTAGCAGC Messenger 336621 (GAM336621) oligonucleotides modulates expression of respective target

AGGAGCAGGT genes whose function and utility is known in the art.

AACATTCATT GAM336621 is a novel bioinformatically detectable regulatory, non protein

TAGAGTTGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336621 was detected

ATGTGCCACA is described with additional reference to Figs. 9-15.

CCCTGCTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AATGCTTTAT encoded by the human genome.

GGATATCAAG GAM336621 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCC GAM336621 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336621 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336621 precursor RNA is designated SEQ ID:6722, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6722 is located from position 32661984 to position 32662086 relative to chromosome 7 on the `+` strand.

GAM336621 precursor RNA folds onto itself, forming GAM336621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336621 precursor RNA, designated SEQ ID NO: 6722, and a schematic representation of a predicted secondary folding of GAM336621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336621 folded precursor RNA yielding a GAM336621 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336621 RNA, hereby incorporated herein.

GAM336621 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336621 target RNA, herein designated GAM TARGET RNA.

GAM336621 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336621 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336621 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336621 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336621 RNA, herein designated GAM RNA, to target binding sites on GAM336621 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336621 target RNA into GAM336621 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336621 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336621 target genes. The mRNA of each one of this plurality of GAM336621 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336621 RNA, herein designated GAM RNA, and which when bound by GAM336621 RNA causes inhibition of translation of the GAM336621 target mRNA into a corresponding GAM336621 target protein.

The mechanism of the translational inhibition exerted by GAM336621 RNA, herein designated GAM RNA, on one or more GAM336621 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336621 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336621 RNA, herein designated GAM RNA, of GAM336621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336621 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336621 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336621 RNA correlate with, and may be deduced from, the identity of the GAM336621 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336622 6544 GCTGCTTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TATCTTACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCTGCTCT Messenger 336622 (GAM336622) oligonucleotides modulates expression of respective target

CCTTTTTGTA genes whose function and utility is known in the art.

GTGATGAGGA GAM336622 is a novel bioinformatically detectable regulatory, non protein

ACAATGAAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336622 was detected

AGAGGTAGTG is described with additional reference to Figs. 9-15.

TAAGGAATTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGGCTGGG encoded by the human genome.

CATGGTGGC GAM336622 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336622 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336622 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336622 precursor RNA is designated SEQ ID:6544, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6544 is located from position 32800023 to position 32800121 relative to chromosome 12 on the `-` strand.

GAM336622 precursor RNA folds onto itself, forming GAM336622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336622 precursor RNA, designated SEQ ID NO: 6544, and a schematic representation of a predicted secondary folding of GAM336622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336622 folded precursor RNA yielding a GAM336622 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336622 RNA, hereby incorporated herein.

GAM336622 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336622 target RNA, herein designated GAM TARGET RNA.

GAM336622 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336622 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336622 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336622 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336622 RNA, herein designated GAM RNA, to target binding sites on GAM336622 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336622 target RNA into GAM336622 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336622 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336622 target genes. The mRNA of each one of this plurality of GAM336622 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336622 RNA, herein designated GAM RNA, and which when bound by GAM336622 RNA causes inhibition of translation of the GAM336622 target mRNA into a corresponding GAM336622 target protein.

The mechanism of the translational inhibition exerted by GAM336622 RNA, herein designated GAM RNA, on one or more GAM336622 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336622 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336622 RNA, herein designated GAM RNA, of GAM336622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336622 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336622 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336622 RNA correlate with, and may be deduced from, the identity of the GAM336622 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336626 5856 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336626 (GAM336626) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA TGTGCCATGT TGGTGTGCTG CACCCATTAA CT

GAM336626 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336626 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336626 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336626 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336626 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336626 precursor RNA is designated SEQ ID:5856, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5856 is located from position 33075772 to position 33075853 relative to chromosome 3 on the `+` strand.

GAM336626 precursor RNA folds onto itself, forming GAM336626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336626 precursor RNA, designated SEQ ID NO: 5856, and a schematic representation of a predicted secondary folding of GAM336626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336626 folded precursor RNA yielding a GAM336626 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336626 RNA, hereby incorporated herein.

GAM336626 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336626 target RNA, herein designated GAM TARGET RNA.

GAM336626 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336626 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336626 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336626 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336626 RNA, herein designated GAM RNA, to target binding sites on GAM336626 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336626 target RNA into GAM336626 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336626 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336626 target genes. The mRNA of each one of this plurality of GAM336626 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336626 RNA, herein designated GAM RNA, and which when bound by GAM336626 RNA causes inhibition of translation of the GAM336626 target mRNA into a corresponding GAM336626 target protein.

The mechanism of the translational inhibition exerted by GAM336626 RNA, herein designated GAM RNA, on one or more GAM336626 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336626 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336626 RNA, herein designated GAM RNA, of GAM336626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336626 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336626 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336626 RNA correlate with, and may be deduced from, the identity of the GAM336626 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336628 5734 AGAGTCACCT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGAAGCATT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAATAATTA Messenger 336628 (GAM336628) oligonucleotides modulates expression of respective target
AAGTGTCTGA genes whose function and utility is known in the art.

GGCCTTCCCC GAM336628 is a novel bioinformatically detectable regulatory, non protein
TTCAATAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336628 was detected
CTGGGATTGG is described with additional reference to Figs. 9-15.

GCCCAGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGTGTTTTT encoded by the human genome.

TAAGCACCCA GAM336628 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GGTTATTCT GAM336628 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336628 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336628 precursor RNA is designated SEQ ID:5734, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5734 is located from position 33138955 to position 33139063 relative to chromosome 17 on the `+` strand.

GAM336628 precursor RNA folds onto itself, forming GAM336628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336628 precursor RNA, designated SEQ ID NO: 5734, and a schematic representation of a predicted secondary folding of GAM336628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336628 folded precursor RNA yielding a GAM336628 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336628 RNA, hereby incorporated herein.

GAM336628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336628 target RNA, herein designated GAM TARGET RNA.

GAM336628 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336628 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336628 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336628 RNA, herein designated GAM RNA, to target binding sites on GAM336628 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336628 target RNA into GAM336628 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336628 target genes. The mRNA of each one of this plurality of GAM336628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336628 RNA, herein designated GAM RNA, and which when bound by GAM336628 RNA causes inhibition of translation of the GAM336628 target mRNA into a corresponding GAM336628 target protein.

The mechanism of the translational inhibition exerted by GAM336628 RNA, herein designated GAM RNA, on one or more GAM336628 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336628 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336628 RNA, herein designated GAM RNA, of GAM336628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336628 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336628 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336628 RNA correlate with, and may be deduced from, the identity of the GAM336628 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336629 6501 GCATTAAAAT AATTAAAGTG TCTGAGGCCT TCCCCTTCAA TAAATCTGGG ATTGGGCCCA GGCAACTGTG TTTTTTAAGC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336629 (GAM336629) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336629 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336629 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336629 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336629 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336629 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336629 precursor RNA is designated SEQ ID:6501, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6501 is located from position 33138970 to position 33139049 relative to chromosome 17 on the `+` strand.

GAM336629 precursor RNA folds onto itself, forming GAM336629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336629 precursor RNA, designated SEQ ID NO: 6501, and a schematic representation of a predicted secondary folding of GAM336629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336629 folded precursor RNA yielding a GAM336629 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336629 RNA, hereby incorporated herein.

GAM336629 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336629 target RNA, herein designated GAM TARGET RNA.

GAM336629 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336629 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336629 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336629 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336629 RNA, herein designated GAM RNA, to target binding sites on GAM336629 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336629 target RNA into GAM336629 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336629 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336629 target genes. The mRNA of each one of this plurality of GAM336629 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336629 RNA, herein designated GAM RNA, and which when bound by GAM336629 RNA causes inhibition of translation of the GAM336629 target mRNA into a corresponding GAM336629 target protein.

The mechanism of the translational inhibition exerted by GAM336629 RNA, herein designated GAM RNA, on one or more GAM336629 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336629 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336629 RNA, herein designated GAM RNA, of GAM336629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336629 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336629 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336629 RNA correlate with, and may be deduced from, the identity of the GAM336629 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336630 7165 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCGGGAG Messenger 336630 (GAM336630) oligonucleotides modulates expression of respective target
GCGGATGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336630 is a novel bioinformatically detectable regulatory, non protein
ATATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336630 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCAAG encoded by the human genome.

ACTCCGTCTC GAM336630 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
G GAM336630 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336630 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336630 precursor RNA is designated SEQ ID:7165, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7165 is located from position 33338251 to position 33338351 relative to chromosome 9 on the `+` strand.

GAM336630 precursor RNA folds onto itself, forming GAM336630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336630 precursor RNA, designated SEQ ID NO: 7165, and a schematic representation of a predicted secondary folding of GAM336630 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336630 folded precursor RNA yielding a GAM336630 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336630 RNA, hereby incorporated herein. Expression of GAM336630 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336630 target RNA, herein designated GAM TARGET RNA.

GAM336630 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336630 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336630 RNA, herein designated GAM RNA, to target binding sites on GAM336630 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336630 target RNA into GAM336630 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336630 target genes. The mRNA of each one of this plurality of GAM336630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336630 RNA, herein designated GAM RNA, and which when bound by GAM336630 RNA causes inhibition of translation of the GAM336630 target mRNA into a corresponding GAM336630 target protein.

The mechanism of the translational inhibition exerted by GAM336630 RNA, herein designated GAM RNA, on one or more GAM336630 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336630 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336630 RNA, herein designated GAM RNA, of GAM336630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336630 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336630 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336630 RNA correlate with, and may be deduced from, the identity of the GAM336630 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336631 6699 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGATG Messenger 336631 (GAM336631) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCAATATCGC GAM336631 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336631 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTCC encoded by the human genome.

GAM336631 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336631 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336631 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336631 precursor RNA is designated SEQ ID:6699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6699 is located from position 33338258 to position 33338345 relative to chromosome 9 on the `+` strand.

GAM336631 precursor RNA folds onto itself, forming GAM336631 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336631 precursor RNA, designated SEQ ID NO: 6699, and a schematic representation of a predicted secondary folding of GAM336631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336631 folded precursor RNA yielding a GAM336631 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336631 RNA, hereby incorporated herein. Expression of GAM336631 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336631 target RNA, herein designated GAM TARGET RNA.

GAM336631 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336631 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336631 RNA, herein designated GAM RNA, to target binding sites on GAM336631 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336631 target RNA into GAM336631 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336631 target genes. The mRNA of each one of this

plurality of GAM336631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336631 RNA, herein designated GAM RNA, and which when bound by GAM336631 RNA causes inhibition of translation of the GAM336631 target mRNA into a corresponding GAM336631 target protein.

The mechanism of the translational inhibition exerted by GAM336631 RNA, herein designated GAM RNA, on one or more GAM336631 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336631 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336631 RNA, herein designated GAM RNA, of GAM336631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336631 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336631 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336631 RNA correlate with, and may be deduced from, the identity of the GAM336631 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336632 6063 CCATGTTAAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCTGGTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGATGACAGC Messenger 336632 (GAM336632) oligonucleotides modulates expression of respective target

ACTGTGATTA genes whose function and utility is known in the art.

TATAGGAGTG GAM336632 is a novel bioinformatically detectable regulatory, non protein

TGTCCTTGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336632 was detected

GTTTGGGAAT is described with additional reference to Figs. 9-15.

TACATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336632 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336632 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336632 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336632 precursor RNA is designated SEQ ID:6063, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6063 is located from position 33407353 to position 33407429 relative to chromosome 17 on the `-` strand.

GAM336632 precursor RNA folds onto itself, forming GAM336632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336632 precursor RNA, designated SEQ ID NO: 6063, and a schematic representation of a predicted secondary folding of GAM336632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336632 folded precursor RNA yielding a GAM336632 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336632 RNA, hereby incorporated herein.

GAM336632 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336632 target RNA, herein designated GAM TARGET RNA.

GAM336632 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336632 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336632 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336632 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336632 RNA, herein designated GAM RNA, to target binding sites on GAM336632 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336632 target RNA into GAM336632 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336632 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336632 target genes. The mRNA of each one of this plurality of GAM336632 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336632 RNA, herein designated GAM RNA, and which when bound by GAM336632 RNA causes inhibition of translation of the GAM336632 target mRNA into a corresponding GAM336632 target protein.

The mechanism of the translational inhibition exerted by GAM336632 RNA, herein designated GAM RNA, on one or more GAM336632 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336632 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336632 RNA, herein designated GAM RNA, of GAM336632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336632 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336632 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336632 RNA correlate with, and may be deduced from, the identity of the GAM336632 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336633 7318 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGATTGCAG Messenger 336633 (GAM336633) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

TCATGCCACT GAM336633 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336633 was detected

CTGGGCGACA is described with additional reference to Figs. 9-15.

GAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336633 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336633 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336633 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336633 precursor RNA is designated SEQ ID:7318, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7318 is located from position 33688439 to position 33688514 relative to chromosome 20 on the `+` strand.

GAM336633 precursor RNA folds onto itself, forming GAM336633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336633 precursor RNA, designated SEQ ID NO: 7318, and a schematic representation of a predicted secondary folding of GAM336633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336633 folded precursor RNA yielding a GAM336633 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336633 RNA, hereby incorporated herein.

GAM336633 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336633 target RNA, herein designated GAM TARGET RNA.

GAM336633 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336633 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336633 RNA, herein designated GAM RNA, to target binding sites on GAM336633 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336633 target RNA into GAM336633 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336633 target genes. The mRNA of each one of this plurality of GAM336633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336633 RNA, herein designated GAM RNA, and which when bound by GAM336633 RNA causes inhibition of translation of the GAM336633 target mRNA into a corresponding GAM336633 target protein.

The mechanism of the translational inhibition exerted by GAM336633 RNA, herein designated GAM RNA, on one or more GAM336633 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336633 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336633 RNA, herein designated GAM RNA, of GAM336633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336633 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336633 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336633 RNA correlate with, and may be deduced from, the identity of the GAM336633 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336634 6318 GAGAAGATAA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGCGTTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGGATGTCA Messenger 336634 (GAM336634) oligonucleotides modulates expression of respective target

TCTTGGGCCT genes whose function and utility is known in the art.

GCTTTTCTCT GAM336634 is a novel bioinformatically detectable regulatory, non protein
GATCGTGTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336634 was detected
CGATGGGCTC is described with additional reference to Figs. 9-15.

ATTTTGCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATTTATACC encoded by the human genome.

TGATGGCCGT GAM336634 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAACCTATCT GAM336634 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TCTC GAM336634 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336634 precursor RNA is designated SEQ ID:6318, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6318 is located from position 33692940 to position 33693053 relative to chromosome 10 on the `+` strand.

GAM336634 precursor RNA folds onto itself, forming GAM336634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336634 precursor RNA, designated SEQ ID NO: 6318, and a schematic representation of a predicted secondary folding of GAM336634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336634 folded precursor RNA yielding a GAM336634 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336634 RNA, hereby incorporated herein.

GAM336634 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336634 target RNA, herein designated GAM TARGET RNA.

GAM336634 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336634 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336634 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336634 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336634 RNA, herein designated GAM RNA, to target binding sites on GAM336634 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336634 target RNA into GAM336634 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336634 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336634 target genes. The mRNA of each one of this plurality of GAM336634 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336634 RNA, herein designated GAM RNA, and which when bound by GAM336634 RNA causes inhibition of translation of the GAM336634 target mRNA into a corresponding GAM336634 target protein.

The mechanism of the translational inhibition exerted by GAM336634 RNA, herein designated GAM RNA, on one or more GAM336634 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336634 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336634 RNA, herein designated GAM RNA, of GAM336634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336634 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336634 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336634 RNA correlate with, and may be deduced from, the identity of the GAM336634 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336637 6869 GTATGGGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
ACTTGGGGCG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGATGTCAGC Messenger 336637 (GAM336637) oligonucleotides modulates expression of respective target
CAGAGTCCTT genes whose function and utility is known in the art.

CCACCAAGGC GAM336637 is a novel bioinformatically detectable regulatory, non protein
TTTTATGGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336637 was detected
TTACGTGATC is described with additional reference to Figs. 9-15.

CACCACCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTAAC encoded by the human genome.

GAM336637 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336637 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336637 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336637 precursor RNA is designated SEQ ID:6869, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6869 is located from position 33804195 to position 33804279 relative to chromosome 11 on the `+` strand.

GAM336637 precursor RNA folds onto itself, forming GAM336637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336637 precursor RNA, designated SEQ ID NO: 6869, and a schematic representation of a predicted secondary folding of GAM336637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336637 folded precursor RNA yielding a GAM336637 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336637 RNA, hereby incorporated herein.

GAM336637 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336637 target RNA, herein designated GAM TARGET RNA.

GAM336637 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336637 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336637 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336637 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336637 RNA, herein designated GAM RNA, to target binding sites on GAM336637 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336637 target RNA into GAM336637 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336637 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336637 target genes. The mRNA of each one of this plurality of GAM336637 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336637 RNA, herein designated GAM RNA, and which when bound by GAM336637 RNA causes inhibition of translation of the GAM336637 target mRNA into a corresponding GAM336637 target protein.

The mechanism of the translational inhibition exerted by GAM336637 RNA, herein designated GAM RNA, on one or more GAM336637 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336637 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336637 RNA, herein designated GAM RNA, of GAM336637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336637 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336637 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336637 RNA correlate with, and may be deduced from, the identity of the GAM336637 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336638 5857 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336638 (GAM336638) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336638 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336638 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336638 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336638 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336638 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336638 precursor RNA is designated SEQ ID:5857, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5857 is located from position 33909250 to position 33909331 relative to chromosome 13 on the `+` strand.

GAM336638 precursor RNA folds onto itself, forming GAM336638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336638 precursor RNA, designated SEQ ID NO: 5857, and a schematic representation of a predicted secondary folding of GAM336638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336638 folded precursor RNA yielding a GAM336638 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336638 RNA, hereby incorporated herein.

GAM336638 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336638 target RNA, herein designated GAM TARGET RNA.

GAM336638 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336638 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336638 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336638 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336638 RNA, herein designated GAM RNA, to target binding sites on GAM336638 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336638 target RNA into GAM336638 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336638 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336638 target genes. The mRNA of each one of this plurality of GAM336638 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336638 RNA, herein designated GAM RNA, and which when bound by GAM336638 RNA causes inhibition of translation of the GAM336638 target mRNA into a corresponding GAM336638 target protein.

The mechanism of the translational inhibition exerted by GAM336638 RNA, herein designated GAM RNA, on one or more GAM336638 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336638 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336638 RNA, herein designated GAM RNA, of GAM336638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336638 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336638 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336638 RNA correlate with, and may be deduced from, the identity of the GAM336638 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336639 6508 GCCCTTAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGTTATGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTCCCAGA Messenger 336639 (GAM336639) oligonucleotides modulates expression of respective target

AATCCAGGCT genes whose function and utility is known in the art.

TAAATGATAC GAM336639 is a novel bioinformatically detectable regulatory, non protein

TCAGGTGTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336639 was detected

TATTCAAGAT is described with additional reference to Figs. 9-15.

AAGGGTCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGAATATAA encoded by the human genome.

AATATTAATT GAM336639 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGAGGGT GAM336639 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336639 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336639 precursor RNA is designated SEQ ID:6508, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6508 is located from position 33928191 to position 33928297 relative to chromosome 11 on the `-` strand.

GAM336639 precursor RNA folds onto itself, forming GAM336639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336639 precursor RNA, designated SEQ ID NO: 6508, and a schematic representation of a predicted secondary folding of GAM336639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336639 folded precursor RNA yielding a GAM336639 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336639 RNA, hereby incorporated herein.

GAM336639 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336639 target RNA, herein designated GAM TARGET RNA.

GAM336639 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336639 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336639 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336639 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336639 RNA, herein designated GAM RNA, to target binding sites on GAM336639 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336639 target RNA into GAM336639 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336639 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336639 target genes. The mRNA of each one of this plurality of GAM336639 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336639 RNA, herein designated GAM RNA, and which when bound by GAM336639 RNA causes inhibition of translation of the GAM336639 target mRNA into a corresponding GAM336639 target protein.

The mechanism of the translational inhibition exerted by GAM336639 RNA, herein designated GAM RNA, on one or more GAM336639 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336639 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336639 RNA, herein designated GAM RNA, of GAM336639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336639 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336639 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336639 RNA correlate with, and may be deduced from, the identity of the GAM336639 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336640 6857 GGTTGGAATG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGAAGGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGTCTTCGG Messenger 336640 (GAM336640) oligonucleotides modulates expression of respective target

CTAAAATTTG genes whose function and utility is known in the art.

CATAAAACGG GAM336640 is a novel bioinformatically detectable regulatory, non protein

AACCCATCCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336640 was detected

GGCGATTCCA is described with additional reference to Figs. 9-15.

ACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336640 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336640 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336640 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336640 precursor RNA is designated SEQ ID:6857, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6857 is located from position 33934627 to position 33934699 relative to chromosome 21 on the `-` strand.

GAM336640 precursor RNA folds onto itself, forming GAM336640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336640 precursor RNA, designated SEQ ID NO: 6857, and a schematic representation of a predicted secondary folding of GAM336640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336640 folded precursor RNA yielding a GAM336640 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336640 RNA, hereby incorporated herein.

GAM336640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336640 target RNA, herein designated GAM TARGET RNA.

GAM336640 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336640 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336640 RNA, herein designated GAM RNA, to target binding sites on GAM336640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336640 target RNA into GAM336640 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336640 target genes. The mRNA of each one of this plurality of GAM336640 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336640 RNA, herein designated GAM RNA, and which when bound by GAM336640 RNA causes inhibition of translation of the GAM336640 target mRNA into a corresponding GAM336640 target protein.

The mechanism of the translational inhibition exerted by GAM336640 RNA, herein designated GAM RNA, on one or more GAM336640 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336640 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336640 RNA, herein designated GAM RNA, of GAM336640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336640 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336640 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336640 RNA correlate with, and may be deduced from, the identity of the GAM336640 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336642 6849 GGTGGTAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCTGGAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGGAAC Messenger 336642 (GAM336642) oligonucleotides modulates expression of respective target
CCCAAAGCCC genes whose function and utility is known in the art.

TATGACACCC GAM336642 is a novel bioinformatically detectable regulatory, non protein
CATATAGGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336642 was detected
CCCCCAAACC is described with additional reference to Figs. 9-15.

TGCCTATACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAGGCCAGG encoded by the human genome.

CCCC GAM336642 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336642 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336642 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336642 precursor RNA is designated SEQ ID:6849, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6849 is located from position 34257285 to position 34257378 relative to chromosome 21 on the `+` strand.

GAM336642 precursor RNA folds onto itself, forming GAM336642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336642 precursor RNA, designated SEQ ID NO: 6849, and a schematic representation of a predicted secondary folding of GAM336642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336642 folded precursor RNA yielding a GAM336642 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336642 RNA, hereby incorporated herein.

GAM336642 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336642 target RNA, herein designated GAM TARGET RNA.

GAM336642 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336642 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336642 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336642 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336642 RNA, herein designated GAM RNA, to target binding sites on GAM336642 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336642 target RNA into GAM336642 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336642 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336642 target genes. The mRNA of each one of this plurality of GAM336642 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336642 RNA, herein designated GAM RNA, and which when bound by GAM336642 RNA causes inhibition of translation of the GAM336642 target mRNA into a corresponding GAM336642 target protein.

The mechanism of the translational inhibition exerted by GAM336642 RNA, herein designated GAM RNA, on one or more GAM336642 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336642 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336642 RNA, herein designated GAM RNA, of GAM336642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336642 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336642 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336642 RNA correlate with, and may be deduced from, the identity of the GAM336642 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336643 6850 GGTGGTAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCTGGAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCAGGAAC Messenger 336643 (GAM336643) oligonucleotides modulates expression of respective target

CCCAAAGCCC genes whose function and utility is known in the art.

TATGACACCC GAM336643 is a novel bioinformatically detectable regulatory, non protein

CATATAGGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336643 was detected

CCCCCAAACC is described with additional reference to Figs. 9-15.

TGCCTATACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCAGGCCAGG encoded by the human genome.

CCCCC GAM336643 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336643 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336643 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336643 precursor RNA is designated SEQ ID:6850, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6850 is located from position 34257285 to position 34257379 relative to chromosome 21 on the `+` strand.

GAM336643 precursor RNA folds onto itself, forming GAM336643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336643 precursor RNA, designated SEQ ID NO: 6850, and a schematic representation of a predicted secondary folding of GAM336643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336643 folded precursor RNA yielding a GAM336643 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336643 RNA, hereby incorporated herein.

GAM336643 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336643 target RNA, herein designated GAM TARGET RNA.

GAM336643 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336643 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336643 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336643 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336643 RNA, herein designated GAM RNA, to target binding sites on GAM336643 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336643 target RNA into GAM336643 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336643 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336643 target genes. The mRNA of each one of this plurality of GAM336643 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336643 RNA, herein designated GAM RNA, and which when bound by GAM336643 RNA causes inhibition of translation of the GAM336643 target mRNA into a corresponding GAM336643 target protein.

The mechanism of the translational inhibition exerted by GAM336643 RNA, herein designated GAM RNA, on one or more GAM336643 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336643 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336643 RNA, herein designated GAM RNA, of GAM336643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336643 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336643 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336643 RNA correlate with, and may be deduced from, the identity of the GAM336643 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336646 6571 GGAAAAGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CATGGGTTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCTTTTTGG Messenger 336646 (GAM336646) oligonucleotides modulates expression of respective target

GAAGAGACAG genes whose function and utility is known in the art.

TTCAGCTTTT GAM336646 is a novel bioinformatically detectable regulatory, non protein

GATGTAAAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336646 was detected

AGCTGTACCT is described with additional reference to Figs. 9-15.

TCTGAGAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTAGCCCCAT encoded by the human genome.

GTCTTCATC GAM336646 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336646 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336646 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336646 precursor RNA is designated SEQ ID:6571, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6571 is located from position 34615664 to position 34615762 relative to chromosome 17 on the `+` strand.

GAM336646 precursor RNA folds onto itself, forming GAM336646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336646 precursor RNA, designated SEQ ID NO: 6571, and a schematic representation of a predicted secondary folding of GAM336646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336646 folded precursor RNA yielding a GAM336646 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336646 RNA, hereby incorporated herein.

GAM336646 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336646 target RNA, herein designated GAM TARGET RNA.

GAM336646 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336646 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336646 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336646 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336646 RNA, herein designated GAM RNA, to target binding sites on GAM336646 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336646 target RNA into GAM336646 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336646 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336646 target genes. The mRNA of each one of this plurality of GAM336646 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336646 RNA, herein designated GAM RNA, and which when bound by GAM336646 RNA causes inhibition of translation of the GAM336646 target mRNA into a corresponding GAM336646 target protein.

The mechanism of the translational inhibition exerted by GAM336646 RNA, herein designated GAM RNA, on one or more GAM336646 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336646 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336646 RNA, herein designated GAM RNA, of GAM336646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336646 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336646 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336646

RNA correlate with, and may be deduced from, the identity of the GAM336646 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336651 6157 CTCAGACTCA CCAAACAGTC TGCTTCTTAC CCCAGTGTAA GCACTGAACA GGCAGGTGGG TGTATGGGTC TGAG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336651 (GAM336651) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336651 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336651 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336651 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336651 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336651 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336651 precursor RNA is designated SEQ ID:6157, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6157 is located from position 34790992 to position 34791065 relative to chromosome 7 on the `+` strand.

GAM336651 precursor RNA folds onto itself, forming GAM336651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336651 precursor RNA, designated SEQ ID NO: 6157, and a schematic representation of a predicted secondary folding of GAM336651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336651 folded precursor RNA yielding a GAM336651 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336651 RNA, hereby incorporated herein.

GAM336651 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336651 target RNA, herein designated GAM TARGET RNA.

GAM336651 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336651 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336651 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336651 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336651 RNA, herein designated GAM RNA, to target binding sites on GAM336651 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336651 target RNA into GAM336651 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336651 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336651 target genes. The mRNA of each one of this plurality of GAM336651 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336651 RNA, herein designated GAM RNA, and which when bound by GAM336651 RNA causes inhibition of translation of the GAM336651 target mRNA into a corresponding GAM336651 target protein.

The mechanism of the translational inhibition exerted by GAM336651 RNA, herein designated GAM RNA, on one or more GAM336651 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336651 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336651 RNA, herein designated GAM RNA, of GAM336651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336651 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336651 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336651 RNA correlate with, and may be deduced from, the identity of the GAM336651 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336652 5787 AGGGAGAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGGGGTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTTGAG Messenger 336652 (GAM336652) oligonucleotides modulates expression of respective target
CCTTCTCCTG genes whose function and utility is known in the art.

CTCTGTCCGT GAM336652 is a novel bioinformatically detectable regulatory, non protein
GGAGCAAGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336652 was detected
AAATAAATGC is described with additional reference to Figs. 9-15.

TGAGACCGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCTCCTCAT encoded by the human genome.

TTCTCCTT GAM336652 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336652 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336652 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336652 precursor RNA is designated SEQ ID:5787, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5787 is located from position 34813290 to position 34813387 relative to chromosome 21 on the `-` strand.

GAM336652 precursor RNA folds onto itself, forming GAM336652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336652 precursor RNA, designated SEQ ID NO: 5787, and a schematic representation of a predicted secondary folding of GAM336652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336652 folded precursor RNA yielding a GAM336652 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336652 RNA, hereby incorporated herein.

GAM336652 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336652 target RNA, herein designated GAM TARGET RNA.

GAM336652 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336652 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336652 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336652 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336652 RNA, herein designated GAM RNA, to target binding sites on GAM336652 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336652 target RNA into GAM336652 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336652 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336652 target genes. The mRNA of each one of this plurality of GAM336652 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336652 RNA, herein designated GAM RNA, and which when bound by GAM336652 RNA causes inhibition of translation of the GAM336652 target mRNA into a corresponding GAM336652 target protein.

The mechanism of the translational inhibition exerted by GAM336652 RNA, herein designated GAM RNA, on one or more GAM336652 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336652 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336652 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336652 RNA, herein designated GAM RNA, of GAM336652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336652 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336652 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336652 RNA correlate with, and may be deduced from, the identity of the GAM336652 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336653 6455 GAGGTGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCAGGAGG Messenger 336653 (GAM336653) oligonucleotides modulates expression of respective target

TCAAGGCTGC genes whose function and utility is known in the art.

AGTGAGTTGT GAM336653 is a novel bioinformatically detectable regulatory, non protein

GATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336653 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAGCAAGA encoded by the human genome.

CCCCATCTC GAM336653 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336653 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336653 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336653 precursor RNA is designated SEQ ID:6455, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6455 is located from position 34876504 to position 34876602 relative to chromosome 19 on the `-` strand.

GAM336653 precursor RNA folds onto itself, forming GAM336653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336653 precursor RNA, designated SEQ ID NO: 6455, and a schematic representation of a predicted secondary folding of GAM336653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336653 folded precursor RNA yielding a GAM336653 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336653 RNA, hereby incorporated herein. Expression of GAM336653 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336653 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336653 target RNA, herein designated GAM TARGET RNA.

GAM336653 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336653 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336653 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336653 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336653 RNA, herein designated GAM RNA, to target binding sites on GAM336653 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336653 target RNA into GAM336653 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336653 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336653 target genes. The mRNA of each one of this plurality of GAM336653 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336653 RNA, herein designated GAM RNA, and which when bound by GAM336653 RNA causes inhibition of

translation of the GAM336653 target mRNA into a corresponding GAM336653 target protein.

The mechanism of the translational inhibition exerted by GAM336653 RNA, herein designated GAM RNA, on one or more GAM336653 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336653 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336653 RNA, herein designated GAM RNA, of GAM336653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336653 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336653 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336653 RNA correlate with, and may be deduced from, the identity of the GAM336653 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336656 5858 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336656 (GAM336656) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336656 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336656 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336656 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336656 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336656 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336656 precursor RNA is designated SEQ ID:5858, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5858 is located from position 35023682 to position 35023763 relative to chromosome 3 on the `+` strand.

GAM336656 precursor RNA folds onto itself, forming GAM336656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336656 precursor RNA, designated SEQ ID NO: 5858, and a schematic representation of a predicted secondary folding of GAM336656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336656 folded precursor RNA yielding a GAM336656 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336656 RNA, hereby incorporated herein.

GAM336656 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336656 target RNA, herein designated GAM TARGET RNA.

GAM336656 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336656 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336656 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336656 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336656 RNA, herein designated GAM RNA, to target binding sites on GAM336656 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336656 target RNA into GAM336656 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336656 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336656 target genes. The mRNA of each one of this plurality of GAM336656 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336656 RNA, herein designated GAM RNA, and which when bound by GAM336656 RNA causes inhibition of translation of the GAM336656 target mRNA into a corresponding GAM336656 target protein.

The mechanism of the translational inhibition exerted by GAM336656 RNA, herein designated GAM RNA, on one or more GAM336656 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336656 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336656 RNA, herein designated GAM RNA, of GAM336656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336656 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336656 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336656 RNA correlate with, and may be deduced from, the identity of the GAM336656 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336657 7258 TGGTTGTTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGTCTGGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTAAGTGCT Messenger 336657 (GAM336657) oligonucleotides modulates expression of respective target

GGTTGTTAGT genes whose function and utility is known in the art.

TGTTAAAGTA GAM336657 is a novel bioinformatically detectable regulatory, non protein

GAGAAAACCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336657 was detected

CTAGCACAGT is described with additional reference to Figs. 9-15.

GCTTGGCACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CACTAAAGCC encoded by the human genome.

ATCATAAACC GAM336657 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336657 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336657 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336657 precursor RNA is designated SEQ ID:7258, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7258 is located from position 35289635 to position 35289735 relative to chromosome 11 on the `+` strand.

GAM336657 precursor RNA folds onto itself, forming GAM336657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336657 precursor RNA, designated SEQ ID NO: 7258, and a schematic representation of a predicted secondary folding of GAM336657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336657 folded precursor RNA yielding a GAM336657 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336657 RNA, hereby incorporated herein.

GAM336657 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336657 target RNA, herein designated GAM TARGET RNA.

GAM336657 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336657 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336657 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336657 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336657 RNA, herein designated GAM RNA, to target binding sites on GAM336657 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336657 target RNA into GAM336657 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336657 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336657 target genes. The mRNA of each one of this plurality of GAM336657 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336657 RNA, herein designated GAM RNA, and which when bound by GAM336657 RNA causes inhibition of translation of the GAM336657 target mRNA into a corresponding GAM336657 target protein.

The mechanism of the translational inhibition exerted by GAM336657 RNA, herein designated GAM RNA, on one or more GAM336657 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336657 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336657 RNA, herein designated GAM RNA, of GAM336657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336657 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336657 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336657 RNA correlate with, and may be deduced from, the identity of the GAM336657 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336658 6775 GGGAAGAACT Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCAATCTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCACACGTC Messenger 336658 (GAM336658) oligonucleotides modulates expression of respective target

TCTCTGAATT genes whose function and utility is known in the art.

GTTGATTATG GAM336658 is a novel bioinformatically detectable regulatory, non protein
CGCTTTATGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336658 was detected
AGAGATTTTT is described with additional reference to Figs. 9-15.

CAATCTCGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCTTTACTT encoded by the human genome.

TGTGTGGTTT GAM336658 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AGACCC GAM336658 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336658 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336658 precursor RNA is designated SEQ ID:6775, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6775 is located from position 35608725 to position 35608830 relative to chromosome 17 on the `-` strand.

GAM336658 precursor RNA folds onto itself, forming GAM336658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336658 precursor RNA, designated SEQ ID NO: 6775, and a schematic representation of a predicted secondary folding of GAM336658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336658 folded precursor RNA yielding a GAM336658 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336658 RNA, hereby incorporated herein.

GAM336658 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336658 target RNA, herein designated GAM TARGET RNA.

GAM336658 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336658 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336658 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336658 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336658 RNA, herein designated GAM RNA, to target binding sites on GAM336658 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336658 target RNA into GAM336658 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336658 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336658 target genes. The mRNA of each one of this plurality of GAM336658 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336658 RNA, herein designated GAM RNA, and which when bound by GAM336658 RNA causes inhibition of translation of the GAM336658 target mRNA into a corresponding GAM336658 target protein.

The mechanism of the translational inhibition exerted by GAM336658 RNA, herein designated GAM RNA, on one or more GAM336658 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336658 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336658 RNA, herein designated GAM RNA, of GAM336658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336658 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336658 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336658 RNA correlate with, and may be deduced from, the identity of the GAM336658 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336659 6335 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAACCCGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGGAGGT Messenger 336659 (GAM336659) oligonucleotides modulates expression of respective target

TGCAGTGACT genes whose function and utility is known in the art.

GAGATCGGGC GAM336659 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336659 was detected

CAGCCTGGGC is described with additional reference to Figs. 9-15.

AACAGAGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACTC encoded by the human genome.

GAM336659 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336659 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336659 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336659 precursor RNA is designated SEQ ID:6335, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6335 is located from position 35681759 to position 35681843 relative to chromosome 22 on the `-` strand.

GAM336659 precursor RNA folds onto itself, forming GAM336659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336659 precursor RNA, designated SEQ ID NO: 6335, and a schematic representation of a predicted secondary folding of GAM336659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336659 folded precursor RNA yielding a GAM336659 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336659 RNA, hereby incorporated herein. Expression of GAM336659 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336659 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336659 target RNA, herein designated GAM TARGET RNA.

GAM336659 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336659 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336659 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336659 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336659 RNA, herein designated GAM RNA, to target binding sites on GAM336659 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336659 target RNA into GAM336659 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336659 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336659 target genes. The mRNA of each one of this plurality of GAM336659 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336659 RNA, herein designated GAM RNA, and which when bound by GAM336659 RNA causes inhibition of translation of the GAM336659 target mRNA into a corresponding GAM336659 target protein.

The mechanism of the translational inhibition exerted by GAM336659 RNA, herein designated GAM RNA, on one or more GAM336659 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336659 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336659 RNA, herein designated GAM RNA, of GAM336659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336659 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336659 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336659 RNA correlate with, and may be deduced from, the identity of the GAM336659 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336660 5859 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336660 (GAM336660) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336660 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336660 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336660 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336660 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336660 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336660 precursor RNA is designated SEQ ID:5859, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5859 is located from position 35708263 to position 35708344 relative to chromosome X on the `-` strand.

GAM336660 precursor RNA folds onto itself, forming GAM336660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336660 precursor RNA, designated SEQ ID NO: 5859, and a schematic representation of a predicted secondary folding of GAM336660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336660 folded precursor

RNA yielding a GAM336660 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336660 RNA, hereby incorporated herein.

GAM336660 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336660 target RNA, herein designated GAM TARGET RNA.

GAM336660 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336660 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336660 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336660 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336660 RNA, herein designated GAM RNA, to target binding sites on GAM336660 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336660 target RNA into GAM336660 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336660 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336660 target genes. The mRNA of each one of this plurality of GAM336660 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336660 RNA, herein designated GAM RNA, and which when bound by GAM336660 RNA causes inhibition of translation of the GAM336660 target mRNA into a corresponding GAM336660 target protein.

The mechanism of the translational inhibition exerted by GAM336660 RNA, herein designated GAM RNA, on one or more GAM336660 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336660 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336660 RNA, herein designated GAM RNA, of GAM336660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336660 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336660 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336660 RNA correlate with, and may be deduced from, the identity of the GAM336660 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336661 6437 GAGGCGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 336661 (GAM336661) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM336661 is a novel bioinformatically detectable regulatory, non protein

GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336661 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAGA encoded by the human genome.

CTCTGTCTC GAM336661 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336661 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336661 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336661 precursor RNA is designated SEQ ID:6437, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6437 is located from position 35736486 to position 35736584 relative to chromosome 20 on the `+` strand.

GAM336661 precursor RNA folds onto itself, forming GAM336661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336661 precursor RNA, designated SEQ ID NO: 6437, and a schematic representation of a predicted secondary folding of GAM336661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336661 folded precursor RNA yielding a GAM336661 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336661 RNA, hereby incorporated herein. Expression of GAM336661 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336661 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336661 target RNA, herein designated GAM TARGET RNA.

GAM336661 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336661 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336661 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336661 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336661 RNA, herein designated GAM RNA, to target binding sites on GAM336661 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336661 target RNA into GAM336661 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336661 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336661 target genes. The mRNA of each one of this plurality of GAM336661 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336661 RNA, herein designated GAM RNA, and which when bound by GAM336661 RNA causes inhibition of translation of the GAM336661 target mRNA into a corresponding GAM336661 target protein.

The mechanism of the translational inhibition exerted by GAM336661 RNA, herein designated GAM RNA, on one or more GAM336661 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336661 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336661 RNA, herein designated GAM RNA, of GAM336661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336661 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336661 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336661 RNA correlate with, and may be deduced from, the identity of the GAM336661 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336662 6753 GGCGGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCGGGAGGTG Messenger 336662 (GAM336662) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TGAGCCGAGA GAM336662 is a novel bioinformatically detectable regulatory, non protein

TCGCGCCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336662 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCAAGACT encoded by the human genome.

CTGTC GAM336662 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336662 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336662 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336662 precursor RNA is designated SEQ

ID:6753, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6753 is located from position 35736488 to position 35736582 relative to chromosome 20 on the `+` strand.

GAM336662 precursor RNA folds onto itself, forming GAM336662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336662 precursor RNA, designated SEQ ID NO: 6753, and a schematic representation of a predicted secondary folding of GAM336662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336662 folded precursor RNA yielding a GAM336662 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336662 RNA, hereby incorporated herein. Expression of GAM336662 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336662 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336662 target RNA, herein designated GAM TARGET RNA.

GAM336662 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336662 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336662 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336662 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336662 RNA, herein designated GAM RNA, to target binding sites on GAM336662 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336662 target RNA

into GAM336662 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336662 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336662 target genes. The mRNA of each one of this plurality of GAM336662 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336662 RNA, herein designated GAM RNA, and which when bound by GAM336662 RNA causes inhibition of translation of the GAM336662 target mRNA into a corresponding GAM336662 target protein.

The mechanism of the translational inhibition exerted by GAM336662 RNA, herein designated GAM RNA, on one or more GAM336662 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336662 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336662 RNA, herein designated GAM RNA, of GAM336662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336662 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336662 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336662 RNA correlate with, and may be deduced from, the identity of the GAM336662 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336663 6689 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336663 (GAM336663) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336663 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336663 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGACTCT encoded by the human genome.

GAM336663 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336663 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336663 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336663 precursor RNA is designated SEQ ID:6689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6689 is located from position 35736492 to position 35736579 relative to chromosome 20 on the `+` strand.

GAM336663 precursor RNA folds onto itself, forming GAM336663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336663 precursor RNA, designated SEQ ID NO: 6689, and a schematic representation of a predicted secondary folding of GAM336663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336663 folded precursor RNA yielding a GAM336663 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336663 RNA, hereby incorporated herein. Expression of GAM336663 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336663 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336663 target RNA, herein designated GAM TARGET RNA.

GAM336663 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336663 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336663 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336663 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336663 RNA, herein designated GAM RNA, to target binding sites on GAM336663 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336663 target RNA into GAM336663 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336663 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336663 target genes. The mRNA of each one of this plurality of GAM336663 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336663 RNA, herein designated GAM RNA, and which when bound by GAM336663 RNA causes inhibition of translation of the GAM336663 target mRNA into a corresponding GAM336663 target protein.

The mechanism of the translational inhibition exerted by GAM336663 RNA, herein designated GAM RNA, on one or more GAM336663 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336663 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336663 RNA, herein designated GAM RNA, of GAM336663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336663 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336663 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336663 RNA correlate with, and may be deduced from, the identity of the GAM336663 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336664 7320 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336664 (GAM336664) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TCGCGCCATT GAM336664 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336664 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336664 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336664 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336664 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336664 precursor RNA is designated SEQ ID:7320, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7320 is located from position 35736498 to position 35736573 relative to chromosome 20 on the `+` strand.

GAM336664 precursor RNA folds onto itself, forming GAM336664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336664 precursor RNA, designated SEQ ID NO: 7320, and a schematic representation of a predicted secondary folding of GAM336664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336664 folded precursor RNA yielding a GAM336664 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336664 RNA, hereby incorporated herein. Expression of GAM336664 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336664 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336664 target RNA, herein designated GAM TARGET RNA.

GAM336664 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336664 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336664 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336664 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336664 RNA, herein designated GAM RNA, to target binding sites on GAM336664 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336664 target RNA into GAM336664 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336664 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336664 target genes. The mRNA of each one of this plurality of GAM336664 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336664 RNA, herein designated GAM RNA, and which when bound by GAM336664 RNA causes inhibition of translation of the GAM336664 target mRNA into a corresponding GAM336664 target protein.

The mechanism of the translational inhibition exerted by GAM336664 RNA, herein designated GAM RNA, on one or more GAM336664 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336664 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336664 RNA, herein designated GAM RNA, of GAM336664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336664 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336664 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336664 RNA correlate with, and may be deduced from, the identity of the GAM336664 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336665 6511 GCCTCTGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
AATACTGTTA detected oligonucleotides of the present invention, referred to here as Genomic Address
AAACTAAATA Messenger 336665 (GAM336665) oligonucleotides modulates expression of respective target
CTTGCCAGGT genes whose function and utility is known in the art.

GTGGTGGCTC GAM336665 is a novel bioinformatically detectable regulatory, non protein
ACACCTGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336665 was detected
TAGTTCTTTT is described with additional reference to Figs. 9-15.

GGAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336665 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336665 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336665 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336665 precursor RNA is designated SEQ ID:6511, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6511 is located from position 35840280 to position 35840355 relative to chromosome 17 on the `+` strand.

GAM336665 precursor RNA folds onto itself, forming GAM336665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336665 precursor RNA, designated SEQ ID NO: 6511, and a schematic representation of a predicted secondary folding of GAM336665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336665 folded precursor RNA yielding a GAM336665 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336665 RNA, hereby incorporated herein.

GAM336665 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336665 target RNA, herein designated GAM TARGET RNA.

GAM336665 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336665 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336665 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336665 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336665 RNA, herein designated GAM RNA, to target binding sites on GAM336665 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336665 target RNA into GAM336665 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336665 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336665 target genes. The mRNA of each one of this plurality of GAM336665 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336665 RNA, herein designated GAM RNA, and which when bound by GAM336665 RNA causes inhibition of translation of the GAM336665 target mRNA into a corresponding GAM336665 target protein.

The mechanism of the translational inhibition exerted by GAM336665 RNA, herein designated GAM RNA, on one or more GAM336665 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336665 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336665 RNA, herein designated GAM RNA, of GAM336665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336665 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336665 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336665 RNA correlate with, and may be deduced from, the identity of the GAM336665 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336669 5860 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336669 (GAM336669) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336669 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336669 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336669 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336669 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336669 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336669 precursor RNA is designated SEQ ID:5860, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5860 is located from position 36383567 to position 36383648 relative to chromosome 2 on the `+` strand.

GAM336669 precursor RNA folds onto itself, forming GAM336669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336669 precursor RNA, designated SEQ ID NO: 5860, and a schematic representation of a predicted secondary folding of GAM336669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336669 folded precursor RNA yielding a GAM336669 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336669 RNA, hereby incorporated herein.

GAM336669 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336669 target RNA, herein designated GAM TARGET RNA.

GAM336669 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336669 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336669 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336669 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336669 RNA, herein designated GAM RNA, to target binding sites on GAM336669 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336669 target RNA into GAM336669 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336669 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336669 target genes. The mRNA of each one of this plurality of GAM336669 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336669 RNA, herein designated GAM RNA, and which when bound by GAM336669 RNA causes inhibition of translation of the GAM336669 target mRNA into a corresponding GAM336669 target protein.

The mechanism of the translational inhibition exerted by GAM336669 RNA, herein designated GAM RNA, on one or more GAM336669 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336669 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336669 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336669 RNA, herein designated GAM RNA, of GAM336669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336669 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336669 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336669 RNA correlate with, and may be deduced from, the identity of the GAM336669 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336670 5653 AAATAGCCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCCTCGTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCGACAGTT Messenger 336670 (GAM336670) oligonucleotides modulates expression of respective target

CCATTCCTAA genes whose function and utility is known in the art.

TGCAGACTTA GAM336670 is a novel bioinformatically detectable regulatory, non protein

CAAAAACTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336670 was detected

GTGTAAGGCT is described with additional reference to Figs. 9-15.

GGCATTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGGCCAGG encoded by the human genome.

ATGAGAGCAG GAM336670 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGCTTTTT GAM336670 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336670 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336670 precursor RNA is designated SEQ ID:5653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5653 is located from position 36386596 to position 36386703 relative to chromosome 10 on the `-` strand.

GAM336670 precursor RNA folds onto itself, forming GAM336670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336670 precursor RNA, designated SEQ ID NO: 5653, and a schematic representation of a predicted secondary folding of GAM336670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336670 folded precursor RNA yielding a GAM336670 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336670 RNA, hereby incorporated herein.

GAM336670 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336670 target RNA, herein designated GAM TARGET RNA.

GAM336670 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336670 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336670 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336670 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336670 RNA, herein designated GAM RNA, to target binding sites on GAM336670 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336670 target RNA into GAM336670 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336670 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336670 target genes. The mRNA of each one of this plurality of GAM336670 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336670 RNA, herein designated GAM RNA, and which when bound by GAM336670 RNA causes inhibition of translation of the GAM336670 target mRNA into a corresponding GAM336670 target protein.

The mechanism of the translational inhibition exerted by GAM336670 RNA, herein designated GAM RNA, on one or more GAM336670 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336670 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336670 RNA, herein designated GAM RNA, of GAM336670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336670 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336670 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336670 RNA correlate with, and may be deduced from, the identity of the GAM336670 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336671 5748 AGCCATTCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGTGCTGCG detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAGTTCCAT Messenger 336671 (GAM336671) oligonucleotides modulates expression of respective target

TCCTAATGCA genes whose function and utility is known in the art.

GACTTACAAA GAM336671 is a novel bioinformatically detectable regulatory, non protein

AACTAGGTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336671 was detected

AAGGCTGGCA is described with additional reference to Figs. 9-15.

TTAGGGTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCAGGATGA encoded by the human genome.

GAGCAGGGCT GAM336671 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336671 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336671 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336671 precursor RNA is designated SEQ

ID:5748, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5748 is located from position 36386600 to position 36386699 relative to chromosome 10 on the `-` strand.

GAM336671 precursor RNA folds onto itself, forming GAM336671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336671 precursor RNA, designated SEQ ID NO: 5748, and a schematic representation of a predicted secondary folding of GAM336671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336671 folded precursor RNA yielding a GAM336671 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336671 RNA, hereby incorporated herein.

GAM336671 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336671 target RNA, herein designated GAM TARGET RNA.

GAM336671 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336671 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336671 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336671 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336671 RNA, herein designated GAM RNA, to target binding sites on GAM336671 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336671 target RNA into GAM336671 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336671 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336671 target genes. The mRNA of each one of this plurality of GAM336671 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336671 RNA, herein designated GAM RNA, and which when bound by GAM336671 RNA causes inhibition of translation of the GAM336671 target mRNA into a corresponding GAM336671 target protein.

The mechanism of the translational inhibition exerted by GAM336671 RNA, herein designated GAM RNA, on one or more GAM336671 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336671 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336671 RNA, herein designated GAM RNA, of GAM336671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336671 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336671 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336671 RNA correlate with, and may be deduced from, the identity of the GAM336671 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336672 6170 CTCGTGCTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

GACAGTTCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCTAATGC Messenger 336672 (GAM336672) oligonucleotides modulates expression of respective target

AGACTTACAA genes whose function and utility is known in the art.

AAACTAGGTG GAM336672 is a novel bioinformatically detectable regulatory, non protein

TAAGGCTGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336672 was detected

ATTAGGGTGA is described with additional reference to Figs. 9-15.

GGCCAGGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM336672 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336672 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336672 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336672 precursor RNA is designated SEQ ID:6170, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6170 is located from position 36386609 to position 36386690 relative to chromosome 10 on the `-` strand.

GAM336672 precursor RNA folds onto itself, forming GAM336672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336672 precursor RNA, designated SEQ ID NO: 6170, and a schematic representation of a predicted secondary folding of GAM336672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336672 folded precursor RNA yielding a GAM336672 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336672 RNA, hereby incorporated herein.

GAM336672 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336672 target RNA, herein designated GAM TARGET RNA.

GAM336672 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336672 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336672 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336672 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336672 RNA, herein designated GAM RNA, to target binding sites on GAM336672 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336672 target RNA into GAM336672 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336672 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336672 target genes. The mRNA of each one of this plurality of GAM336672 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336672 RNA, herein designated GAM RNA, and which when bound by GAM336672 RNA causes inhibition of translation of the GAM336672 target mRNA into a corresponding GAM336672 target protein.

The mechanism of the translational inhibition exerted by GAM336672 RNA, herein designated GAM RNA, on one or more GAM336672 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336672 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336672 RNA, herein designated GAM RNA, of GAM336672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336672 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336672 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336672 RNA correlate with, and may be deduced from, the identity of the GAM336672 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336673 7091 TGACCCTCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACCTCACAT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTTCTGGA Messenger 336673 (GAM336673) oligonucleotides modulates expression of respective target

GCCCATACTC genes whose function and utility is known in the art.

ACCAATCAGC GAM336673 is a novel bioinformatically detectable regulatory, non protein
TTTAGCTTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336673 was detected
GGTCGAGATG is described with additional reference to Figs. 9-15.

AGGTTTCTCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGGTCTCT encoded by the human genome.

GCAGGGTCA GAM336673 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336673 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336673 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336673 precursor RNA is designated SEQ ID:7091, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7091 is located from position 36425183 to position 36425281 relative to chromosome 21 on the `-` strand.

GAM336673 precursor RNA folds onto itself, forming GAM336673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336673 precursor RNA, designated SEQ ID NO: 7091, and a schematic representation of a predicted secondary folding of GAM336673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336673 folded precursor RNA yielding a GAM336673 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336673 RNA, hereby incorporated herein.

GAM336673 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336673 target RNA, herein designated GAM TARGET RNA.

GAM336673 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336673 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336673 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336673 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336673 RNA, herein designated GAM RNA, to target binding sites on GAM336673 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336673 target RNA into GAM336673 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336673 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336673 target genes. The mRNA of each one of this plurality of GAM336673 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336673 RNA, herein designated GAM RNA, and which when bound by GAM336673 RNA causes inhibition of translation of the GAM336673 target mRNA into a corresponding GAM336673 target protein.

The mechanism of the translational inhibition exerted by GAM336673 RNA, herein designated GAM RNA, on one or more GAM336673 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336673 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336673 RNA, herein designated GAM RNA, of GAM336673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336673 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336673 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336673 RNA correlate with, and may be deduced from, the identity of the GAM336673 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336674 6128 CCTTGGCATT Fig. 8 further provides a conceptual description of another novel bioinformatically
CATTATTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTCCAGTTC Messenger 336674 (GAM336674) oligonucleotides modulates expression of respective target
TCAGCACAGC genes whose function and utility is known in the art.

GCTTGGCACA GAM336674 is a novel bioinformatically detectable regulatory, non protein
TAGTAGGAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336674 was detected
TCAGGAAGTG is described with additional reference to Figs. 9-15.

TTTATGGGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAATGGGGT encoded by the human genome.

GATGATGTTG GAM336674 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AGG GAM336674 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336674 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336674 precursor RNA is designated SEQ ID:6128, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6128 is located from position 36639912 to position 36640014 relative to chromosome 22 on the `+` strand.

GAM336674 precursor RNA folds onto itself, forming GAM336674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336674 precursor RNA, designated SEQ ID NO: 6128, and a schematic representation of a predicted secondary folding of GAM336674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336674 folded precursor RNA yielding a GAM336674 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336674 RNA, hereby incorporated herein.

GAM336674 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336674 target RNA, herein designated GAM TARGET RNA.

GAM336674 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336674 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336674 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336674 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336674 RNA, herein designated GAM RNA, to target binding sites on GAM336674 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336674 target RNA into GAM336674 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336674 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336674 target genes. The mRNA of each one of this plurality of GAM336674 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336674 RNA, herein designated GAM RNA, and which when bound by GAM336674 RNA causes inhibition of translation of the GAM336674 target mRNA into a corresponding GAM336674 target protein.

The mechanism of the translational inhibition exerted by GAM336674 RNA, herein designated GAM RNA, on one or more GAM336674 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336674 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336674 RNA, herein designated GAM RNA, of GAM336674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336674 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336674 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336674 RNA correlate with, and may be deduced from, the identity of the GAM336674 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336675 6339 GAGACAGGAG AATCACTTGA ATCTGAGAGG TGGAAGTTGC AGTGAGCCGA GATTGTGCCA CTGCACTCCA GCCTGGGTGA CAGAGTGAAA CTCCATCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336675 (GAM336675) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336675 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336675 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336675 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336675 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336675 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336675 precursor RNA is designated SEQ ID:6339, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6339 is located from position 36669197 to position 36669295 relative to chromosome 9 on the `+` strand.

GAM336675 precursor RNA folds onto itself, forming GAM336675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336675 precursor RNA, designated SEQ ID NO: 6339, and a schematic representation of a predicted secondary folding of GAM336675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336675 folded precursor RNA yielding a GAM336675 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336675 RNA, hereby incorporated herein.

GAM336675 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336675 target RNA, herein designated GAM TARGET RNA.

GAM336675 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336675 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336675 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336675 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336675 RNA, herein designated GAM RNA, to target binding sites on GAM336675 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336675 target RNA into GAM336675 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336675 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336675 target genes. The mRNA of each one of this plurality of GAM336675 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336675 RNA, herein designated GAM RNA, and which when bound by GAM336675 RNA causes inhibition of translation of the GAM336675 target mRNA into a corresponding GAM336675 target protein.

The mechanism of the translational inhibition exerted by GAM336675 RNA, herein designated GAM RNA, on one or more GAM336675 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336675 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336675 RNA, herein designated GAM RNA, of

GAM336675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336675 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336675 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336675 RNA correlate with, and may be deduced from, the identity of the GAM336675 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336676 7229 TGGCTTCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGTGCTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTACAGGTG Messenger 336676 (GAM336676) oligonucleotides modulates expression of respective target

TGAGCCACCG genes whose function and utility is known in the art.

CACCTGGCCA GAM336676 is a novel bioinformatically detectable regulatory, non protein

TCCCGGCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336676 was detected

TTTCTATTCT is described with additional reference to Figs. 9-15.

GCTGTGAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TA encoded by the human genome.

GAM336676 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336676 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336676 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336676 precursor RNA is designated SEQ ID:7229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7229 is located from position 36951386 to position 36951467 relative to chromosome 22 on the `+` strand.

GAM336676 precursor RNA folds onto itself, forming GAM336676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336676 precursor RNA, designated SEQ ID NO: 7229, and

a schematic representation of a predicted secondary folding of GAM336676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336676 folded precursor RNA yielding a GAM336676 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336676 RNA, hereby incorporated herein.

GAM336676 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336676 target RNA, herein designated GAM TARGET RNA.

GAM336676 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336676 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336676 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336676 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336676 RNA, herein designated GAM RNA, to target binding sites on GAM336676 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336676 target RNA into GAM336676 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336676 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336676 target genes. The mRNA of each one of this plurality of GAM336676 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336676 RNA, herein designated GAM RNA, and which when bound by GAM336676 RNA causes inhibition of translation of the GAM336676 target mRNA into a corresponding GAM336676 target protein.

The mechanism of the translational inhibition exerted by GAM336676 RNA, herein designated GAM RNA, on one or more GAM336676 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336676 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336676 RNA, herein designated GAM RNA, of GAM336676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336676 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336676 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336676 RNA correlate with, and may be deduced from, the identity of the GAM336676 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336677 6989 TCAATACTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGGCACAC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTCTGCTT Messenger 336677 (GAM336677) oligonucleotides modulates expression of respective target

TCTACACTGT genes whose function and utility is known in the art.

TGCCGGAGAA GAM336677 is a novel bioinformatically detectable regulatory, non protein

GGGTCATAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336677 was detected

GTGAAGTTTG is described with additional reference to Figs. 9-15.

GCAGAAAAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGGCCATTG encoded by the human genome.

TCTAGTACTG GAM336677 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336677 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336677 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336677 precursor RNA is designated SEQ ID:6989, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6989 is located from position 36970296 to position 36970396 relative to chromosome 17 on the `+` strand.

GAM336677 precursor RNA folds onto itself, forming GAM336677 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336677 precursor RNA, designated SEQ ID NO: 6989, and a schematic representation of a predicted secondary folding of GAM336677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336677 folded precursor RNA yielding a GAM336677 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336677 RNA, hereby incorporated herein.

GAM336677 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336677 target RNA, herein designated GAM TARGET RNA.

GAM336677 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336677 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336677 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336677 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336677 RNA, herein designated GAM RNA, to target binding sites on GAM336677 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336677 target RNA into GAM336677 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336677 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336677 target genes. The mRNA of each one of this plurality of GAM336677 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336677 RNA,

herein designated GAM RNA, and which when bound by GAM336677 RNA causes inhibition of translation of the GAM336677 target mRNA into a corresponding GAM336677 target protein.

The mechanism of the translational inhibition exerted by GAM336677 RNA, herein designated GAM RNA, on one or more GAM336677 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336677 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336677 RNA, herein designated GAM RNA, of GAM336677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336677 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336677 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336677 RNA correlate with, and may be deduced from, the identity of the GAM336677 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336681 5716 AGAATCGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACCCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCACAGGTT Messenger 336681 (GAM336681) oligonucleotides modulates expression of respective target

GCAGTAGGCC genes whose function and utility is known in the art.

GAGATTGTGC GAM336681 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336681 was detected

CAGCCTGGGT is described with additional reference to Figs. 9-15.

GGCAGAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACT encoded by the human genome.

GAM336681 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336681 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336681 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336681 precursor RNA is designated SEQ ID:5716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5716 is located from position 37422585 to position 37422668 relative to chromosome 9 on the `+` strand.

GAM336681 precursor RNA folds onto itself, forming GAM336681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336681 precursor RNA, designated SEQ ID NO: 5716, and a schematic representation of a predicted secondary folding of GAM336681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336681 folded precursor RNA yielding a GAM336681 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336681 RNA, hereby incorporated herein.

GAM336681 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336681 target RNA, herein designated GAM TARGET RNA.

GAM336681 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336681 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336681 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336681 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336681 RNA, herein designated GAM RNA, to target binding sites on GAM336681 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336681 target RNA

into GAM336681 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336681 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336681 target genes. The mRNA of each one of this plurality of GAM336681 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336681 RNA, herein designated GAM RNA, and which when bound by GAM336681 RNA causes inhibition of translation of the GAM336681 target mRNA into a corresponding GAM336681 target protein.

The mechanism of the translational inhibition exerted by GAM336681 RNA, herein designated GAM RNA, on one or more GAM336681 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336681 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336681 RNA, herein designated GAM RNA, of GAM336681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336681 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336681 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336681 RNA correlate with, and may be deduced from, the identity of the GAM336681 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336683 7156 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336683 (GAM336683) oligonucleotides modulates expression of respective target

GCGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336683 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336683 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACTCCGTCTC GAM336683 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336683 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336683 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336683 precursor RNA is designated SEQ ID:7156, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7156 is located from position 37445099 to position 37445199 relative to chromosome 21 on the `-` strand.

GAM336683 precursor RNA folds onto itself, forming GAM336683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336683 precursor RNA, designated SEQ ID NO: 7156, and a schematic representation of a predicted secondary folding of GAM336683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336683 folded precursor RNA yielding a GAM336683 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336683 RNA, hereby incorporated herein. Expression of GAM336683 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336683 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336683 target RNA, herein designated GAM TARGET RNA.

GAM336683 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336683 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336683 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336683 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336683 RNA, herein designated GAM RNA, to target binding sites on GAM336683 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336683 target RNA into GAM336683 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336683 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336683 target genes. The mRNA of each one of this plurality of GAM336683 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336683 RNA, herein designated GAM RNA, and which when bound by GAM336683 RNA causes inhibition of translation of the GAM336683 target mRNA into a corresponding GAM336683 target protein.

The mechanism of the translational inhibition exerted by GAM336683 RNA, herein designated GAM RNA, on one or more GAM336683 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336683 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336683 RNA, herein designated GAM RNA, of GAM336683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336683 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336683 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336683 RNA correlate with, and may be deduced from, the identity of the GAM336683 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336685 7081 TCTTTCTCTA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTGTCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGTAGTATG Messenger 336685 (GAM336685) oligonucleotides modulates expression of respective target
CATCTTTTTC genes whose function and utility is known in the art.

TCCACTAGCC GAM336685 is a novel bioinformatically detectable regulatory, non protein
AGGGGCTATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336685 was detected
GAGGCCCTGA is described with additional reference to Figs. 9-15.

ATAGAACAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGCAGCTA encoded by the human genome.

GCAAGGGCGG GAM336685 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AAGGAAGAGA GAM336685 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAGA GAM336685 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336685 precursor RNA is designated SEQ ID:7081, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7081 is located from position 37606073 to position 37606186 relative to chromosome 20 on the `+` strand.

GAM336685 precursor RNA folds onto itself, forming GAM336685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336685 precursor RNA, designated SEQ ID NO: 7081, and a schematic representation of a predicted secondary folding of GAM336685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336685 folded precursor RNA yielding a GAM336685 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336685 RNA, hereby incorporated herein.

GAM336685 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336685 target RNA, herein designated GAM TARGET RNA.

GAM336685 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336685 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336685 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336685 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336685 RNA, herein designated GAM RNA, to target binding sites on GAM336685 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336685 target RNA into GAM336685 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336685 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336685 target genes. The mRNA of each one of this plurality of GAM336685 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336685 RNA, herein designated GAM RNA, and which when bound by GAM336685 RNA causes inhibition of translation of the GAM336685 target mRNA into a corresponding GAM336685 target protein.

The mechanism of the translational inhibition exerted by GAM336685 RNA, herein designated GAM RNA, on one or more GAM336685 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336685 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336685 RNA, herein designated GAM RNA, of GAM336685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336685 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336685 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336685 RNA correlate with, and may be deduced from, the identity of the GAM336685 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336686 7142 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGAAG Messenger 336686 (GAM336686) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCTG GAM336686 is a novel bioinformatically detectable regulatory, non protein
AGATTGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336686 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATAAGAGCAA encoded by the human genome.

AACTCTGTCT GAM336686 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336686 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336686 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336686 precursor RNA is designated SEQ ID:7142, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7142 is located from position 37624000 to position 37624101 relative to chromosome 3 on the `+` strand.

GAM336686 precursor RNA folds onto itself, forming GAM336686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336686 precursor RNA, designated SEQ ID NO: 7142, and a schematic representation of a predicted secondary folding of GAM336686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336686 folded precursor RNA yielding a GAM336686 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336686 RNA, hereby incorporated herein. Expression of GAM336686 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336686 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336686 target RNA, herein designated GAM TARGET RNA.

GAM336686 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336686 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336686 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336686 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336686 RNA, herein designated GAM RNA, to target binding sites on GAM336686 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336686 target RNA into GAM336686 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336686 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336686 target genes. The mRNA of each one of this plurality of GAM336686 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336686 RNA, herein designated GAM RNA, and which when bound by GAM336686 RNA causes inhibition of translation of the GAM336686 target mRNA into a corresponding GAM336686 target protein.

The mechanism of the translational inhibition exerted by GAM336686 RNA, herein designated GAM RNA, on one or more GAM336686 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336686 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336686 RNA, herein designated GAM RNA, of

GAM336686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336686 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336686 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336686 RNA correlate with, and may be deduced from, the identity of the GAM336686 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336689 6246 CTGTTGCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTGGAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTGGCACC Messenger 336689 (GAM336689) oligonucleotides modulates expression of respective target

ATCTCAGCTC genes whose function and utility is known in the art.

ACTGGAGCGT GAM336689 is a novel bioinformatically detectable regulatory, non protein

CTGCCTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336689 was detected

GTTCAAGTGA is described with additional reference to Figs. 9-15.

TTCTCCTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCAGCATCCC encoded by the human genome.

AAGTAGCTGG GAM336689 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GACTACAG GAM336689 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336689 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336689 precursor RNA is designated SEQ ID:6246, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6246 is located from position 37948104 to position 37948211 relative to chromosome 7 on the `+` strand.

GAM336689 precursor RNA folds onto itself, forming GAM336689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336689 precursor RNA, designated SEQ ID NO: 6246, and a schematic representation of a predicted secondary folding of GAM336689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336689 folded precursor RNA yielding a GAM336689 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336689 RNA, hereby incorporated herein.

GAM336689 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336689 target RNA, herein designated GAM TARGET RNA.

GAM336689 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336689 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336689 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336689 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336689 RNA, herein designated GAM RNA, to target binding sites on GAM336689 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336689 target RNA into GAM336689 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336689 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336689 target genes. The mRNA of each one of this plurality of GAM336689 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336689 RNA, herein designated GAM RNA, and which when bound by GAM336689 RNA causes inhibition of translation of the GAM336689 target mRNA into a corresponding GAM336689 target protein.

The mechanism of the translational inhibition exerted by GAM336689 RNA, herein designated GAM RNA, on one or more GAM336689 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336689 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336689 RNA, herein designated GAM RNA, of GAM336689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336689 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336689 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336689 RNA correlate with, and may be deduced from, the identity of the GAM336689 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336690 7092 TGAGAAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTCATTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCCTAGGC Messenger 336690 (GAM336690) oligonucleotides modulates expression of respective target

CGGAGTGCAG genes whose function and utility is known in the art.

TGACATGATC GAM336690 is a novel bioinformatically detectable regulatory, non protein

TTGGCTCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336690 was detected

GCAATCTCCA is described with additional reference to Figs. 9-15.

CCTCCAGGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGTGATTC encoded by the human genome.

TCCTGCCTCA GAM336690 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336690 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336690 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336690 precursor RNA is designated SEQ ID:7092, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7092 is located from position 37983831 to position 37983930 relative to chromosome 7 on the `-` strand.

GAM336690 precursor RNA folds onto itself, forming GAM336690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336690 precursor RNA, designated SEQ ID NO: 7092, and a schematic representation of a predicted secondary folding of GAM336690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336690 folded precursor RNA yielding a GAM336690 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336690 RNA, hereby incorporated herein.

GAM336690 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336690 target RNA, herein designated GAM TARGET RNA.

GAM336690 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336690 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336690 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336690 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336690 RNA, herein designated GAM RNA, to target binding sites on GAM336690 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336690 target RNA into GAM336690 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336690 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336690 target genes. The mRNA of each one of this plurality of GAM336690 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336690 RNA, herein designated GAM RNA, and which when bound by GAM336690 RNA causes inhibition of translation of the GAM336690 target mRNA into a corresponding GAM336690 target protein.

The mechanism of the translational inhibition exerted by GAM336690 RNA, herein designated GAM RNA, on one or more GAM336690 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336690 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336690 RNA, herein designated GAM RNA, of GAM336690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336690 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336690 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336690 RNA correlate with, and may be deduced from, the identity of the GAM336690 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336691 6926 GTGTGACTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTGCTACTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGATTTTACT Messenger 336691 (GAM336691) oligonucleotides modulates expression of respective target
GTTCAGGAAA genes whose function and utility is known in the art.

GTGAAGCAGA GAM336691 is a novel bioinformatically detectable regulatory, non protein
GAGGTTCAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336691 was detected
GTCTTACTCA is described with additional reference to Figs. 9-15.

AGGTCACAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336691 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336691 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336691 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336691 precursor RNA is designated SEQ ID:6926, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6926 is located from position 38081171 to position 38081249 relative to chromosome 20 on the `+` strand.

GAM336691 precursor RNA folds onto itself, forming GAM336691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336691 precursor RNA, designated SEQ ID NO: 6926, and a schematic representation of a predicted secondary folding of GAM336691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336691 folded precursor RNA yielding a GAM336691 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336691 RNA, hereby incorporated herein.

GAM336691 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336691 target RNA, herein designated GAM TARGET RNA.

GAM336691 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336691 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336691 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336691 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336691 RNA, herein designated GAM RNA, to target binding sites on GAM336691 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336691 target RNA

into GAM336691 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336691 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336691 target genes. The mRNA of each one of this plurality of GAM336691 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336691 RNA, herein designated GAM RNA, and which when bound by GAM336691 RNA causes inhibition of translation of the GAM336691 target mRNA into a corresponding GAM336691 target protein.

The mechanism of the translational inhibition exerted by GAM336691 RNA, herein designated GAM RNA, on one or more GAM336691 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336691 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336691 RNA, herein designated GAM RNA, of GAM336691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336691 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336691 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336691 RNA correlate with, and may be deduced from, the identity of the GAM336691 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336697 7005 TCACTTGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCTGCAG Messenger 336697 (GAM336697) oligonucleotides modulates expression of respective target

TGAGCTATGA genes whose function and utility is known in the art.

TTGCACCACT GAM336697 is a novel bioinformatically detectable regulatory, non protein

GTACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336697 was detected

CTGGGTGACA is described with additional reference to Figs. 9-15.

GAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336697 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336697 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336697 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336697 precursor RNA is designated SEQ ID:7005, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7005 is located from position 38541864 to position 38541939 relative to chromosome 8 on the `+` strand.

GAM336697 precursor RNA folds onto itself, forming GAM336697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336697 precursor RNA, designated SEQ ID NO: 7005, and a schematic representation of a predicted secondary folding of GAM336697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336697 folded precursor RNA yielding a GAM336697 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336697 RNA, hereby incorporated herein.

GAM336697 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336697 target RNA, herein designated GAM TARGET RNA.

GAM336697 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336697 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336697 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336697 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336697 RNA, herein designated GAM RNA, to target binding sites on GAM336697 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336697 target RNA into GAM336697 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336697 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336697 target genes. The mRNA of each one of this plurality of GAM336697 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336697 RNA, herein designated GAM RNA, and which when bound by GAM336697 RNA causes inhibition of translation of the GAM336697 target mRNA into a corresponding GAM336697 target protein.

The mechanism of the translational inhibition exerted by GAM336697 RNA, herein designated GAM RNA, on one or more GAM336697 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336697 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336697 RNA, herein designated GAM RNA, of GAM336697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336697 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336697 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336697 RNA correlate with, and may be deduced from, the identity of the GAM336697 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336699 6107 CCTATCACAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCTGCCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCTCTGGT Messenger 336699 (GAM336699) oligonucleotides modulates expression of respective target

AAACTGCAGG genes whose function and utility is known in the art.

TTCCCTCTGC GAM336699 is a novel bioinformatically detectable regulatory, non protein
CTCAGTTGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336699 was detected
GCCAGGGATT is described with additional reference to Figs. 9-15.

CTGACCAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATGATGGG encoded by the human genome.

GAM336699 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336699 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336699 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336699 precursor RNA is designated SEQ ID:6107, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6107 is located from position 38679676 to position 38679764 relative to chromosome 15 on the `+` strand.

GAM336699 precursor RNA folds onto itself, forming GAM336699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336699 precursor RNA, designated SEQ ID NO: 6107, and a schematic representation of a predicted secondary folding of GAM336699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336699 folded precursor RNA yielding a GAM336699 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336699 RNA, hereby incorporated herein.

GAM336699 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336699 target RNA, herein designated GAM TARGET RNA.

GAM336699 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336699 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336699 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336699 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336699 RNA, herein designated GAM RNA, to target binding sites on GAM336699 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336699 target RNA into GAM336699 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336699 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336699 target genes. The mRNA of each one of this plurality of GAM336699 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336699 RNA, herein designated GAM RNA, and which when bound by GAM336699 RNA causes inhibition of translation of the GAM336699 target mRNA into a corresponding GAM336699 target protein.

The mechanism of the translational inhibition exerted by GAM336699 RNA, herein designated GAM RNA, on one or more GAM336699 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336699 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336699 RNA, herein designated GAM RNA, of GAM336699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336699 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336699 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336699 RNA correlate with, and may be deduced from, the identity of the GAM336699 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336701 6936 GTTACTTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAGTAGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGGATATTT Messenger 336701 (GAM336701) oligonucleotides modulates expression of respective target
TTGATGCCCA genes whose function and utility is known in the art.

GAGTGTTGTC GAM336701 is a novel bioinformatically detectable regulatory, non protein
TTCCCCGTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336701 was detected
AGGGTATCTC is described with additional reference to Figs. 9-15.

ATTCTGATCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACCGAATTG encoded by the human genome.

GCCATCCATA GAM336701 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTGAGAAGTG GAM336701 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GC GAM336701 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336701 precursor RNA is designated SEQ ID:6936, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6936 is located from position 38828150 to position 38828261 relative to chromosome 22 on the `+` strand.

GAM336701 precursor RNA folds onto itself, forming GAM336701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336701 precursor RNA, designated SEQ ID NO: 6936, and a schematic representation of a predicted secondary folding of GAM336701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336701 folded precursor RNA yielding a GAM336701 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336701 RNA, hereby incorporated herein.

GAM336701 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336701 target RNA, herein designated GAM TARGET RNA.

GAM336701 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336701 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336701 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336701 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336701 RNA, herein designated GAM RNA, to target binding sites on GAM336701 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336701 target RNA into GAM336701 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336701 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336701 target genes. The mRNA of each one of this plurality of GAM336701 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336701 RNA, herein designated GAM RNA, and which when bound by GAM336701 RNA causes inhibition of translation of the GAM336701 target mRNA into a corresponding GAM336701 target protein.

The mechanism of the translational inhibition exerted by GAM336701 RNA, herein designated GAM RNA, on one or more GAM336701 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336701 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336701 RNA, herein designated GAM RNA, of GAM336701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336701 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336701 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336701 RNA correlate with, and may be deduced from, the identity of the GAM336701 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336702 5861 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336702 (GAM336702) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336702 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336702 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336702 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336702 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336702 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336702 precursor RNA is designated SEQ ID:5861, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5861 is located from position 38853404 to position 38853485 relative to chromosome 6 on the `+` strand.

GAM336702 precursor RNA folds onto itself, forming GAM336702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336702 precursor RNA, designated SEQ ID NO: 5861, and a schematic representation of a predicted secondary folding of GAM336702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336702 folded precursor RNA yielding a GAM336702 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336702 RNA, hereby incorporated herein.

GAM336702 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336702 target RNA, herein designated GAM TARGET RNA.

GAM336702 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336702 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336702 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336702 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336702 RNA, herein designated GAM RNA, to target binding sites on GAM336702 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336702 target RNA into GAM336702 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336702 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336702 target genes. The mRNA of each one of this plurality of GAM336702 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336702 RNA, herein designated GAM RNA, and which when bound by GAM336702 RNA causes inhibition of translation of the GAM336702 target mRNA into a corresponding GAM336702 target protein.

The mechanism of the translational inhibition exerted by GAM336702 RNA, herein designated GAM RNA, on one or more GAM336702 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336702 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336702 RNA, herein designated GAM RNA, of GAM336702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336702 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336702 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336702 RNA correlate with, and may be deduced from, the identity of the GAM336702 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336703 6358 GAGATTGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGCCCAGGT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTTGAGACT Messenger 336703 (GAM336703) oligonucleotides modulates expression of respective target

GCAGTGAACC genes whose function and utility is known in the art.

ATGATTGTGC GAM336703 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336703 was detected

AGCCTGGGTG is described with additional reference to Figs. 9-15.

ACAGTTAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCTGTCTC encoded by the human genome.

GAM336703 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336703 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336703 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336703 precursor RNA is designated SEQ ID:6358, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6358 is located from position 39141230 to position 39141318 relative to chromosome 21 on the `-` strand.

GAM336703 precursor RNA folds onto itself, forming GAM336703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336703 precursor RNA, designated SEQ ID NO: 6358, and a schematic representation of a predicted secondary folding of GAM336703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336703 folded precursor RNA yielding a GAM336703 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336703 RNA, hereby incorporated herein.

GAM336703 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336703 target RNA, herein designated GAM TARGET RNA.

GAM336703 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336703 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336703 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336703 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336703 RNA, herein designated GAM RNA, to target binding sites on GAM336703 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336703 target RNA into GAM336703 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336703 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336703 target genes. The mRNA of each one of this plurality of GAM336703 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336703 RNA, herein designated GAM RNA, and which when bound by GAM336703 RNA causes inhibition of translation of the GAM336703 target mRNA into a corresponding GAM336703 target protein.

The mechanism of the translational inhibition exerted by GAM336703 RNA, herein designated GAM RNA, on one or more GAM336703 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336703 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336703 RNA, herein designated GAM RNA, of GAM336703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336703 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336703 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336703 RNA correlate with, and may be deduced from, the identity of the GAM336703 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336704 6697 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACGCCG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGTCGGAGG Messenger 336704 (GAM336704) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCATGATCGC GAM336704 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336704 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCT encoded by the human genome.

GAM336704 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336704 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336704 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336704 precursor RNA is designated SEQ ID:6697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6697 is located from position 39394031 to position 39394118 relative to chromosome 1 on the `+` strand.

GAM336704 precursor RNA folds onto itself, forming GAM336704 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336704 precursor RNA, designated SEQ ID NO: 6697, and a schematic representation of a predicted secondary folding of GAM336704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336704 folded precursor RNA yielding a GAM336704 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336704 RNA, hereby incorporated herein. Expression of GAM336704 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336704 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336704 target RNA, herein designated GAM TARGET RNA.

GAM336704 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336704 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336704 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336704 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336704 RNA, herein designated GAM RNA, to target binding sites on GAM336704 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336704 target RNA into GAM336704 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336704 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336704 target genes. The mRNA of each one of this

plurality of GAM336704 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336704 RNA, herein designated GAM RNA, and which when bound by GAM336704 RNA causes inhibition of translation of the GAM336704 target mRNA into a corresponding GAM336704 target protein.

The mechanism of the translational inhibition exerted by GAM336704 RNA, herein designated GAM RNA, on one or more GAM336704 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336704 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336704 RNA, herein designated GAM RNA, of GAM336704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336704 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336704 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336704 RNA correlate with, and may be deduced from, the identity of the GAM336704 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336705 6334 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACGCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTCGGAGGT Messenger 336705 (GAM336705) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CATGATCGCG GAM336705 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336705 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTC encoded by the human genome.

GAM336705 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336705 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336705 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336705 precursor RNA is designated SEQ ID:6334, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6334 is located from position 39394032 to position 39394117 relative to chromosome 1 on the `+` strand.

GAM336705 precursor RNA folds onto itself, forming GAM336705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336705 precursor RNA, designated SEQ ID NO: 6334, and a schematic representation of a predicted secondary folding of GAM336705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336705 folded precursor RNA yielding a GAM336705 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336705 RNA, hereby incorporated herein. Expression of GAM336705 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336705 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336705 target RNA, herein designated GAM TARGET RNA.

GAM336705 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336705 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336705 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336705 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336705 RNA, herein designated GAM RNA, to target binding sites on GAM336705 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336705 target RNA into GAM336705 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336705 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336705 target genes. The mRNA of each one of this plurality of GAM336705 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336705 RNA, herein designated GAM RNA, and which when bound by GAM336705 RNA causes inhibition of translation of the GAM336705 target mRNA into a corresponding GAM336705 target protein.

The mechanism of the translational inhibition exerted by GAM336705 RNA, herein designated GAM RNA, on one or more GAM336705 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336705 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336705 RNA, herein designated GAM RNA, of GAM336705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336705 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336705 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336705 RNA correlate with, and may be deduced from, the identity of the GAM336705 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336706 6372 GAGGCAGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCCAGTGAT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCATTTGGTT Messenger 336706 (GAM336706) oligonucleotides modulates expression of respective target

GTTCATTTTG genes whose function and utility is known in the art.

TTGGGACTGA GAM336706 is a novel bioinformatically detectable regulatory, non protein

GAACAGCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336706 was detected

ATGACTGGAT is described with additional reference to Figs. 9-15.

CCACACTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TC encoded by the human genome.

GAM336706 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336706 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336706 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336706 precursor RNA is designated SEQ ID:6372, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6372 is located from position 39568547 to position 39568628 relative to chromosome X on the `+` strand.

GAM336706 precursor RNA folds onto itself, forming GAM336706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336706 precursor RNA, designated SEQ ID NO: 6372, and a schematic representation of a predicted secondary folding of GAM336706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336706 folded precursor RNA yielding a GAM336706 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336706 RNA, hereby incorporated herein.

GAM336706 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336706 target RNA, herein designated GAM TARGET RNA.

GAM336706 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336706 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336706 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336706 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336706 RNA, herein designated GAM RNA, to target binding sites on GAM336706 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336706 target RNA into GAM336706 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336706 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336706 target genes. The mRNA of each one of this plurality of GAM336706 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336706 RNA, herein designated GAM RNA, and which when bound by GAM336706 RNA causes inhibition of translation of the GAM336706 target mRNA into a corresponding GAM336706 target protein.

The mechanism of the translational inhibition exerted by GAM336706 RNA, herein designated GAM RNA, on one or more GAM336706 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336706 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336706 RNA, herein designated GAM RNA, of GAM336706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336706 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336706 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336706 RNA correlate with, and may be deduced from, the identity of the GAM336706 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336707 6510 GCCGTAGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAGCCAGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGTGTGGCA Messenger 336707 (GAM336707) oligonucleotides modulates expression of respective target
GAAGGCTCTG genes whose function and utility is known in the art.

GATTAGTCCT GAM336707 is a novel bioinformatically detectable regulatory, non protein
GGGTTCTAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336707 was detected
TCTGGGTCTT is described with additional reference to Figs. 9-15.

CTACAAACCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTCCATGAA encoded by the human genome.

TTAGGC GAM336707 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336707 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336707 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336707 precursor RNA is designated SEQ ID:6510, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6510 is located from position 39605027 to position 39605122 relative to chromosome 22 on the `+` strand.

GAM336707 precursor RNA folds onto itself, forming GAM336707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336707 precursor RNA, designated SEQ ID NO: 6510, and a schematic representation of a predicted secondary folding of GAM336707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336707 folded precursor RNA yielding a GAM336707 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336707 RNA, hereby incorporated herein.

GAM336707 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336707 target RNA, herein designated GAM TARGET RNA.

GAM336707 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336707 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336707 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336707 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336707 RNA, herein designated GAM RNA, to target binding sites on GAM336707 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336707 target RNA into GAM336707 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336707 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336707 target genes. The mRNA of each one of this plurality of GAM336707 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336707 RNA, herein designated GAM RNA, and which when bound by GAM336707 RNA causes inhibition of translation of the GAM336707 target mRNA into a corresponding GAM336707 target protein.

The mechanism of the translational inhibition exerted by GAM336707 RNA, herein designated GAM RNA, on one or more GAM336707 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336707 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336707 RNA, herein designated GAM RNA, of GAM336707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336707 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336707 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336707 RNA correlate with, and may be deduced from, the identity of the GAM336707 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336709 6353 GAGATGAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCCAGGAGG Messenger 336709 (GAM336709) oligonucleotides modulates expression of respective target
TGGAGGCTGT genes whose function and utility is known in the art.

AGTGAGCTAT GAM336709 is a novel bioinformatically detectable regulatory, non protein
GATTGTGGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336709 was detected
CAGCAGTCCA is described with additional reference to Figs. 9-15.

GCCTGGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CACAAGGATA encoded by the human genome.

CCCTGTCTT GAM336709 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336709 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336709 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336709 precursor RNA is designated SEQ ID:6353, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6353 is located from position 39769473 to position 39769571 relative to chromosome 22 on the `+` strand.

GAM336709 precursor RNA folds onto itself, forming GAM336709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336709 precursor RNA, designated SEQ ID NO: 6353, and a schematic representation of a predicted secondary folding of GAM336709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336709 folded precursor RNA yielding a GAM336709 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336709 RNA, hereby incorporated herein.

GAM336709 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336709 target RNA, herein designated GAM TARGET RNA.

GAM336709 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336709 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336709 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336709 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336709 RNA, herein designated GAM RNA, to target binding sites on GAM336709 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336709 target RNA into GAM336709 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336709 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336709 target genes. The mRNA of each one of this plurality of GAM336709 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336709 RNA, herein designated GAM RNA, and which when bound by GAM336709 RNA causes inhibition of translation of the GAM336709 target mRNA into a corresponding GAM336709 target protein.

The mechanism of the translational inhibition exerted by GAM336709 RNA, herein designated GAM RNA, on one or more GAM336709 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336709 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336709 RNA, herein designated GAM RNA, of GAM336709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336709 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336709 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336709 RNA correlate with, and may be deduced from, the identity of the GAM336709 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336710 6224 CTGGAGGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAAGATTAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTATTTATT Messenger 336710 (GAM336710) oligonucleotides modulates expression of respective target
TTATTTTGTT genes whose function and utility is known in the art.

TTCTGCTATA GAM336710 is a novel bioinformatically detectable regulatory, non protein
TTTAGAGTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336710 was detected
CAAAAAAATA is described with additional reference to Figs. 9-15.

GAGCAGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCTGCTGT encoded by the human genome.

CTCCAG GAM336710 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336710 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336710 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336710 precursor RNA is designated SEQ ID:6224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6224 is located from position 39771457 to position 39771552 relative to chromosome 15 on the `-` strand.

GAM336710 precursor RNA folds onto itself, forming GAM336710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336710 precursor RNA, designated SEQ ID NO: 6224, and a schematic representation of a predicted secondary folding of GAM336710 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336710 folded precursor RNA yielding a GAM336710 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336710 RNA, hereby incorporated herein.

GAM336710 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336710 target RNA, herein designated GAM TARGET RNA.

GAM336710 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336710 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336710 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336710 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336710 RNA, herein designated GAM RNA, to target binding sites on GAM336710 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336710 target RNA into GAM336710 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336710 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336710 target genes. The mRNA of each one of this plurality of GAM336710 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336710 RNA, herein designated GAM RNA, and which when bound by GAM336710 RNA causes inhibition of translation of the GAM336710 target mRNA into a corresponding GAM336710 target protein.

The mechanism of the translational inhibition exerted by GAM336710 RNA, herein designated GAM RNA, on one or more GAM336710 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336710 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336710 RNA, herein designated GAM RNA, of GAM336710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336710 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336710 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336710 RNA correlate with, and may be deduced from, the identity of the GAM336710 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336713 6084 CCCTACTATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCTTGGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACATCCAGCA Messenger 336713 (GAM336713) oligonucleotides modulates expression of respective target

CATACTCAAG genes whose function and utility is known in the art.

GTGGGAGGGC GAM336713 is a novel bioinformatically detectable regulatory, non protein

AGTAAGCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336713 was detected

ATGGTGGCTA is described with additional reference to Figs. 9-15.

GATGTTTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGACAAGAG encoded by the human genome.

TAGGG GAM336713 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336713 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336713 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336713 precursor RNA is designated SEQ ID:6084, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6084 is located from position 39876405 to position 39876499 relative to chromosome 19 on the `-` strand.

GAM336713 precursor RNA folds onto itself, forming GAM336713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336713 precursor RNA, designated SEQ ID NO: 6084, and a schematic representation of a predicted secondary folding of GAM336713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336713 folded precursor RNA yielding a GAM336713 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336713 RNA, hereby incorporated herein.

GAM336713 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336713 target RNA, herein designated GAM TARGET RNA.

GAM336713 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336713 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336713 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336713 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336713 RNA, herein designated GAM RNA, to target binding sites on GAM336713 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336713 target RNA into GAM336713 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336713 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336713 target genes. The mRNA of each one of this plurality of GAM336713 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336713 RNA, herein designated GAM RNA, and which when bound by GAM336713 RNA causes inhibition of translation of the GAM336713 target mRNA into a corresponding GAM336713 target protein.

The mechanism of the translational inhibition exerted by GAM336713 RNA, herein designated GAM RNA, on one or more GAM336713 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336713 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336713 RNA, herein designated GAM RNA, of GAM336713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336713 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336713 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336713 RNA correlate with, and may be deduced from, the identity of the GAM336713 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336715 6326 GAGAATCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCAGAGGT Messenger 336715 (GAM336715) oligonucleotides modulates expression of respective target

GGTGGTGAGT genes whose function and utility is known in the art.

CGAGATAGCA GAM336715 is a novel bioinformatically detectable regulatory, non protein

CCATTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336715 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAACTC encoded by the human genome.

GAM336715 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336715 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336715 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336715 precursor RNA is designated SEQ

ID:6326, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6326 is located from position 39935490 to position 39935576 relative to chromosome X on the `+` strand.

GAM336715 precursor RNA folds onto itself, forming GAM336715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336715 precursor RNA, designated SEQ ID NO: 6326, and a schematic representation of a predicted secondary folding of GAM336715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336715 folded precursor RNA yielding a GAM336715 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336715 RNA, hereby incorporated herein. Expression of GAM336715 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336715 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336715 target RNA, herein designated GAM TARGET RNA.

GAM336715 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336715 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336715 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336715 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336715 RNA, herein designated GAM RNA, to target binding sites on GAM336715 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336715 target RNA

into GAM336715 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336715 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336715 target genes. The mRNA of each one of this plurality of GAM336715 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336715 RNA, herein designated GAM RNA, and which when bound by GAM336715 RNA causes inhibition of translation of the GAM336715 target mRNA into a corresponding GAM336715 target protein.

The mechanism of the translational inhibition exerted by GAM336715 RNA, herein designated GAM RNA, on one or more GAM336715 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336715 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336715 RNA, herein designated GAM RNA, of GAM336715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336715 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336715 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336715 RNA correlate with, and may be deduced from, the identity of the GAM336715 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336716 6606 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGACGGAGT Messenger 336716 (GAM336716) oligonucleotides modulates expression of respective target

TTGTGGTGAG genes whose function and utility is known in the art.

CCGAGATCAC GAM336716 is a novel bioinformatically detectable regulatory, non protein

ACCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336716 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAAACTCC encoded by the human genome.

GAM336716 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336716 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336716 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336716 precursor RNA is designated SEQ ID:6606, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6606 is located from position 40002861 to position 40002949 relative to chromosome 4 on the `+` strand.

GAM336716 precursor RNA folds onto itself, forming GAM336716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336716 precursor RNA, designated SEQ ID NO: 6606, and a schematic representation of a predicted secondary folding of GAM336716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336716 folded precursor RNA yielding a GAM336716 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336716 RNA, hereby incorporated herein. Expression of GAM336716 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336716 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336716 target RNA, herein designated GAM TARGET RNA.

GAM336716 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336716 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336716 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336716 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336716 RNA, herein designated GAM RNA, to target binding sites on GAM336716 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336716 target RNA into GAM336716 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336716 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336716 target genes. The mRNA of each one of this plurality of GAM336716 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336716 RNA, herein designated GAM RNA, and which when bound by GAM336716 RNA causes inhibition of translation of the GAM336716 target mRNA into a corresponding GAM336716 target protein.

The mechanism of the translational inhibition exerted by GAM336716 RNA, herein designated GAM RNA, on one or more GAM336716 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336716 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336716 RNA, herein designated GAM RNA, of GAM336716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336716 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336716 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336716 RNA correlate with, and may be deduced from, the identity of the GAM336716 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336717 7000 TCACTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAGGAGACG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTTGTGG Messenger 336717 (GAM336717) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TCACACCATT GCACTCCAGC CTGGGCAACA ACAGTGA GAM336717 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336717 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336717 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336717 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336717 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336717 precursor RNA is designated SEQ ID:7000, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7000 is located from position 40002867 to position 40002943 relative to chromosome 4 on the `+` strand.

GAM336717 precursor RNA folds onto itself, forming GAM336717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336717 precursor RNA, designated SEQ ID NO: 7000, and a schematic representation of a predicted secondary folding of GAM336717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336717 folded precursor RNA yielding a GAM336717 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336717 RNA, hereby incorporated herein. Expression of GAM336717 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336717 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336717 target RNA, herein designated GAM TARGET RNA.

GAM336717 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336717 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336717 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336717 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336717 RNA, herein designated GAM RNA, to target binding sites on GAM336717 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336717 target RNA into GAM336717 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336717 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336717 target genes. The mRNA of each one of this plurality of GAM336717 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336717 RNA, herein designated GAM RNA, and which when bound by GAM336717 RNA causes inhibition of translation of the GAM336717 target mRNA into a corresponding GAM336717 target protein.

The mechanism of the translational inhibition exerted by GAM336717 RNA, herein designated GAM RNA, on one or more GAM336717 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336717 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336717 RNA, herein designated GAM RNA, of GAM336717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336717 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336717 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336717 RNA correlate with, and may be deduced from, the identity of the GAM336717 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336718 5753 AGCTGCAGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTTCTTCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TATGAGCTTG Messenger 336718 (GAM336718) oligonucleotides modulates expression of respective target
GACACATCAA genes whose function and utility is known in the art.

TCCTAAACTA GAM336718 is a novel bioinformatically detectable regulatory, non protein
GGAGTGTGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336718 was detected
GGAGGAAGGG is described with additional reference to Figs. 9-15.

AGGAGCAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCAGCAGTT encoded by the human genome.

GAM336718 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336718 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336718 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336718 precursor RNA is designated SEQ ID:5753, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5753 is located from position 40074931 to position 40075020 relative to chromosome 22 on the `+` strand.

GAM336718 precursor RNA folds onto itself, forming GAM336718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336718 precursor RNA, designated SEQ ID NO: 5753, and a schematic representation of a predicted secondary folding of GAM336718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336718 folded precursor RNA yielding a GAM336718 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM336718 RNA, hereby incorporated herein.

GAM336718 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336718 target RNA, herein designated GAM TARGET RNA.

GAM336718 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336718 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336718 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336718 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336718 RNA, herein designated GAM RNA, to target binding sites on GAM336718 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336718 target RNA into GAM336718 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336718 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336718 target genes. The mRNA of each one of this plurality of GAM336718 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336718 RNA, herein designated GAM RNA, and which when bound by GAM336718 RNA causes inhibition of translation of the GAM336718 target mRNA into a corresponding GAM336718 target protein.

The mechanism of the translational inhibition exerted by GAM336718 RNA, herein designated GAM RNA, on one or more GAM336718 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336718 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336718 RNA, herein designated GAM RNA, of GAM336718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336718 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336718 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336718 RNA correlate with, and may be deduced from, the identity of the GAM336718 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336719 6655 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCGGAGG Messenger 336719 (GAM336719) oligonucleotides modulates expression of respective target
TTGCGGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336719 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336719 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAAACTCC encoded by the human genome.

GAM336719 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336719 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336719 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336719 precursor RNA is designated SEQ ID:6655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6655 is located from position 40082689 to position 40082777 relative to chromosome 22 on the `-` strand.

GAM336719 precursor RNA folds onto itself, forming GAM336719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336719 precursor RNA, designated SEQ ID NO: 6655, and a schematic representation of a predicted secondary folding of GAM336719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336719 folded precursor RNA yielding a GAM336719 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336719 RNA, hereby incorporated herein. Expression of GAM336719 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336719 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336719 target RNA, herein designated GAM TARGET RNA.

GAM336719 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336719 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336719 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336719 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336719 RNA, herein designated GAM RNA, to target binding sites on GAM336719 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336719 target RNA into GAM336719 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336719 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336719 target genes. The mRNA of each one of this plurality of GAM336719 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336719 RNA, herein designated GAM RNA, and which when bound by GAM336719 RNA causes inhibition of translation of the GAM336719 target mRNA into a corresponding GAM336719 target protein.

The mechanism of the translational inhibition exerted by GAM336719 RNA, herein designated GAM RNA, on one or more GAM336719 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336719 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336719 RNA, herein designated GAM RNA, of GAM336719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336719 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336719 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336719 RNA correlate with, and may be deduced from, the identity of the GAM336719 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336720 5800 AGTATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACCAGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCAGAGGCT Messenger 336720 (GAM336720) oligonucleotides modulates expression of respective target

GCATGCAGTG genes whose function and utility is known in the art.

AGCCAAGATT GAM336720 is a novel bioinformatically detectable regulatory, non protein

GCACCACTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336720 was detected

ACTCTAACCT is described with additional reference to Figs. 9-15.

GGGCAACAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGATACT encoded by the human genome.

GAM336720 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336720 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336720 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336720 precursor RNA is designated SEQ ID:5800, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5800 is located from position 40086888 to position 40086975 relative to chromosome 17 on the `+` strand.

GAM336720 precursor RNA folds onto itself, forming GAM336720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336720 precursor RNA, designated SEQ ID NO: 5800, and a schematic representation of a predicted secondary folding of GAM336720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336720 folded precursor RNA yielding a GAM336720 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336720 RNA, hereby incorporated herein.

GAM336720 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336720 target RNA, herein designated GAM TARGET RNA.

GAM336720 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336720 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336720 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336720 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336720 RNA, herein designated GAM RNA, to target binding sites on GAM336720 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336720 target RNA into GAM336720 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336720 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336720 target genes. The mRNA of each one of this plurality of GAM336720 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336720 RNA, herein designated GAM RNA, and which when bound by GAM336720 RNA causes inhibition of translation of the GAM336720 target mRNA into a corresponding GAM336720 target protein.

The mechanism of the translational inhibition exerted by GAM336720 RNA, herein designated GAM RNA, on one or more GAM336720 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336720 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336720 RNA, herein designated GAM RNA, of GAM336720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336720 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336720 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336720 RNA correlate with, and may be deduced from, the identity of the GAM336720 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336722 5862 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336722 (GAM336722) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336722 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336722 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336722 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336722 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336722 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336722 precursor RNA is designated SEQ

ID:5862, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5862 is located from position 40227896 to position 40227977 relative to chromosome 8 on the `+` strand.

GAM336722 precursor RNA folds onto itself, forming GAM336722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336722 precursor RNA, designated SEQ ID NO: 5862, and a schematic representation of a predicted secondary folding of GAM336722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336722 folded precursor RNA yielding a GAM336722 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336722 RNA, hereby incorporated herein.

GAM336722 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336722 target RNA, herein designated GAM TARGET RNA.

GAM336722 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336722 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336722 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336722 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336722 RNA, herein designated GAM RNA, to target binding sites on GAM336722 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336722 target RNA into GAM336722 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336722 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336722 target genes. The mRNA of each one of this plurality of GAM336722 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336722 RNA, herein designated GAM RNA, and which when bound by GAM336722 RNA causes inhibition of translation of the GAM336722 target mRNA into a corresponding GAM336722 target protein.

The mechanism of the translational inhibition exerted by GAM336722 RNA, herein designated GAM RNA, on one or more GAM336722 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336722 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336722 RNA, herein designated GAM RNA, of GAM336722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336722 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336722 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336722 RNA correlate with, and may be deduced from, the identity of the GAM336722 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336723 6319 GAGAATCACT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCAGAGGT Messenger 336723 (GAM336723) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

TGAGATTATG GAM336723 is a novel bioinformatically detectable regulatory, non protein

CCATTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336723 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

TGACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAACTC encoded by the human genome.

GAM336723 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336723 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336723 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336723 precursor RNA is designated SEQ ID:6319, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6319 is located from position 40285217 to position 40285302 relative to chromosome 19 on the `+` strand.

GAM336723 precursor RNA folds onto itself, forming GAM336723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336723 precursor RNA, designated SEQ ID NO: 6319, and a schematic representation of a predicted secondary folding of GAM336723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336723 folded precursor RNA yielding a GAM336723 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336723 RNA, hereby incorporated herein.

GAM336723 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336723 target RNA, herein designated GAM TARGET RNA.

GAM336723 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336723 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336723 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336723 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336723 RNA, herein designated GAM RNA, to target binding sites on GAM336723 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336723 target RNA into GAM336723 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336723 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336723 target genes. The mRNA of each one of this plurality of GAM336723 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336723 RNA, herein designated GAM RNA, and which when bound by GAM336723 RNA causes inhibition of translation of the GAM336723 target mRNA into a corresponding GAM336723 target protein.

The mechanism of the translational inhibition exerted by GAM336723 RNA, herein designated GAM RNA, on one or more GAM336723 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336723 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336723 RNA, herein designated GAM RNA, of GAM336723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336723 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336723 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336723 RNA correlate with, and may be deduced from, the identity of the GAM336723 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336727 6918 GTGGTCATAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTCCTTTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTCTAATA Messenger 336727 (GAM336727) oligonucleotides modulates expression of respective target

ACCTGAGCTT genes whose function and utility is known in the art.

CTGTTATGAA GAM336727 is a novel bioinformatically detectable regulatory, non protein
GCTGGGACCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336727 was detected
TTAGAGCCTC is described with additional reference to Figs. 9-15.

AGGATGATCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTGTTTGTT encoded by the human genome.

TGTGAAGC GAM336727 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336727 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336727 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336727 precursor RNA is designated SEQ ID:6918, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6918 is located from position 40420544 to position 40420641 relative to chromosome 22 on the `+` strand.

GAM336727 precursor RNA folds onto itself, forming GAM336727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336727 precursor RNA, designated SEQ ID NO: 6918, and a schematic representation of a predicted secondary folding of GAM336727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336727 folded precursor RNA yielding a GAM336727 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336727 RNA, hereby incorporated herein.

GAM336727 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336727 target RNA, herein designated GAM TARGET RNA.

GAM336727 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336727 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336727 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336727 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336727 RNA, herein designated GAM RNA, to target binding sites on GAM336727 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336727 target RNA into GAM336727 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336727 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336727 target genes. The mRNA of each one of this plurality of GAM336727 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336727 RNA, herein designated GAM RNA, and which when bound by GAM336727 RNA causes inhibition of translation of the GAM336727 target mRNA into a corresponding GAM336727 target protein.

The mechanism of the translational inhibition exerted by GAM336727 RNA, herein designated GAM RNA, on one or more GAM336727 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336727 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336727 RNA, herein designated GAM RNA, of GAM336727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336727 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336727 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336727 RNA correlate with, and may be deduced from, the identity of the GAM336727 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336728 5808 AGTCTCACTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTTGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTGAAGTCA Messenger 336728 (GAM336728) oligonucleotides modulates expression of respective target
ACGGCATGAT genes whose function and utility is known in the art.

CTCAGCTCAC GAM336728 is a novel bioinformatically detectable regulatory, non protein
TGCAACCTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336728 was detected
ACCTCCTGGG is described with additional reference to Figs. 9-15.

TTCAAGCAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTCGTGCCT encoded by the human genome.

CAGCCTCCCA GAM336728 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AGTAGCTTGG GAM336728 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
ATT GAM336728 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336728 precursor RNA is designated SEQ ID:5808, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5808 is located from position 40578117 to position 40578229 relative to chromosome 19 on the `+` strand.

GAM336728 precursor RNA folds onto itself, forming GAM336728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336728 precursor RNA, designated SEQ ID NO: 5808, and a schematic representation of a predicted secondary folding of GAM336728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336728 folded precursor RNA yielding a GAM336728 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336728 RNA, hereby incorporated herein.

GAM336728 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336728 target RNA, herein designated GAM TARGET RNA.

GAM336728 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336728 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336728 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336728 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336728 RNA, herein designated GAM RNA, to target binding sites on GAM336728 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336728 target RNA into GAM336728 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336728 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336728 target genes. The mRNA of each one of this plurality of GAM336728 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336728 RNA, herein designated GAM RNA, and which when bound by GAM336728 RNA causes inhibition of translation of the GAM336728 target mRNA into a corresponding GAM336728 target protein.

The mechanism of the translational inhibition exerted by GAM336728 RNA, herein designated GAM RNA, on one or more GAM336728 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336728 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336728 RNA, herein designated GAM RNA, of GAM336728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336728 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336728 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336728 RNA correlate with, and may be deduced from, the identity of the GAM336728 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336729 6705 GGAGACCCAG GACCCGGGAG AGAGGTAGAG GGGAGCAGAG ACAGCCACCA GCTTCTATCT TCTGCTCTAA GCACATTCTT TCACGAGTTT AAGTTTCC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336729 (GAM336729) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336729 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336729 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336729 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336729 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336729 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336729 precursor RNA is designated SEQ ID:6705, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6705 is located from position 40608767 to position 40608864 relative to chromosome 15 on the `+` strand.

GAM336729 precursor RNA folds onto itself, forming GAM336729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336729 precursor RNA, designated SEQ ID NO: 6705, and a schematic representation of a predicted secondary folding of GAM336729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336729 folded precursor RNA yielding a GAM336729 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336729 RNA, hereby incorporated herein.

GAM336729 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336729 target RNA, herein designated GAM TARGET RNA.

GAM336729 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336729 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336729 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336729 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336729 RNA, herein designated GAM RNA, to target binding sites on GAM336729 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336729 target RNA into GAM336729 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336729 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336729 target genes. The mRNA of each one of this plurality of GAM336729 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336729 RNA, herein designated GAM RNA, and which when bound by GAM336729 RNA causes inhibition of translation of the GAM336729 target mRNA into a corresponding GAM336729 target protein.

The mechanism of the translational inhibition exerted by GAM336729 RNA, herein designated GAM RNA, on one or more GAM336729 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336729 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336729 RNA, herein designated GAM RNA, of

GAM336729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336729 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336729 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336729 RNA correlate with, and may be deduced from, the identity of the GAM336729 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336730 6472 GATCCCAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCATCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCTATGTCC Messenger 336730 (GAM336730) oligonucleotides modulates expression of respective target

TTGCTATGTA genes whose function and utility is known in the art.

TGTACAAAAA GAM336730 is a novel bioinformatically detectable regulatory, non protein

TGAGAAATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336730 was detected

AAATTGTGTT is described with additional reference to Figs. 9-15.

TAAAAACCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATCTCATTAC encoded by the human genome.

ATACTTTCTC GAM336730 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAACCACTCT GAM336730 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TTGAGTGTCA GAM336730 precursor RNA does not encode a protein. A nucleotide sequence identical or

TTTTTGGGTC highly similar to the nucleotide sequence of GAM336730 precursor RNA is designated SEQ

ID:6472, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6472 is located from position 40623807 to position 40623936 relative to chromosome 11 on the `-` strand.

GAM336730 precursor RNA folds onto itself, forming GAM336730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336730 precursor RNA, designated SEQ ID NO: 6472, and a schematic representation of a predicted secondary folding of GAM336730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336730 folded precursor RNA yielding a GAM336730 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336730 RNA, hereby incorporated herein.

GAM336730 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336730 target RNA, herein designated GAM TARGET RNA.

GAM336730 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336730 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336730 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336730 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336730 RNA, herein designated GAM RNA, to target binding sites on GAM336730 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336730 target RNA into GAM336730 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336730 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336730 target genes. The mRNA of each one of this plurality of GAM336730 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336730 RNA, herein designated GAM RNA, and which when bound by GAM336730 RNA causes inhibition of translation of the GAM336730 target mRNA into a corresponding GAM336730 target protein.

The mechanism of the translational inhibition exerted by GAM336730 RNA, herein designated GAM RNA, on one or more GAM336730 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336730 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336730 RNA, herein designated GAM RNA, of GAM336730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336730 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336730 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336730 RNA correlate with, and may be deduced from, the identity of the GAM336730 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336731 7333 TTGGGCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGCTTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAAGCCTTC Messenger 336731 (GAM336731) oligonucleotides modulates expression of respective target

TCTGTGTACT genes whose function and utility is known in the art.

CTGGAGATAG GAM336731 is a novel bioinformatically detectable regulatory, non protein

ATGGAGAAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336731 was detected

GTTTTCAGAT is described with additional reference to Figs. 9-15.

TCCTGGGAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM336731 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336731 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336731 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336731 precursor RNA is designated SEQ ID:7333, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7333 is located from position 40762540 to position 40762621 relative to chromosome 17 on the `-` strand.

GAM336731 precursor RNA folds onto itself, forming GAM336731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336731 precursor RNA, designated SEQ ID NO: 7333, and a schematic representation of a predicted secondary folding of GAM336731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336731 folded precursor RNA yielding a GAM336731 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336731 RNA, hereby incorporated herein.

GAM336731 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336731 target RNA, herein designated GAM TARGET RNA.

GAM336731 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336731 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336731 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336731 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336731 RNA, herein designated GAM RNA, to target binding sites on GAM336731 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336731 target RNA into GAM336731 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336731 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336731 target genes. The mRNA of each one of this

plurality of GAM336731 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336731 RNA, herein designated GAM RNA, and which when bound by GAM336731 RNA causes inhibition of translation of the GAM336731 target mRNA into a corresponding GAM336731 target protein.

The mechanism of the translational inhibition exerted by GAM336731 RNA, herein designated GAM RNA, on one or more GAM336731 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336731 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336731 RNA, herein designated GAM RNA, of GAM336731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336731 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336731 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336731 RNA correlate with, and may be deduced from, the identity of the GAM336731 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336732 7235 TGGGCCCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGCTTTGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAGCCTTCT Messenger 336732 (GAM336732) oligonucleotides modulates expression of respective target

CTGTGTACTC genes whose function and utility is known in the art.

TGGAGATAGA GAM336732 is a novel bioinformatically detectable regulatory, non protein

TGGAGAAGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336732 was detected

TTTTCAGATT is described with additional reference to Figs. 9-15.

CCTGGGAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336732 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336732 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336732 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336732 precursor RNA is designated SEQ ID:7235, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7235 is located from position 40762541 to position 40762620 relative to chromosome 17 on the `-` strand.

GAM336732 precursor RNA folds onto itself, forming GAM336732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336732 precursor RNA, designated SEQ ID NO: 7235, and a schematic representation of a predicted secondary folding of GAM336732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336732 folded precursor RNA yielding a GAM336732 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336732 RNA, hereby incorporated herein.

GAM336732 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336732 target RNA, herein designated GAM TARGET RNA.

GAM336732 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336732 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336732 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336732 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336732 RNA, herein designated GAM RNA, to target binding sites on GAM336732 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336732 target RNA into GAM336732 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336732 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336732 target genes. The mRNA of each one of this plurality of GAM336732 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336732 RNA, herein designated GAM RNA, and which when bound by GAM336732 RNA causes inhibition of translation of the GAM336732 target mRNA into a corresponding GAM336732 target protein.

The mechanism of the translational inhibition exerted by GAM336732 RNA, herein designated GAM RNA, on one or more GAM336732 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336732 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336732 RNA, herein designated GAM RNA, of GAM336732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336732 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336732 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336732 RNA correlate with, and may be deduced from, the identity of the GAM336732 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336734 6487 GCAGAGGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGGGACTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGCCCATTG Messenger 336734 (GAM336734) oligonucleotides modulates expression of respective target
AAGAACTTGG genes whose function and utility is known in the art.

GAGTGTATTC GAM336734 is a novel bioinformatically detectable regulatory, non protein
TGGGAACAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336734 was detected
CACCCATCTT is described with additional reference to Figs. 9-15.

CTCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336734 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336734 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336734 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336734 precursor RNA is designated SEQ ID:6487, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6487 is located from position 40925498 to position 40925573 relative to chromosome 8 on the `-` strand.

GAM336734 precursor RNA folds onto itself, forming GAM336734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336734 precursor RNA, designated SEQ ID NO: 6487, and a schematic representation of a predicted secondary folding of GAM336734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336734 folded precursor RNA yielding a GAM336734 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336734 RNA, hereby incorporated herein.

GAM336734 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336734 target RNA, herein designated GAM TARGET RNA.

GAM336734 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336734 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336734 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336734 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336734 RNA, herein designated GAM RNA, to target binding sites on GAM336734 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336734 target RNA into GAM336734 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336734 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336734 target genes. The mRNA of each one of this plurality of GAM336734 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336734 RNA, herein designated GAM RNA, and which when bound by GAM336734 RNA causes inhibition of translation of the GAM336734 target mRNA into a corresponding GAM336734 target protein.

The mechanism of the translational inhibition exerted by GAM336734 RNA, herein designated GAM RNA, on one or more GAM336734 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336734 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336734 RNA, herein designated GAM RNA, of GAM336734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336734 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336734 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336734 RNA correlate with, and may be deduced from, the identity of the GAM336734 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336736 5863 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336736 (GAM336736) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336736 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336736 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336736 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336736 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336736 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336736 precursor RNA is designated SEQ ID:5863, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5863 is located from position 41122390 to position 41122471 relative to chromosome 4 on the `+` strand.

GAM336736 precursor RNA folds onto itself, forming GAM336736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336736 precursor RNA, designated SEQ ID NO: 5863, and a schematic representation of a predicted secondary folding of GAM336736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336736 folded precursor RNA yielding a GAM336736 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336736 RNA, hereby incorporated herein.

GAM336736 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336736 target RNA, herein designated GAM TARGET RNA.

GAM336736 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336736 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336736 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336736 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336736 RNA, herein designated GAM RNA, to target binding sites on GAM336736 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336736 target RNA into GAM336736 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336736 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336736 target genes. The mRNA of each one of this plurality of GAM336736 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336736 RNA, herein designated GAM RNA, and which when bound by GAM336736 RNA causes inhibition of translation of the GAM336736 target mRNA into a corresponding GAM336736 target protein.

The mechanism of the translational inhibition exerted by GAM336736 RNA, herein designated GAM RNA, on one or more GAM336736 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336736 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336736 RNA, herein designated GAM RNA, of GAM336736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336736 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336736 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336736 RNA correlate with, and may be deduced from, the identity of the GAM336736 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336738 7131 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGGAG Messenger 336738 (GAM336738) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM336738 is a novel bioinformatically detectable regulatory, non protein
AGATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336738 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGGGCGA encoded by the human genome.

GACTCTGTCT GAM336738 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336738 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336738 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336738 precursor RNA is designated SEQ ID:7131, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7131 is located from position 41382416 to position 41382517 relative to chromosome 17 on the `+` strand.

GAM336738 precursor RNA folds onto itself, forming GAM336738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336738 precursor RNA, designated SEQ ID NO: 7131, and a schematic representation of a predicted secondary folding of GAM336738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336738 folded precursor RNA yielding a GAM336738 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336738 RNA, hereby incorporated herein. Expression of GAM336738 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336738 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336738 target RNA, herein designated GAM TARGET RNA.

GAM336738 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336738 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336738 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336738 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336738 RNA, herein designated GAM RNA, to target binding sites on GAM336738 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336738 target RNA into GAM336738 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336738 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336738 target genes. The mRNA of each one of this plurality of GAM336738 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336738 RNA, herein designated GAM RNA, and which when bound by GAM336738 RNA causes inhibition of translation of the GAM336738 target mRNA into a corresponding GAM336738 target protein.

The mechanism of the translational inhibition exerted by GAM336738 RNA, herein designated GAM RNA, on one or more GAM336738 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336738 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336738 RNA, herein designated GAM RNA, of GAM336738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336738 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336738 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336738 RNA correlate with, and may be deduced from, the identity of the GAM336738 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336739 6225 CTGGAGGCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGAGTCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TATCTGCAAT Messenger 336739 (GAM336739) oligonucleotides modulates expression of respective target
AGGACAATGA genes whose function and utility is known in the art.

TTCTCCTAGC GAM336739 is a novel bioinformatically detectable regulatory, non protein
AGATCTGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336739 was detected
CTCCTATGCT is described with additional reference to Figs. 9-15.

CAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336739 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336739 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336739 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336739 precursor RNA is designated SEQ ID:6225, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6225 is located from position 41425604 to position 41425676 relative to chromosome 20 on the `+` strand.

GAM336739 precursor RNA folds onto itself, forming GAM336739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336739 precursor RNA, designated SEQ ID NO: 6225, and a schematic representation of a predicted secondary folding of GAM336739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336739 folded precursor RNA yielding a GAM336739 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336739 RNA, hereby incorporated herein.

GAM336739 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336739 target RNA, herein designated GAM TARGET RNA.

GAM336739 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336739 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336739 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336739 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336739 RNA, herein designated GAM RNA, to target binding sites on GAM336739 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336739 target RNA into GAM336739 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336739 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336739 target genes. The mRNA of each one of this plurality of GAM336739 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336739 RNA, herein designated GAM RNA, and which when bound by GAM336739 RNA causes inhibition of translation of the GAM336739 target mRNA into a corresponding GAM336739 target protein.

The mechanism of the translational inhibition exerted by GAM336739 RNA, herein designated GAM RNA, on one or more GAM336739 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336739 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336739 RNA, herein designated GAM RNA, of GAM336739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336739 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336739 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336739 RNA correlate with, and may be deduced from, the identity of the GAM336739 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336740 5959 ATCTGCATGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTGTTGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTGTTGTA Messenger 336740 (GAM336740) oligonucleotides modulates expression of respective target

CAGTGGAGGA genes whose function and utility is known in the art.

GAAACAATGC GAM336740 is a novel bioinformatically detectable regulatory, non protein

ATTTTGGGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336740 was detected

CAGCTAGGAC is described with additional reference to Figs. 9-15.

CCATGCAGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336740 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336740 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336740 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336740 precursor RNA is designated SEQ ID:5959, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5959 is located from position 41446302 to position 41446381 relative to chromosome 17 on the `-` strand.

GAM336740 precursor RNA folds onto itself, forming GAM336740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336740 precursor RNA, designated SEQ ID NO: 5959, and a schematic representation of a predicted secondary folding of GAM336740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336740 folded precursor RNA yielding a GAM336740 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336740 RNA, hereby incorporated herein.

GAM336740 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336740 target RNA, herein designated GAM TARGET RNA.

GAM336740 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336740 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336740 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336740 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336740 RNA, herein designated GAM RNA, to target binding sites on GAM336740 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336740 target RNA into GAM336740 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336740 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336740 target genes. The mRNA of each one of this plurality of GAM336740 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336740 RNA, herein designated GAM RNA, and which when bound by GAM336740 RNA causes inhibition of translation of the GAM336740 target mRNA into a corresponding GAM336740 target protein.

The mechanism of the translational inhibition exerted by GAM336740 RNA, herein designated GAM RNA, on one or more GAM336740 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336740 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336740 RNA, herein designated GAM RNA, of GAM336740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336740 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336740 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336740 RNA correlate with, and may be deduced from, the identity of the GAM336740 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336743 6138 CGCACATCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTACTCCACA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAGAGACTT Messenger 336743 (GAM336743) oligonucleotides modulates expression of respective target
CATTTTGTTG genes whose function and utility is known in the art.

ATAAACCCTA GAM336743 is a novel bioinformatically detectable regulatory, non protein
TGAATGTAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336743 was detected
GAATGTGGGA is described with additional reference to Figs. 9-15.

AGGCGTTCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTGCG encoded by the human genome.

GAM336743 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336743 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336743 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336743 precursor RNA is designated SEQ ID:6138, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6138 is located from position 41560746 to position 41560831 relative to chromosome 19 on the `-` strand.

GAM336743 precursor RNA folds onto itself, forming GAM336743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336743 precursor RNA, designated SEQ ID NO: 6138, and a schematic representation of a predicted secondary folding of GAM336743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336743 folded precursor RNA yielding a GAM336743 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336743 RNA, hereby incorporated herein.

GAM336743 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336743 target RNA, herein designated GAM TARGET RNA.

GAM336743 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336743 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336743 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336743 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336743 RNA, herein designated GAM RNA, to target binding sites on GAM336743 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336743 target RNA into GAM336743 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336743 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336743 target genes. The mRNA of each one of this

plurality of GAM336743 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336743 RNA, herein designated GAM RNA, and which when bound by GAM336743 RNA causes inhibition of translation of the GAM336743 target mRNA into a corresponding GAM336743 target protein.

The mechanism of the translational inhibition exerted by GAM336743 RNA, herein designated GAM RNA, on one or more GAM336743 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336743 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336743 RNA, herein designated GAM RNA, of GAM336743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336743 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336743 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336743 RNA correlate with, and may be deduced from, the identity of the GAM336743 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336744 6958 TAAGGAATGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAAAACCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTATTTGTGG Messenger 336744 (GAM336744) oligonucleotides modulates expression of respective target

CTCAGACCTT genes whose function and utility is known in the art.

ACTCGACATC GAM336744 is a novel bioinformatically detectable regulatory, non protein

ACAGAATTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336744 was detected

CACTGGTGAG is described with additional reference to Figs. 9-15.

AAACCCTATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AATGTAAGGA encoded by the human genome.

ATGTGGGAAA GAM336744 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GCCTTTAGTA GAM336744 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GTGGTTCAAA GAM336744 precursor RNA does not encode a protein. A nucleotide sequence identical or

CTTCACTCGA highly similar to the nucleotide sequence of GAM336744 precursor RNA is designated SEQ

ID:6958, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6958 is located from position 41616369 to position 41616498 relative to chromosome 19 on the `-` strand.

GAM336744 precursor RNA folds onto itself, forming GAM336744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336744 precursor RNA, designated SEQ ID NO: 6958, and a schematic representation of a predicted secondary folding of GAM336744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336744 folded precursor RNA yielding a GAM336744 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336744 RNA, hereby incorporated herein.

GAM336744 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336744 target RNA, herein designated GAM TARGET RNA.

GAM336744 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336744 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336744 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336744 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336744 RNA, herein designated GAM RNA, to target binding sites on GAM336744 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336744 target RNA into GAM336744 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336744 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336744 target genes. The mRNA of each one of this plurality of GAM336744 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336744 RNA, herein designated GAM RNA, and which when bound by GAM336744 RNA causes inhibition of translation of the GAM336744 target mRNA into a corresponding GAM336744 target protein.

The mechanism of the translational inhibition exerted by GAM336744 RNA, herein designated GAM RNA, on one or more GAM336744 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336744 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336744 RNA, herein designated GAM RNA, of GAM336744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336744 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336744 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336744 RNA correlate with, and may be deduced from, the identity of the GAM336744 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336745 5756 AGGAATGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAAACCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTTGTGGCT Messenger 336745 (GAM336745) oligonucleotides modulates expression of respective target

CAGACCTTAC genes whose function and utility is known in the art.

TCGACATCAC GAM336745 is a novel bioinformatically detectable regulatory, non protein

AGAATTCACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336745 was detected

CTGGTGAGAA is described with additional reference to Figs. 9-15.

ACCCTATGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTAAGGAAT encoded by the human genome.

GTGGGAAAGC GAM336745 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTTTAGTAGT GAM336745 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GGTTCAAACT GAM336745 precursor RNA does not encode a protein. A nucleotide sequence identical or

TCACT highly similar to the nucleotide sequence of GAM336745 precursor RNA is designated SEQ ID:5756, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5756 is located from position 41616372 to position 41616496 relative to chromosome 19 on the `-` strand.

GAM336745 precursor RNA folds onto itself, forming GAM336745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336745 precursor RNA, designated SEQ ID NO: 5756, and a schematic representation of a predicted secondary folding of GAM336745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336745 folded precursor RNA yielding a GAM336745 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336745 RNA, hereby incorporated herein.

GAM336745 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336745 target RNA, herein designated GAM TARGET RNA.

GAM336745 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336745 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336745 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336745 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336745 RNA, herein designated GAM RNA, to target binding sites on GAM336745 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336745 target RNA into GAM336745 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336745 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336745 target genes. The mRNA of each one of this plurality of GAM336745 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336745 RNA, herein designated GAM RNA, and which when bound by GAM336745 RNA causes inhibition of translation of the GAM336745 target mRNA into a corresponding GAM336745 target protein.

The mechanism of the translational inhibition exerted by GAM336745 RNA, herein designated GAM RNA, on one or more GAM336745 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336745 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336745 RNA, herein designated GAM RNA, of GAM336745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336745 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336745 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336745 RNA correlate with, and may be deduced from, the identity of the GAM336745 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336746 6324 GAGAATCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTGGAGGC Messenger 336746 (GAM336746) oligonucleotides modulates expression of respective target
TGCAGTAAGC genes whose function and utility is known in the art.

CGAGATTGTG GAM336746 is a novel bioinformatically detectable regulatory, non protein
CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336746 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAAACTATCT encoded by the human genome.

C GAM336746 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336746 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336746 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336746 precursor RNA is designated SEQ ID:6324, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6324 is located from position 41616885 to position 41616975 relative to chromosome 8 on the `+` strand.

GAM336746 precursor RNA folds onto itself, forming GAM336746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336746 precursor RNA, designated SEQ ID NO: 6324, and a schematic representation of a predicted secondary folding of GAM336746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336746 folded precursor RNA yielding a GAM336746 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336746 RNA, hereby incorporated herein. Expression of GAM336746 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336746 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336746 target RNA, herein designated GAM TARGET RNA.

GAM336746 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336746 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336746 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336746 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336746 RNA, herein designated GAM RNA, to target binding sites on GAM336746 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336746 target RNA into GAM336746 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336746 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336746 target genes. The mRNA of each one of this plurality of GAM336746 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336746 RNA, herein designated GAM RNA, and which when bound by GAM336746 RNA causes inhibition of translation of the GAM336746 target mRNA into a corresponding GAM336746 target protein.

The mechanism of the translational inhibition exerted by GAM336746 RNA, herein designated GAM RNA, on one or more GAM336746 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336746 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336746 RNA, herein designated GAM RNA, of GAM336746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336746 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336746 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336746 RNA correlate with, and may be deduced from, the identity of the GAM336746 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336747 6561 GCTTGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGAGGTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTGCAGTA Messenger 336747 (GAM336747) oligonucleotides modulates expression of respective target
AGCCGAGATT genes whose function and utility is known in the art.

GTGCCACTGC GAM336747 is a novel bioinformatically detectable regulatory, non protein
ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336747 was detected
GGGCAACAAG is described with additional reference to Figs. 9-15.

AGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336747 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336747 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336747 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336747 precursor RNA is designated SEQ ID:6561, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6561 is located from position 41616892 to position 41616964 relative to chromosome 8 on the `+` strand.

GAM336747 precursor RNA folds onto itself, forming GAM336747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336747 precursor RNA, designated SEQ ID NO: 6561, and a schematic representation of a predicted secondary folding of GAM336747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336747 folded precursor RNA yielding a GAM336747 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336747 RNA, hereby incorporated herein. Expression of GAM336747 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336747 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336747 target RNA, herein designated GAM TARGET RNA.

GAM336747 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336747 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336747 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336747 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336747 RNA, herein designated GAM RNA, to target binding sites on GAM336747 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336747 target RNA into GAM336747 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336747 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336747 target genes. The mRNA of each one of this plurality of GAM336747 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336747 RNA, herein designated GAM RNA, and which when bound by GAM336747 RNA causes inhibition of translation of the GAM336747 target mRNA into a corresponding GAM336747 target protein.

The mechanism of the translational inhibition exerted by GAM336747 RNA, herein designated GAM RNA, on one or more GAM336747 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336747 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336747 RNA, herein designated GAM RNA, of GAM336747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336747 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336747 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336747 RNA correlate with, and may be deduced from, the identity of the GAM336747 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336749 6865 GTAGTCCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCATAAAATC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAAAGTATT Messenger 336749 (GAM336749) oligonucleotides modulates expression of respective target
ACTGGTCTCC genes whose function and utility is known in the art.

CACTTTTAGG GAM336749 is a novel bioinformatically detectable regulatory, non protein
CTATTAACGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336749 was detected
TTGTAGTGAG is described with additional reference to Figs. 9-15.

AGTTTGTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCTTGTCG encoded by the human genome.

TGGTTGCCAG GAM336749 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GGGCTGGGGG GAM336749 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
C GAM336749 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336749 precursor RNA is designated SEQ ID:6865, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6865 is located from position 41749003 to position 41749113 relative to chromosome 19 on the `+` strand.

GAM336749 precursor RNA folds onto itself, forming GAM336749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336749 precursor RNA, designated SEQ ID NO: 6865, and a schematic representation of a predicted secondary folding of GAM336749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336749 folded precursor RNA yielding a GAM336749 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336749 RNA, hereby incorporated herein.

GAM336749 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336749 target RNA, herein designated GAM TARGET RNA.

GAM336749 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336749 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336749 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336749 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336749 RNA, herein designated GAM RNA, to target binding sites on GAM336749 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336749 target RNA into GAM336749 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336749 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336749 target genes. The mRNA of each one of this plurality of GAM336749 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336749 RNA, herein designated GAM RNA, and which when bound by GAM336749 RNA causes inhibition of translation of the GAM336749 target mRNA into a corresponding GAM336749 target protein.

The mechanism of the translational inhibition exerted by GAM336749 RNA, herein

designated GAM RNA, on one or more GAM336749 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336749 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336749 RNA, herein designated GAM RNA, of GAM336749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336749 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336749 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336749 RNA correlate with, and may be deduced from, the identity of the GAM336749 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336750 7157 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336750 (GAM336750) oligonucleotides modulates expression of respective target

GCGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM336750 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336750 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACTCCGTCTC GAM336750 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336750 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336750 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336750 precursor RNA is designated SEQ ID:7157, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:7157 is located from position 41757315 to position 41757415 relative to chromosome 6 on the `-` strand.

GAM336750 precursor RNA folds onto itself, forming GAM336750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336750 precursor RNA, designated SEQ ID NO: 7157, and a schematic representation of a predicted secondary folding of GAM336750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336750 folded precursor RNA yielding a GAM336750 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336750 RNA, hereby incorporated herein. Expression of GAM336750 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336750 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336750 target RNA, herein designated GAM TARGET RNA.

GAM336750 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336750 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336750 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336750 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336750 RNA, herein designated GAM RNA, to target binding sites on GAM336750 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336750 target RNA into GAM336750 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336750 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336750 target genes. The mRNA of each one of this plurality of GAM336750 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336750 RNA, herein designated GAM RNA, and which when bound by GAM336750 RNA causes inhibition of translation of the GAM336750 target mRNA into a corresponding GAM336750 target protein.

The mechanism of the translational inhibition exerted by GAM336750 RNA, herein designated GAM RNA, on one or more GAM336750 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336750 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336750 RNA, herein designated GAM RNA, of GAM336750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336750 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336750 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336750 RNA correlate with, and may be deduced from, the identity of the GAM336750 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336751 5761 AGGATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGCCTGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTCGAGGCT Messenger 336751 (GAM336751) oligonucleotides modulates expression of respective target

GCAGTGAGCT genes whose function and utility is known in the art.

ATGATCGTGC GAM336751 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336751 was detected

CAACCAGGCT is described with additional reference to Figs. 9-15.

GACCGAGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACCCT encoded by the human genome.

GAM336751 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336751 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336751 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336751 precursor RNA is designated SEQ ID:5761, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5761 is located from position 41765141 to position 41765226 relative to chromosome 8 on the `+` strand.

GAM336751 precursor RNA folds onto itself, forming GAM336751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336751 precursor RNA, designated SEQ ID NO: 5761, and a schematic representation of a predicted secondary folding of GAM336751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336751 folded precursor RNA yielding a GAM336751 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336751 RNA, hereby incorporated herein.

GAM336751 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336751 target RNA, herein designated GAM TARGET RNA.

GAM336751 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336751 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336751 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336751 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336751 RNA, herein designated GAM RNA, to target binding sites on GAM336751 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336751 target RNA into GAM336751 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336751 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336751 target genes. The mRNA of each one of this plurality of GAM336751 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336751 RNA, herein designated GAM RNA, and which when bound by GAM336751 RNA causes inhibition of translation of the GAM336751 target mRNA into a corresponding GAM336751 target protein.

The mechanism of the translational inhibition exerted by GAM336751 RNA, herein designated GAM RNA, on one or more GAM336751 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336751 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336751 RNA, herein designated GAM RNA, of GAM336751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336751 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336751 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336751 RNA correlate with, and may be deduced from, the identity of the GAM336751 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336752 5970 ATGCCTAATT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGCACATAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCCTGTCCC Messenger 336752 (GAM336752) oligonucleotides modulates expression of respective target

CAAAATCTAA genes whose function and utility is known in the art.

TAAACTCAGA GAM336752 is a novel bioinformatically detectable regulatory, non protein
AGTAATAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336752 was detected
TTTCTGGGTT is described with additional reference to Figs. 9-15.

TTTGTGGGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCCCTCTGA encoded by the human genome.

GCTAGGGTAG GAM336752 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTAAAAGTTG GAM336752 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CAT GAM336752 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336752 precursor RNA is designated SEQ ID:5970, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5970 is located from position 41880845 to position 41880957 relative to chromosome 7 on the `-` strand.

GAM336752 precursor RNA folds onto itself, forming GAM336752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336752 precursor RNA, designated SEQ ID NO: 5970, and a schematic representation of a predicted secondary folding of GAM336752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336752 folded precursor RNA yielding a GAM336752 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336752 RNA, hereby incorporated herein.

GAM336752 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336752 target RNA, herein designated GAM TARGET RNA.

GAM336752 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336752 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336752 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336752 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336752 RNA, herein designated GAM RNA, to target binding sites on GAM336752 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336752 target RNA into GAM336752 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336752 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336752 target genes. The mRNA of each one of this plurality of GAM336752 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336752 RNA, herein designated GAM RNA, and which when bound by GAM336752 RNA causes inhibition of translation of the GAM336752 target mRNA into a corresponding GAM336752 target protein.

The mechanism of the translational inhibition exerted by GAM336752 RNA, herein designated GAM RNA, on one or more GAM336752 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336752 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336752 RNA, herein designated GAM RNA, of GAM336752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336752 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336752 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336752 RNA correlate with, and may be deduced from, the identity of the GAM336752 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336755 7138 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 336755 (GAM336755) oligonucleotides modulates expression of respective target
GTGGAGGCTG genes whose function and utility is known in the art.

TGGTGAGCTG GAM336755 is a novel bioinformatically detectable regulatory, non protein
AGATTGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336755 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGA encoded by the human genome.

AACTCCATCT GAM336755 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336755 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336755 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336755 precursor RNA is designated SEQ ID:7138, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7138 is located from position 42527933 to position 42528034 relative to chromosome 17 on the `-` strand.

GAM336755 precursor RNA folds onto itself, forming GAM336755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336755 precursor RNA, designated SEQ ID NO: 7138, and a schematic representation of a predicted secondary folding of GAM336755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336755 folded precursor RNA yielding a GAM336755 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336755 RNA, hereby incorporated herein. Expression of GAM336755 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336755 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336755 target RNA, herein designated GAM TARGET RNA.

GAM336755 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336755 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336755 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336755 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336755 RNA, herein designated GAM RNA, to target binding sites on GAM336755 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336755 target RNA into GAM336755 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336755 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336755 target genes. The mRNA of each one of this plurality of GAM336755 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336755 RNA, herein designated GAM RNA, and which when bound by GAM336755 RNA causes inhibition of translation of the GAM336755 target mRNA into a corresponding GAM336755 target protein.

The mechanism of the translational inhibition exerted by GAM336755 RNA, herein designated GAM RNA, on one or more GAM336755 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336755 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336755 RNA, herein designated GAM RNA, of GAM336755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336755 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336755 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336755 RNA correlate with, and may be deduced from, the identity of the GAM336755 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336756 6632 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336756 (GAM336756) oligonucleotides modulates expression of respective target
CTGTGGTGAG genes whose function and utility is known in the art.

CTGAGATTGC GAM336756 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336756 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAAACTCC encoded by the human genome.

GAM336756 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336756 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336756 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336756 precursor RNA is designated SEQ ID:6632, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6632 is located from position 42527939 to position 42528027 relative to chromosome 17 on the `-` strand.

GAM336756 precursor RNA folds onto itself, forming GAM336756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336756 precursor RNA, designated SEQ ID NO: 6632, and a schematic representation of a predicted secondary folding of GAM336756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336756 folded precursor

RNA yielding a GAM336756 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336756 RNA, hereby incorporated herein. Expression of GAM336756 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336756 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336756 target RNA, herein designated GAM TARGET RNA.

GAM336756 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336756 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336756 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336756 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336756 RNA, herein designated GAM RNA, to target binding sites on GAM336756 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336756 target RNA into GAM336756 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336756 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336756 target genes. The mRNA of each one of this plurality of GAM336756 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336756 RNA, herein designated GAM RNA, and which when bound by GAM336756 RNA causes inhibition of translation of the GAM336756 target mRNA into a corresponding GAM336756 target protein.

The mechanism of the translational inhibition exerted by GAM336756 RNA, herein designated GAM RNA, on one or more GAM336756 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336756 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336756 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336756 RNA, herein designated GAM RNA, of GAM336756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336756 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336756 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336756 RNA correlate with, and may be deduced from, the identity of the GAM336756 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336757 6189 CTCTTTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTGTTGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAAAAATTT Messenger 336757 (GAM336757) oligonucleotides modulates expression of respective target
CTTGGAAAAT genes whose function and utility is known in the art.

ATGATTGTTC GAM336757 is a novel bioinformatically detectable regulatory, non protein
ATGGACAACG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336757 was detected
GACCTCATCA is described with additional reference to Figs. 9-15.

CCCAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336757 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336757 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336757 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336757 precursor RNA is designated SEQ ID:6189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6189 is located from position 42675594 to position 42675671 relative to chromosome 8 on the `+` strand.

GAM336757 precursor RNA folds onto itself, forming GAM336757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336757 precursor RNA, designated SEQ ID NO: 6189, and a schematic representation of a predicted secondary folding of GAM336757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336757 folded precursor RNA yielding a GAM336757 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336757 RNA, hereby incorporated herein.

GAM336757 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336757 target RNA, herein designated GAM TARGET RNA.

GAM336757 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336757 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336757 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336757 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336757 RNA, herein designated GAM RNA, to target binding sites on GAM336757 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336757 target RNA into GAM336757 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336757 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336757 target genes. The mRNA of each one of this plurality of GAM336757 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336757 RNA, herein designated GAM RNA, and which when bound by GAM336757 RNA causes inhibition of translation of the GAM336757 target mRNA into a corresponding GAM336757 target protein.

The mechanism of the translational inhibition exerted by GAM336757 RNA, herein

designated GAM RNA, on one or more GAM336757 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336757 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336757 RNA, herein designated GAM RNA, of GAM336757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336757 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336757 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336757 RNA correlate with, and may be deduced from, the identity of the GAM336757 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336760 7313 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAAGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 336760 (GAM336760) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

TTGCGCCACT GAM336760 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336760 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

AGAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336760 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336760 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336760 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336760 precursor RNA is designated SEQ ID:7313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7313 is located from position 42757406 to position 42757482

relative to chromosome 6 on the `-` strand.

GAM336760 precursor RNA folds onto itself, forming GAM336760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336760 precursor RNA, designated SEQ ID NO: 7313, and a schematic representation of a predicted secondary folding of GAM336760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336760 folded precursor RNA yielding a GAM336760 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336760 RNA, hereby incorporated herein. Expression of GAM336760 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336760 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336760 target RNA, herein designated GAM TARGET RNA.

GAM336760 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336760 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336760 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336760 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336760 RNA, herein designated GAM RNA, to target binding sites on GAM336760 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336760 target RNA into GAM336760 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336760 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336760 target genes. The mRNA of each one of this plurality of GAM336760 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336760 RNA, herein designated GAM RNA, and which when bound by GAM336760 RNA causes inhibition of translation of the GAM336760 target mRNA into a corresponding GAM336760 target protein.

The mechanism of the translational inhibition exerted by GAM336760 RNA, herein designated GAM RNA, on one or more GAM336760 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336760 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336760 RNA, herein designated GAM RNA, of GAM336760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336760 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336760 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336760 RNA correlate with, and may be deduced from, the identity of the GAM336760 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336761 5693 ACCAGAGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGAGAATGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CACAGCTGTC Messenger 336761 (GAM336761) oligonucleotides modulates expression of respective target
CTGTTCTCCA genes whose function and utility is known in the art.

CATTTGAATA GAM336761 is a novel bioinformatically detectable regulatory, non protein
GGCCGGACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336761 was detected
AGTTTTCTCT is described with additional reference to Figs. 9-15.

GAGTTTTTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

T encoded by the human genome.

GAM336761 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336761 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336761 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336761 precursor RNA is designated SEQ ID:5693, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5693 is located from position 42800191 to position 42800271 relative to chromosome 21 on the `+` strand.

GAM336761 precursor RNA folds onto itself, forming GAM336761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336761 precursor RNA, designated SEQ ID NO: 5693, and a schematic representation of a predicted secondary folding of GAM336761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336761 folded precursor RNA yielding a GAM336761 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336761 RNA, hereby incorporated herein.

GAM336761 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336761 target RNA, herein designated GAM TARGET RNA.

GAM336761 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336761 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336761 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336761 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336761 RNA, herein designated GAM RNA, to target binding sites on GAM336761 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336761 target RNA into GAM336761 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336761 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336761 target genes. The mRNA of each one of this plurality of GAM336761 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336761 RNA, herein designated GAM RNA, and which when bound by GAM336761 RNA causes inhibition of translation of the GAM336761 target mRNA into a corresponding GAM336761 target protein.

The mechanism of the translational inhibition exerted by GAM336761 RNA, herein designated GAM RNA, on one or more GAM336761 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336761 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336761 RNA, herein designated GAM RNA, of GAM336761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336761 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336761 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336761 RNA correlate with, and may be deduced from, the identity of the GAM336761 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336762 7282 TGTTGGCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTGTCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCTCCTGAC Messenger 336762 (GAM336762) oligonucleotides modulates expression of respective target

CTTGTGATCG genes whose function and utility is known in the art.

GCCCACCTCG GAM336762 is a novel bioinformatically detectable regulatory, non protein
GCCTCCCAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336762 was detected
GTACTGAGAT is described with additional reference to Figs. 9-15.

TACAGACGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCCACCA encoded by the human genome.

GAM336762 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336762 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336762 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336762 precursor RNA is designated SEQ ID:7282, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7282 is located from position 42860934 to position 42861021 relative to chromosome 19 on the `-` strand.

GAM336762 precursor RNA folds onto itself, forming GAM336762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336762 precursor RNA, designated SEQ ID NO: 7282, and a schematic representation of a predicted secondary folding of GAM336762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336762 folded precursor RNA yielding a GAM336762 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336762 RNA, hereby incorporated herein.

GAM336762 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336762 target RNA, herein designated GAM TARGET RNA.

GAM336762 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336762 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336762 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336762 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336762 RNA, herein designated GAM RNA, to target binding sites on GAM336762 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336762 target RNA into GAM336762 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336762 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336762 target genes. The mRNA of each one of this plurality of GAM336762 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336762 RNA, herein designated GAM RNA, and which when bound by GAM336762 RNA causes inhibition of translation of the GAM336762 target mRNA into a corresponding GAM336762 target protein.

The mechanism of the translational inhibition exerted by GAM336762 RNA, herein designated GAM RNA, on one or more GAM336762 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336762 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336762 RNA, herein designated GAM RNA, of GAM336762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336762 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336762 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336762 RNA correlate with, and may be deduced from, the identity of the GAM336762 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336763 6708 GGAGATGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCAGTTCAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CGTCAACCCA Messenger 336763 (GAM336763) oligonucleotides modulates expression of respective target
AAAGCTCTCT genes whose function and utility is known in the art.

TCAGGTCATG GAM336763 is a novel bioinformatically detectable regulatory, non protein
GCAAACAGAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336763 was detected
CAGGGCTGTG is described with additional reference to Figs. 9-15.

GGTGTGGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCTTGGCAC encoded by the human genome.

TGACTCC GAM336763 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336763 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336763 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336763 precursor RNA is designated SEQ ID:6708, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6708 is located from position 42899850 to position 42899946 relative to chromosome 22 on the `-` strand.

GAM336763 precursor RNA folds onto itself, forming GAM336763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336763 precursor RNA, designated SEQ ID NO: 6708, and a schematic representation of a predicted secondary folding of GAM336763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336763 folded precursor RNA yielding a GAM336763 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336763 RNA, hereby incorporated herein. Expression of GAM336763 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336763 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336763 target RNA, herein designated GAM TARGET RNA.

GAM336763 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336763 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336763 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336763 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336763 RNA, herein designated GAM RNA, to target binding sites on GAM336763 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336763 target RNA into GAM336763 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336763 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336763 target genes. The mRNA of each one of this plurality of GAM336763 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336763 RNA, herein designated GAM RNA, and which when bound by GAM336763 RNA causes inhibition of translation of the GAM336763 target mRNA into a corresponding GAM336763 target protein.

The mechanism of the translational inhibition exerted by GAM336763 RNA, herein designated GAM RNA, on one or more GAM336763 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336763 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336763 RNA, herein designated GAM RNA, of GAM336763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336763 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336763 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336763 RNA correlate with, and may be deduced from, the identity of the GAM336763 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336764 6369 GAGGATGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAGCCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGAAGT Messenger 336764 (GAM336764) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

TGAAATCATG GAM336764 is a novel bioinformatically detectable regulatory, non protein
CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336764 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

TGATAGAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAACCTT encoded by the human genome.

GAM336764 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336764 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336764 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336764 precursor RNA is designated SEQ ID:6369, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6369 is located from position 42908008 to position 42908094 relative to chromosome 20 on the `+` strand.

GAM336764 precursor RNA folds onto itself, forming GAM336764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336764 precursor RNA, designated SEQ ID NO: 6369, and a schematic representation of a predicted secondary folding of GAM336764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336764 folded precursor RNA yielding a GAM336764 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336764 RNA, hereby incorporated herein.

GAM336764 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336764 target RNA, herein designated GAM TARGET RNA.

GAM336764 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336764 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336764 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336764 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336764 RNA, herein designated GAM RNA, to target binding sites on GAM336764 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336764 target RNA into GAM336764 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336764 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336764 target genes. The mRNA of each one of this plurality of GAM336764 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336764 RNA, herein designated GAM RNA, and which when bound by GAM336764 RNA causes inhibition of translation of the GAM336764 target mRNA into a corresponding GAM336764 target protein.

The mechanism of the translational inhibition exerted by GAM336764 RNA, herein designated GAM RNA, on one or more GAM336764 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336764 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336764 RNA, herein designated GAM RNA, of GAM336764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336764 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336764 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336764 RNA correlate with, and may be deduced from, the identity of the GAM336764 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336765 7261 TGGTTTGAGC CCAGGAGGCA GAAGTTGCAG TGAGCTGAAA TCATGCCACT GCACTCCAGC CTGGGTGATA GAGCCA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336765 (GAM336765) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336765 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336765 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336765 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336765 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336765 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336765 precursor RNA is designated SEQ ID:7261, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7261 is located from position 42908013 to position 42908088 relative to chromosome 20 on the `+` strand.

GAM336765 precursor RNA folds onto itself, forming GAM336765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336765 precursor RNA, designated SEQ ID NO: 7261, and a schematic representation of a predicted secondary folding of GAM336765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336765 folded precursor RNA yielding a GAM336765 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336765 RNA, hereby incorporated herein.

GAM336765 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336765 target RNA, herein designated GAM TARGET RNA.

GAM336765 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336765 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336765 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336765 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336765 RNA, herein designated GAM RNA, to target binding sites on GAM336765 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336765 target RNA into GAM336765 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336765 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336765 target genes. The mRNA of each one of this plurality of GAM336765 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336765 RNA, herein designated GAM RNA, and which when bound by GAM336765 RNA causes inhibition of translation of the GAM336765 target mRNA into a corresponding GAM336765 target protein.

The mechanism of the translational inhibition exerted by GAM336765 RNA, herein designated GAM RNA, on one or more GAM336765 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336765 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336765 RNA, herein designated GAM RNA, of GAM336765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336765 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336765 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336765 RNA correlate with, and may be deduced from, the identity of the GAM336765 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336767 6780 GGGACCGTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGAAATGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTTGATTTT Messenger 336767 (GAM336767) oligonucleotides modulates expression of respective target

AGTGGCTGTG genes whose function and utility is known in the art.

AGCACACATA GAM336767 is a novel bioinformatically detectable regulatory, non protein

AGGATACAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336767 was detected

TCATTTCCCT is described with additional reference to Figs. 9-15.

TATAATTAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCC encoded by the human genome.

GAM336767 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336767 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336767 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336767 precursor RNA is designated SEQ ID:6780, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6780 is located from position 43301518 to position 43301601 relative to chromosome 13 on the `+` strand.

GAM336767 precursor RNA folds onto itself, forming GAM336767 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336767 precursor RNA, designated SEQ ID NO: 6780, and a schematic representation of a predicted secondary folding of GAM336767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336767 folded precursor RNA yielding a GAM336767 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336767 RNA, hereby incorporated herein.

GAM336767 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336767 target RNA, herein designated GAM TARGET RNA.

GAM336767 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336767 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336767 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336767 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336767 RNA, herein designated GAM RNA, to target binding sites on GAM336767 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336767 target RNA into GAM336767 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336767 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336767 target genes. The mRNA of each one of this plurality of GAM336767 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336767 RNA,

herein designated GAM RNA, and which when bound by GAM336767 RNA causes inhibition of translation of the GAM336767 target mRNA into a corresponding GAM336767 target protein.

The mechanism of the translational inhibition exerted by GAM336767 RNA, herein designated GAM RNA, on one or more GAM336767 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336767 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336767 RNA, herein designated GAM RNA, of GAM336767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336767 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336767 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336767 RNA correlate with, and may be deduced from, the identity of the GAM336767 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336768 6434 GAGGCATAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTCGGGAGG Messenger 336768 (GAM336768) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM336768 is a novel bioinformatically detectable regulatory, non protein

GATCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336768 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGCAAGACT encoded by the human genome.

CTGTCTC GAM336768 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336768 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336768 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336768 precursor RNA is designated SEQ ID:6434, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6434 is located from position 43393809 to position 43393905 relative to chromosome 17 on the `-` strand.

GAM336768 precursor RNA folds onto itself, forming GAM336768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336768 precursor RNA, designated SEQ ID NO: 6434, and a schematic representation of a predicted secondary folding of GAM336768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336768 folded precursor RNA yielding a GAM336768 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336768 RNA, hereby incorporated herein.

GAM336768 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336768 target RNA, herein designated GAM TARGET RNA.

GAM336768 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336768 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336768 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336768 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336768 RNA, herein designated GAM RNA, to target binding sites on GAM336768 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336768 target RNA

into GAM336768 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336768 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336768 target genes. The mRNA of each one of this plurality of GAM336768 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336768 RNA, herein designated GAM RNA, and which when bound by GAM336768 RNA causes inhibition of translation of the GAM336768 target mRNA into a corresponding GAM336768 target protein.

The mechanism of the translational inhibition exerted by GAM336768 RNA, herein designated GAM RNA, on one or more GAM336768 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336768 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336768 RNA, herein designated GAM RNA, of GAM336768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336768 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336768 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336768 RNA correlate with, and may be deduced from, the identity of the GAM336768 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336770 6988 TCAAGTCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACTGCTCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCAGTGACC Messenger 336770 (GAM336770) oligonucleotides modulates expression of respective target

ACTAGCCATA genes whose function and utility is known in the art.

TGTGGCTACT GAM336770 is a novel bioinformatically detectable regulatory, non protein

GAGCACTTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336770 was detected

AATGTGGCTA is described with additional reference to Figs. 9-15.

GTTTGAACTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGATGTGCTC encoded by the human genome.

TAAGTACACT GAM336770 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGATTTTGA GAM336770 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336770 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336770 precursor RNA is designated SEQ ID:6988, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6988 is located from position 43586567 to position 43586675 relative to chromosome 13 on the `+` strand.

GAM336770 precursor RNA folds onto itself, forming GAM336770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336770 precursor RNA, designated SEQ ID NO: 6988, and a schematic representation of a predicted secondary folding of GAM336770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336770 folded precursor RNA yielding a GAM336770 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336770 RNA, hereby incorporated herein.

GAM336770 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336770 target RNA, herein designated GAM TARGET RNA.

GAM336770 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336770 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336770 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336770 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336770 RNA, herein designated GAM RNA, to target binding sites on GAM336770 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336770 target RNA into GAM336770 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336770 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336770 target genes. The mRNA of each one of this plurality of GAM336770 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336770 RNA, herein designated GAM RNA, and which when bound by GAM336770 RNA causes inhibition of translation of the GAM336770 target mRNA into a corresponding GAM336770 target protein.

The mechanism of the translational inhibition exerted by GAM336770 RNA, herein designated GAM RNA, on one or more GAM336770 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336770 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336770 RNA, herein designated GAM RNA, of GAM336770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336770 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336770 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336770 RNA correlate with, and may be deduced from, the identity of the GAM336770 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336771 6882 GTCCTGTACT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTCAATTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGACCACTA Messenger 336771 (GAM336771) oligonucleotides modulates expression of respective target

GCCATATGTG genes whose function and utility is known in the art.

GCTACTGAGC GAM336771 is a novel bioinformatically detectable regulatory, non protein
ACTTGAAATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336771 was detected
TGGCTAGTTT is described with additional reference to Figs. 9-15.

GAACTGAGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGCTCTAAG encoded by the human genome.

TACACTGGAT GAM336771 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336771 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336771 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336771 precursor RNA is designated SEQ ID:6882, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6882 is located from position 43586571 to position 43586670 relative to chromosome 13 on the `+` strand.

GAM336771 precursor RNA folds onto itself, forming GAM336771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336771 precursor RNA, designated SEQ ID NO: 6882, and a schematic representation of a predicted secondary folding of GAM336771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336771 folded precursor RNA yielding a GAM336771 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336771 RNA, hereby incorporated herein.

GAM336771 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336771 target RNA, herein designated GAM TARGET RNA.

GAM336771 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336771 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336771 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336771 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336771 RNA, herein designated GAM RNA, to target binding sites on GAM336771 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336771 target RNA into GAM336771 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336771 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336771 target genes. The mRNA of each one of this plurality of GAM336771 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336771 RNA, herein designated GAM RNA, and which when bound by GAM336771 RNA causes inhibition of translation of the GAM336771 target mRNA into a corresponding GAM336771 target protein.

The mechanism of the translational inhibition exerted by GAM336771 RNA, herein designated GAM RNA, on one or more GAM336771 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336771 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336771 RNA, herein designated GAM RNA, of GAM336771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336771 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336771 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336771 RNA correlate with, and may be deduced from, the identity of the GAM336771 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336772 6624 GGAGAATCAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGCAGAGG Messenger 336772 (GAM336772) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATCAC GAM336772 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336772 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336772 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336772 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336772 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336772 precursor RNA is designated SEQ ID:6624, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6624 is located from position 43590234 to position 43590321 relative to chromosome 5 on the `-` strand.

GAM336772 precursor RNA folds onto itself, forming GAM336772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336772 precursor RNA, designated SEQ ID NO: 6624, and a schematic representation of a predicted secondary folding of GAM336772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336772 folded precursor RNA yielding a GAM336772 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336772 RNA, hereby incorporated herein. Expression of GAM336772 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336772 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336772 target RNA, herein designated GAM TARGET RNA.

GAM336772 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336772 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336772 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336772 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336772 RNA, herein designated GAM RNA, to target binding sites on GAM336772 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336772 target RNA into GAM336772 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336772 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336772 target genes. The mRNA of each one of this plurality of GAM336772 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336772 RNA, herein designated GAM RNA, and which when bound by GAM336772 RNA causes inhibition of translation of the GAM336772 target mRNA into a corresponding GAM336772 target protein.

The mechanism of the translational inhibition exerted by GAM336772 RNA, herein designated GAM RNA, on one or more GAM336772 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336772 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336772 RNA, herein designated GAM RNA, of GAM336772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336772 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336772 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336772 RNA correlate with, and may be deduced from, the identity of the GAM336772 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336773 6862 GTAGAGGGTA TGCCTGGGAA AACAGGAGTC ACAGAAGCTT CTGTGACTGT ATTTTCCCAA AGAGGTTTAT TATTTAT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336773 (GAM336773) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336773 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336773 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336773 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336773 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336773 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336773 precursor RNA is designated SEQ ID:6862, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6862 is located from position 43594076 to position 43594152 relative to chromosome 7 on the `+` strand.

GAM336773 precursor RNA folds onto itself, forming GAM336773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336773 precursor RNA, designated SEQ ID NO: 6862, and a schematic representation of a predicted secondary folding of GAM336773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336773 folded precursor RNA yielding a GAM336773 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336773 RNA, hereby incorporated herein.

GAM336773 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336773 target RNA, herein designated GAM TARGET RNA.

GAM336773 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336773 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336773 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336773 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336773 RNA, herein designated GAM RNA, to target binding sites on GAM336773 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336773 target RNA into GAM336773 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336773 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336773 target genes. The mRNA of each one of this plurality of GAM336773 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336773 RNA, herein designated GAM RNA, and which when bound by GAM336773 RNA causes inhibition of translation of the GAM336773 target mRNA into a corresponding GAM336773 target protein.

The mechanism of the translational inhibition exerted by GAM336773 RNA, herein designated GAM RNA, on one or more GAM336773 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336773 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336773 RNA, herein designated GAM RNA, of GAM336773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336773 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336773 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336773 RNA correlate with, and may be deduced from, the identity of the GAM336773 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336775 6912 GTGGCATAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGGGCCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
AATCCAATGT Messenger 336775 (GAM336775) oligonucleotides modulates expression of respective target
GACTGGTGTC genes whose function and utility is known in the art.

CATATAAGAG GAM336775 is a novel bioinformatically detectable regulatory, non protein
GTGGAGAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336775 was detected
GTAGAGACAC is described with additional reference to Figs. 9-15.

AGACACATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGAAGGCCA encoded by the human genome.

TGTGATGGCA GAM336775 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM336775 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336775 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336775 precursor RNA is designated SEQ ID:6912, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6912 is located from position 43900231 to position 43900331 relative to chromosome 10 on the `+` strand.

GAM336775 precursor RNA folds onto itself, forming GAM336775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336775 precursor RNA, designated SEQ ID NO: 6912, and a schematic representation of a predicted secondary folding of GAM336775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336775 folded precursor RNA yielding a GAM336775 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336775 RNA, hereby incorporated herein.

GAM336775 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336775 target RNA, herein designated GAM TARGET RNA.

GAM336775 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336775 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336775 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336775 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336775 RNA, herein designated GAM RNA, to target binding sites on GAM336775 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336775 target RNA into GAM336775 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336775 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336775 target genes. The mRNA of each one of this plurality of GAM336775 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336775 RNA, herein designated GAM RNA, and which when bound by GAM336775 RNA causes inhibition of translation of the GAM336775 target mRNA into a corresponding GAM336775 target protein.

The mechanism of the translational inhibition exerted by GAM336775 RNA, herein

designated GAM RNA, on one or more GAM336775 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336775 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336775 RNA, herein designated GAM RNA, of GAM336775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336775 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336775 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336775 RNA correlate with, and may be deduced from, the identity of the GAM336775 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336776 6978 TAGTGTTCAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACCTACACT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCATCCTCCT Messenger 336776 (GAM336776) oligonucleotides modulates expression of respective target

TTAATTTGCC genes whose function and utility is known in the art.

CAGTGGCCTG GAM336776 is a novel bioinformatically detectable regulatory, non protein

ACACTTGGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336776 was detected

GGGCAAGTGC is described with additional reference to Figs. 9-15.

TGTCATATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGATCTGTT encoded by the human genome.

TACGTGAACA GAM336776 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTA GAM336776 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336776 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336776 precursor RNA is designated SEQ ID:6978, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6978 is located from position 44128391 to position 44128493 relative to chromosome 17 on the `+` strand.

GAM336776 precursor RNA folds onto itself, forming GAM336776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336776 precursor RNA, designated SEQ ID NO: 6978, and a schematic representation of a predicted secondary folding of GAM336776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336776 folded precursor RNA yielding a GAM336776 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336776 RNA, hereby incorporated herein.

GAM336776 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336776 target RNA, herein designated GAM TARGET RNA.

GAM336776 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336776 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336776 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336776 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336776 RNA, herein designated GAM RNA, to target binding sites on GAM336776 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336776 target RNA into GAM336776 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336776 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336776 target genes. The mRNA of each one of this plurality of GAM336776 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336776 RNA, herein designated GAM RNA, and which when bound by GAM336776 RNA causes inhibition of translation of the GAM336776 target mRNA into a corresponding GAM336776 target protein.

The mechanism of the translational inhibition exerted by GAM336776 RNA, herein designated GAM RNA, on one or more GAM336776 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336776 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336776 RNA, herein designated GAM RNA, of GAM336776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336776 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336776 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336776 RNA correlate with, and may be deduced from, the identity of the GAM336776 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336777 5864 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336777 (GAM336777) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336777 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336777 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336777 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336777 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336777 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336777 precursor RNA is designated SEQ ID:5864, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5864 is located from position 44151668 to position 44151749 relative to chromosome 12 on the `+` strand.

GAM336777 precursor RNA folds onto itself, forming GAM336777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336777 precursor RNA, designated SEQ ID NO: 5864, and a schematic representation of a predicted secondary folding of GAM336777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336777 folded precursor RNA yielding a GAM336777 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336777 RNA, hereby incorporated herein.

GAM336777 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336777 target RNA, herein designated GAM TARGET RNA.

GAM336777 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336777 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336777 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336777 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336777 RNA, herein designated GAM RNA, to target binding sites on GAM336777 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336777 target RNA into GAM336777 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336777 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336777 target genes. The mRNA of each one of this plurality of GAM336777 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336777 RNA, herein designated GAM RNA, and which when bound by GAM336777 RNA causes inhibition of translation of the GAM336777 target mRNA into a corresponding GAM336777 target protein.

The mechanism of the translational inhibition exerted by GAM336777 RNA, herein designated GAM RNA, on one or more GAM336777 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336777 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336777 RNA, herein designated GAM RNA, of GAM336777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336777 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336777 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336777 RNA correlate with, and may be deduced from, the identity of the GAM336777 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336778 7013 TCATACTGTA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTTAGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCATGAAAAG Messenger 336778 (GAM336778) oligonucleotides modulates expression of respective target

CTCTGTGGTG genes whose function and utility is known in the art.

CAGTGGCAAA GAM336778 is a novel bioinformatically detectable regulatory, non protein

CAGGGCTAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336778 was detected

GATGTTTGCT is described with additional reference to Figs. 9-15.

GATGTCGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGA encoded by the human genome.

GAM336778 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336778 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336778 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336778 precursor RNA is designated SEQ ID:7013, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7013 is located from position 44172084 to position 44172167 relative to chromosome 10 on the `+` strand.

GAM336778 precursor RNA folds onto itself, forming GAM336778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336778 precursor RNA, designated SEQ ID NO: 7013, and a schematic representation of a predicted secondary folding of GAM336778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336778 folded precursor RNA yielding a GAM336778 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336778 RNA, hereby incorporated herein.

GAM336778 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336778 target RNA, herein designated GAM TARGET RNA.

GAM336778 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336778 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336778 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336778 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336778 RNA, herein designated GAM RNA, to target binding sites on GAM336778 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336778 target RNA into GAM336778 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336778 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336778 target genes. The mRNA of each one of this plurality of GAM336778 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336778 RNA, herein designated GAM RNA, and which when bound by GAM336778 RNA causes inhibition of translation of the GAM336778 target mRNA into a corresponding GAM336778 target protein.

The mechanism of the translational inhibition exerted by GAM336778 RNA, herein designated GAM RNA, on one or more GAM336778 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336778 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336778 RNA, herein designated GAM RNA, of GAM336778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336778 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336778 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336778 RNA correlate with, and may be deduced from, the identity of the GAM336778 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336780 5668 AAGGAGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTAAATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTAATATGG Messenger 336780 (GAM336780) oligonucleotides modulates expression of respective target
CCTTGGTTGC genes whose function and utility is known in the art.

AGAAGTCCTG GAM336780 is a novel bioinformatically detectable regulatory, non protein
ATACTAAGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336780 was detected
AATTCTAGCA is described with additional reference to Figs. 9-15.

ACCTTAATAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTACAGTAG encoded by the human genome.

ATTCCCCCTT GAM336780 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336780 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336780 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336780 precursor RNA is designated SEQ ID:5668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5668 is located from position 44287793 to position 44287892 relative to chromosome 18 on the `+` strand.

GAM336780 precursor RNA folds onto itself, forming GAM336780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336780 precursor RNA, designated SEQ ID NO: 5668, and a schematic representation of a predicted secondary folding of GAM336780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336780 folded precursor RNA yielding a GAM336780 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336780 RNA, hereby incorporated herein.

GAM336780 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336780 target RNA, herein designated GAM TARGET RNA.

GAM336780 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336780 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336780 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336780 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336780 RNA, herein designated GAM RNA, to target binding sites on GAM336780 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336780 target RNA into GAM336780 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336780 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336780 target genes. The mRNA of each one of this plurality of GAM336780 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336780 RNA, herein designated GAM RNA, and which when bound by GAM336780 RNA causes inhibition of translation of the GAM336780 target mRNA into a corresponding GAM336780 target protein.

The mechanism of the translational inhibition exerted by GAM336780 RNA, herein designated GAM RNA, on one or more GAM336780 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336780 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336780 RNA, herein designated GAM RNA, of GAM336780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336780 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336780 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336780 RNA correlate with, and may be deduced from, the identity of the GAM336780 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336781 5750 AGCCTGGGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
ACTGTATGGT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCAGTGTCA Messenger 336781 (GAM336781) oligonucleotides modulates expression of respective target
GCTTCCTGTG genes whose function and utility is known in the art.

TTACACGAGA GAM336781 is a novel bioinformatically detectable regulatory, non protein
TGGCACAGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336781 was detected
GGGTGAAGCT is described with additional reference to Figs. 9-15.

GGTGATGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTATGTGACC encoded by the human genome.

CCTCT GAM336781 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336781 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336781 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336781 precursor RNA is designated SEQ ID:5750, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5750 is located from position 44376402 to position 44376496 relative to chromosome 21 on the `+` strand.

GAM336781 precursor RNA folds onto itself, forming GAM336781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336781 precursor RNA, designated SEQ ID NO: 5750, and a schematic representation of a predicted secondary folding of GAM336781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336781 folded precursor RNA yielding a GAM336781 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336781 RNA, hereby incorporated herein.

GAM336781 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336781 target RNA, herein designated GAM TARGET RNA.

GAM336781 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336781 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336781 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336781 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336781 RNA, herein designated GAM RNA, to target binding sites on GAM336781 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336781 target RNA into GAM336781 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336781 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336781 target genes. The mRNA of each one of this plurality of GAM336781 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336781 RNA, herein designated GAM RNA, and which when bound by GAM336781 RNA causes inhibition of translation of the GAM336781 target mRNA into a corresponding GAM336781 target protein.

The mechanism of the translational inhibition exerted by GAM336781 RNA, herein designated GAM RNA, on one or more GAM336781 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336781 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336781 RNA, herein designated GAM RNA, of GAM336781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336781 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336781 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336781 RNA correlate with, and may be deduced from, the identity of the GAM336781 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336782 6821 GGGTCACTGT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGGTACCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTCAGCTTC Messenger 336782 (GAM336782) oligonucleotides modulates expression of respective target
CTGTGTTACA genes whose function and utility is known in the art.

CGAGATGGCA GAM336782 is a novel bioinformatically detectable regulatory, non protein
CAGTTGGGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336782 was detected
AAGCTGGTGA is described with additional reference to Figs. 9-15.

TGAAGGTATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGACCC encoded by the human genome.

GAM336782 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336782 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336782 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336782 precursor RNA is designated SEQ ID:6821, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6821 is located from position 44376407 to position 44376492 relative to chromosome 21 on the `+` strand.

GAM336782 precursor RNA folds onto itself, forming GAM336782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336782 precursor RNA, designated SEQ ID NO: 6821, and a schematic representation of a predicted secondary folding of GAM336782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336782 folded precursor RNA yielding a GAM336782 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336782 RNA, hereby incorporated herein.

GAM336782 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336782 target RNA, herein designated GAM TARGET RNA.

GAM336782 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336782 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336782 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336782 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336782 RNA, herein designated GAM RNA, to target binding sites on GAM336782 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336782 target RNA into GAM336782 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336782 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336782 target genes. The mRNA of each one of this plurality of GAM336782 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336782 RNA, herein designated GAM RNA, and which when bound by GAM336782 RNA causes inhibition of translation of the GAM336782 target mRNA into a corresponding GAM336782 target protein.

The mechanism of the translational inhibition exerted by GAM336782 RNA, herein designated GAM RNA, on one or more GAM336782 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336782 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336782 RNA, herein designated GAM RNA, of GAM336782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336782 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336782 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336782 RNA correlate with, and may be deduced from, the identity of the GAM336782 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336783 6287 GAACATCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCTGGGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAACCTGGC Messenger 336783 (GAM336783) oligonucleotides modulates expression of respective target

ATACAATGTA genes whose function and utility is known in the art.

GATTTCTGTG GAM336783 is a novel bioinformatically detectable regulatory, non protein

TTCGTTAGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336783 was detected

AACAGCTACA is described with additional reference to Figs. 9-15.

TTGTCTGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTTTCAGGC encoded by the human genome.

TACCTGGAAA GAM336783 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CATGTTC GAM336783 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336783 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336783 precursor RNA is designated SEQ ID:6287, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6287 is located from position 44431916 to position 44432022 relative to chromosome X on the `-` strand.

GAM336783 precursor RNA folds onto itself, forming GAM336783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336783 precursor RNA, designated SEQ ID NO: 6287, and a schematic representation of a predicted secondary folding of GAM336783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336783 folded precursor RNA yielding a GAM336783 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336783 RNA, hereby incorporated herein.

GAM336783 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336783 target RNA, herein designated GAM TARGET RNA.

GAM336783 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336783 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336783 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336783 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336783 RNA, herein designated GAM RNA, to target binding sites on GAM336783 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336783 target RNA into GAM336783 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336783 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336783 target genes. The mRNA of each one of this plurality of GAM336783 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336783 RNA, herein designated GAM RNA, and which when bound by GAM336783 RNA causes inhibition of translation of the GAM336783 target mRNA into a corresponding GAM336783 target protein.

The mechanism of the translational inhibition exerted by GAM336783 RNA, herein designated GAM RNA, on one or more GAM336783 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336783 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336783 RNA, herein designated GAM RNA, of GAM336783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336783 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336783 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336783 RNA correlate with, and may be deduced from, the identity of the GAM336783 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336784 7021 TCCAGGTCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGCATGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGGCATACA Messenger 336784 (GAM336784) oligonucleotides modulates expression of respective target

ATGTAGATTT genes whose function and utility is known in the art.

CTGTGTTCGT GAM336784 is a novel bioinformatically detectable regulatory, non protein

TAGGCAACAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336784 was detected

CTACATTGTC is described with additional reference to Figs. 9-15.

TGCTGGGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGGCTACCT encoded by the human genome.

GGA GAM336784 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336784 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336784 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336784 precursor RNA is designated SEQ

ID:7021, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7021 is located from position 44431925 to position 44432017 relative to chromosome X on the `-` strand.

GAM336784 precursor RNA folds onto itself, forming GAM336784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336784 precursor RNA, designated SEQ ID NO: 7021, and a schematic representation of a predicted secondary folding of GAM336784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336784 folded precursor RNA yielding a GAM336784 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336784 RNA, hereby incorporated herein.

GAM336784 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336784 target RNA, herein designated GAM TARGET RNA.

GAM336784 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336784 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336784 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336784 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336784 RNA, herein designated GAM RNA, to target binding sites on GAM336784 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336784 target RNA into GAM336784 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336784 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336784 target genes. The mRNA of each one of this plurality of GAM336784 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336784 RNA, herein designated GAM RNA, and which when bound by GAM336784 RNA causes inhibition of translation of the GAM336784 target mRNA into a corresponding GAM336784 target protein.

The mechanism of the translational inhibition exerted by GAM336784 RNA, herein designated GAM RNA, on one or more GAM336784 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336784 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336784 RNA, herein designated GAM RNA, of GAM336784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336784 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336784 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336784 RNA correlate with, and may be deduced from, the identity of the GAM336784 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336785 7265 TGTCTATAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATGTGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTTTCTGC Messenger 336785 (GAM336785) oligonucleotides modulates expression of respective target

CCGTAAAATG genes whose function and utility is known in the art.

TTCAAATGTT GAM336785 is a novel bioinformatically detectable regulatory, non protein

TTCTCTCTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336785 was detected

AAAGCTTTGT is described with additional reference to Figs. 9-15.

TCATTGTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTGGAATT encoded by the human genome.

TTGGTTCTCA GAM336785 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGGAGTAGAC GAM336785 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

A GAM336785 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336785 precursor RNA is designated SEQ ID:7265, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7265 is located from position 44596378 to position 44596488 relative to chromosome 17 on the `+` strand.

GAM336785 precursor RNA folds onto itself, forming GAM336785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336785 precursor RNA, designated SEQ ID NO: 7265, and a schematic representation of a predicted secondary folding of GAM336785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336785 folded precursor RNA yielding a GAM336785 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM336785 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336785 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM336785 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336785 target RNA, herein designated GAM TARGET RNA.

GAM336785 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336785 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336785 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336785 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336785 RNA, herein designated GAM RNA, to target binding sites on GAM336785 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336785 target RNA into GAM336785 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336785 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336785 target genes. The mRNA of each one of this plurality of GAM336785 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336785 RNA, herein designated GAM RNA, and which when bound by GAM336785 RNA causes inhibition of translation of the GAM336785 target mRNA into a corresponding GAM336785 target protein.

The mechanism of the translational inhibition exerted by GAM336785 RNA, herein designated GAM RNA, on one or more GAM336785 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336785 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336785 RNA, herein designated GAM RNA, of GAM336785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336785 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336785 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336785 RNA correlate with, and may be deduced from, the identity of the GAM336785 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336786 5865 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336786 (GAM336786) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336786 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336786 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336786 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336786 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336786 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336786 precursor RNA is designated SEQ ID:5865, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5865 is located from position 44812786 to position 44812867 relative to chromosome 10 on the `+` strand.

GAM336786 precursor RNA folds onto itself, forming GAM336786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336786 precursor RNA, designated SEQ ID NO: 5865, and a schematic representation of a predicted secondary folding of GAM336786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336786 folded precursor RNA yielding a GAM336786 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336786 RNA, hereby incorporated herein.

GAM336786 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336786 target RNA, herein designated GAM TARGET RNA.

GAM336786 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336786 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336786 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336786 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336786 RNA, herein designated GAM RNA, to target binding sites on GAM336786 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336786 target RNA into GAM336786 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336786 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336786 target genes. The mRNA of each one of this plurality of GAM336786 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336786 RNA, herein designated GAM RNA, and which when bound by GAM336786 RNA causes inhibition of translation of the GAM336786 target mRNA into a corresponding GAM336786 target protein.

The mechanism of the translational inhibition exerted by GAM336786 RNA, herein designated GAM RNA, on one or more GAM336786 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336786 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336786 RNA, herein designated GAM RNA, of GAM336786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336786 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336786 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336786 RNA correlate with, and may be deduced from, the identity of the GAM336786 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336787 5763 AGGCAAGGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCACTCGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCCAGGTTG Messenger 336787 (GAM336787) oligonucleotides modulates expression of respective target
GAATGCAGTG genes whose function and utility is known in the art.

GTGTGATCAC GAM336787 is a novel bioinformatically detectable regulatory, non protein
AGTTCACTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336787 was detected
AAACTCAAAC is described with additional reference to Figs. 9-15.

TCCTGGGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGAATCTT encoded by the human genome.

CCT GAM336787 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336787 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336787 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336787 precursor RNA is designated SEQ ID:5763, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5763 is located from position 44900341 to position 44900433 relative to chromosome 22 on the `+` strand.

GAM336787 precursor RNA folds onto itself, forming GAM336787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336787 precursor RNA, designated SEQ ID NO: 5763, and a schematic representation of a predicted secondary folding of GAM336787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336787 folded precursor RNA yielding a GAM336787 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336787 RNA, hereby incorporated herein.

GAM336787 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336787 target RNA, herein designated GAM TARGET RNA.

GAM336787 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336787 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336787 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336787 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336787 RNA, herein designated GAM RNA, to target binding sites on GAM336787 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336787 target RNA into GAM336787 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336787 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336787 target genes. The mRNA of each one of this plurality of GAM336787 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336787 RNA, herein designated GAM RNA, and which when bound by GAM336787 RNA causes inhibition of translation of the GAM336787 target mRNA into a corresponding GAM336787 target protein.

The mechanism of the translational inhibition exerted by GAM336787 RNA, herein designated GAM RNA, on one or more GAM336787 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336787 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336787 RNA, herein designated GAM RNA, of GAM336787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336787 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336787 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336787 RNA correlate with, and may be deduced from, the identity of the GAM336787 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336788 6834 GGTATTGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAAAAGTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTATCTAGGT Messenger 336788 (GAM336788) oligonucleotides modulates expression of respective target
AGTCCAGGAA genes whose function and utility is known in the art.

GGTCTTCCTT GAM336788 is a novel bioinformatically detectable regulatory, non protein
TCATGACAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336788 was detected
ACCCATAGAC is described with additional reference to Figs. 9-15.

ACTTAGTCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGACT encoded by the human genome.

GAM336788 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336788 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336788 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336788 precursor RNA is designated SEQ ID:6834, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6834 is located from position 44989605 to position 44989690 relative to chromosome 20 on the `+` strand.

GAM336788 precursor RNA folds onto itself, forming GAM336788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336788 precursor RNA, designated SEQ ID NO: 6834, and a schematic representation of a predicted secondary folding of GAM336788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336788 folded precursor RNA yielding a GAM336788 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336788 RNA, hereby incorporated herein.

GAM336788 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336788 target RNA, herein designated GAM TARGET RNA.

GAM336788 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336788 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336788 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336788 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336788 RNA, herein designated GAM RNA, to target binding sites on GAM336788 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336788 target RNA into GAM336788 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336788 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336788 target genes. The mRNA of each one of this plurality of GAM336788 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336788 RNA, herein designated GAM RNA, and which when bound by GAM336788 RNA causes inhibition of translation of the GAM336788 target mRNA into a corresponding GAM336788 target protein.

The mechanism of the translational inhibition exerted by GAM336788 RNA, herein designated GAM RNA, on one or more GAM336788 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336788 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336788 RNA, herein designated GAM RNA, of GAM336788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336788 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336788 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336788 RNA correlate with, and may be deduced from, the identity of the GAM336788 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336789 6435 GAGGCCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCTGAGATC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCTTGGGCA Messenger 336789 (GAM336789) oligonucleotides modulates expression of respective target
ACTGATTTAT genes whose function and utility is known in the art.

GGTTTGGATT GAM336789 is a novel bioinformatically detectable regulatory, non protein
TGTGTCCATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336789 was detected
CCCTTCCTCT is described with additional reference to Figs. 9-15.

TCTGCCATGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTATAAGTTT encoded by the human genome.

CCTGAGGCCT GAM336789 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM336789 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336789 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336789 precursor RNA is designated SEQ ID:6435, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6435 is located from position 45081110 to position 45081210 relative to chromosome 21 on the `+` strand.

GAM336789 precursor RNA folds onto itself, forming GAM336789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336789 precursor RNA, designated SEQ ID NO: 6435, and a schematic representation of a predicted secondary folding of GAM336789 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336789 folded precursor RNA yielding a GAM336789 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336789 RNA, hereby incorporated herein.

GAM336789 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336789 target RNA, herein designated GAM TARGET RNA.

GAM336789 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336789 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336789 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336789 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336789 RNA, herein designated GAM RNA, to target binding sites on GAM336789 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336789 target RNA into GAM336789 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336789 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336789 target genes. The mRNA of each one of this plurality of GAM336789 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336789 RNA, herein designated GAM RNA, and which when bound by GAM336789 RNA causes inhibition of translation of the GAM336789 target mRNA into a corresponding GAM336789 target protein.

The mechanism of the translational inhibition exerted by GAM336789 RNA, herein designated GAM RNA, on one or more GAM336789 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336789 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336789 RNA, herein designated GAM RNA, of GAM336789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336789 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336789 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336789 RNA correlate with, and may be deduced from, the identity of the GAM336789 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336790 6130 CCTTGGGGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAATGATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCGTGGAAT Messenger 336790 (GAM336790) oligonucleotides modulates expression of respective target

GAGTTTTGTT genes whose function and utility is known in the art.

GTTAGGGTGG GAM336790 is a novel bioinformatically detectable regulatory, non protein

ACAGAAAAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336790 was detected

CCTATGGCAA is described with additional reference to Figs. 9-15.

AGTCACTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCCCTGAGT encoded by the human genome.

GTGCCCTTTG GAM336790 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

G GAM336790 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336790 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336790 precursor RNA is designated SEQ ID:6130, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6130 is located from position 45349110 to position 45349210 relative to chromosome 17 on the `+` strand.

GAM336790 precursor RNA folds onto itself, forming GAM336790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336790 precursor RNA, designated SEQ ID NO: 6130, and a schematic representation of a predicted secondary folding of GAM336790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336790 folded precursor RNA yielding a GAM336790 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336790 RNA, hereby incorporated herein.

GAM336790 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336790 target RNA, herein designated GAM TARGET RNA.

GAM336790 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336790 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336790 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336790 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336790 RNA, herein designated GAM RNA, to target binding sites on GAM336790 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336790 target RNA into GAM336790 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336790 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336790 target genes. The mRNA of each one of this plurality of GAM336790 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336790 RNA, herein designated GAM RNA, and which when bound by GAM336790 RNA causes inhibition of translation of the GAM336790 target mRNA into a corresponding GAM336790 target protein.

The mechanism of the translational inhibition exerted by GAM336790 RNA, herein designated GAM RNA, on one or more GAM336790 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336790 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336790 RNA, herein designated GAM RNA, of GAM336790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336790 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336790 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336790 RNA correlate with, and may be deduced from, the identity of the GAM336790 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336792 5775 AGGCCCTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCGTGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGAAGGTGT Messenger 336792 (GAM336792) oligonucleotides modulates expression of respective target

GTGTGTGGGG genes whose function and utility is known in the art.

TGGCAGGGAG GAM336792 is a novel bioinformatically detectable regulatory, non protein

GAGAAGGAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336792 was detected

CTGCTCTGTG is described with additional reference to Figs. 9-15.

CTTATTCTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCCCGTTTC encoded by the human genome.

TTTTGCAGCC GAM336792 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGCCCACGGC GAM336792 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TT GAM336792 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336792 precursor RNA is designated SEQ ID:5775, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5775 is located from position 45455573 to position 45455684 relative to chromosome 19 on the `-` strand.

GAM336792 precursor RNA folds onto itself, forming GAM336792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336792 precursor RNA, designated SEQ ID NO: 5775, and a schematic representation of a predicted secondary folding of GAM336792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336792 folded precursor RNA yielding a GAM336792 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336792 RNA, hereby incorporated herein.

GAM336792 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336792 target RNA, herein designated GAM TARGET RNA.

GAM336792 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336792 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336792 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336792 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336792 RNA, herein designated GAM RNA, to target binding sites on GAM336792 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336792 target RNA into GAM336792 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336792 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336792 target genes. The mRNA of each one of this plurality of GAM336792 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336792 RNA, herein designated GAM RNA, and which when bound by GAM336792 RNA causes inhibition of translation of the GAM336792 target mRNA into a corresponding GAM336792 target protein.

The mechanism of the translational inhibition exerted by GAM336792 RNA, herein designated GAM RNA, on one or more GAM336792 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336792 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336792 RNA, herein designated GAM RNA, of GAM336792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336792 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336792 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336792 RNA correlate with, and may be deduced from, the identity of the GAM336792 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336793 7248 TGGGTGGCGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGGGGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTGTGTGT Messenger 336793 (GAM336793) oligonucleotides modulates expression of respective target

GGGGTGGCAG genes whose function and utility is known in the art.

GGAGGAGAAG GAM336793 is a novel bioinformatically detectable regulatory, non protein

GAATCTGCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336793 was detected

TGTGCTTATT is described with additional reference to Figs. 9-15.

CTTGTCCCCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTCTTTTGC encoded by the human genome.

AGCCTGCCCA GAM336793 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336793 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336793 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336793 precursor RNA is designated SEQ ID:7248, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7248 is located from position 45455579 to position 45455678 relative to chromosome 19 on the `-` strand.

GAM336793 precursor RNA folds onto itself, forming GAM336793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336793 precursor RNA, designated SEQ ID NO: 7248, and a schematic representation of a predicted secondary folding of GAM336793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336793 folded precursor RNA yielding a GAM336793 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336793 RNA, hereby incorporated herein.

GAM336793 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336793 target RNA, herein designated GAM TARGET RNA.

GAM336793 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336793 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336793 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336793 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336793 RNA, herein designated GAM RNA, to target binding sites on GAM336793 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336793 target RNA into GAM336793 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336793 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336793 target genes. The mRNA of each one of this plurality of GAM336793 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336793 RNA, herein designated GAM RNA, and which when bound by GAM336793 RNA causes inhibition of translation of the GAM336793 target mRNA into a corresponding GAM336793 target protein.

The mechanism of the translational inhibition exerted by GAM336793 RNA, herein designated GAM RNA, on one or more GAM336793 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336793 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336793 RNA, herein designated GAM RNA, of GAM336793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336793 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336793 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336793 RNA correlate with, and may be deduced from, the identity of the GAM336793 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336794 7251 TGGTGGAAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAACCTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTCCAAGGA Messenger 336794 (GAM336794) oligonucleotides modulates expression of respective target

CAGTCCCATG genes whose function and utility is known in the art.

ACAGGGAAGC GAM336794 is a novel bioinformatically detectable regulatory, non protein
TGACACTTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336794 was detected
GTGGCAGGTT is described with additional reference to Figs. 9-15.

AATCCCCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336794 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336794 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336794 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336794 precursor RNA is designated SEQ ID:7251, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7251 is located from position 45732059 to position 45732138 relative to chromosome 10 on the `+` strand.

GAM336794 precursor RNA folds onto itself, forming GAM336794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336794 precursor RNA, designated SEQ ID NO: 7251, and a schematic representation of a predicted secondary folding of GAM336794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336794 folded precursor RNA yielding a GAM336794 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336794 RNA, hereby incorporated herein.

GAM336794 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336794 target RNA, herein designated GAM TARGET RNA.

GAM336794 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336794 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336794 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM336794 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336794 RNA, herein designated GAM RNA, to target binding sites on GAM336794 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336794 target RNA into GAM336794 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336794 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336794 target genes. The mRNA of each one of this plurality of GAM336794 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336794 RNA, herein designated GAM RNA, and which when bound by GAM336794 RNA causes inhibition of translation of the GAM336794 target mRNA into a corresponding GAM336794 target protein.

The mechanism of the translational inhibition exerted by GAM336794 RNA, herein designated GAM RNA, on one or more GAM336794 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336794 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336794 RNA, herein designated GAM RNA, of GAM336794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336794 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336794 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336794 RNA correlate with, and may be deduced from, the identity of the GAM336794 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336795 7073 TCTGCCAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTATGCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTGGCTCTG Messenger 336795 (GAM336795) oligonucleotides modulates expression of respective target

TGCTTCTAGT genes whose function and utility is known in the art.

ATCTGCATTT GAM336795 is a novel bioinformatically detectable regulatory, non protein

AATGCTTAGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336795 was detected

TTCTACCAGA is described with additional reference to Figs. 9-15.

GCTAGTTTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCACAAAGTT encoded by the human genome.

TCCAGA GAM336795 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336795 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336795 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336795 precursor RNA is designated SEQ ID:7073, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7073 is located from position 45867956 to position 45868051 relative to chromosome 22 on the `+` strand.

GAM336795 precursor RNA folds onto itself, forming GAM336795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336795 precursor RNA, designated SEQ ID NO: 7073, and a schematic representation of a predicted secondary folding of GAM336795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336795 folded precursor RNA yielding a GAM336795 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336795 RNA, hereby incorporated herein.

GAM336795 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336795 target RNA, herein designated GAM TARGET RNA.

GAM336795 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336795 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336795 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336795 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336795 RNA, herein designated GAM RNA, to target binding sites on GAM336795 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336795 target RNA into GAM336795 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336795 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336795 target genes. The mRNA of each one of this plurality of GAM336795 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336795 RNA, herein designated GAM RNA, and which when bound by GAM336795 RNA causes inhibition of translation of the GAM336795 target mRNA into a corresponding GAM336795 target protein.

The mechanism of the translational inhibition exerted by GAM336795 RNA, herein designated GAM RNA, on one or more GAM336795 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336795 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336795 RNA, herein designated GAM RNA, of GAM336795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336795 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336795 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336795 RNA correlate with, and may be deduced from, the identity of the GAM336795 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336796 5977 ATGTTCTGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTACTGAGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTAGGGCTTC Messenger 336796 (GAM336796) oligonucleotides modulates expression of respective target
AACTTACGAA genes whose function and utility is known in the art.

TTTGGTGAGT GAM336796 is a novel bioinformatically detectable regulatory, non protein
TCACAGTTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336796 was detected
GCCTGTAACA is described with additional reference to Figs. 9-15.

CATTTCTTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGATTTCCAG encoded by the human genome.

AGCGT GAM336796 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336796 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336796 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336796 precursor RNA is designated SEQ ID:5977, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5977 is located from position 45983536 to position 45983630 relative to chromosome 18 on the `+` strand.

GAM336796 precursor RNA folds onto itself, forming GAM336796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336796 precursor RNA, designated SEQ ID NO: 5977, and a schematic representation of a predicted secondary folding of GAM336796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336796 folded precursor RNA yielding a GAM336796 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336796 RNA, hereby incorporated herein.

GAM336796 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336796 target RNA, herein designated GAM TARGET RNA.

GAM336796 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336796 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336796 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336796 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336796 RNA, herein designated GAM RNA, to target binding sites on GAM336796 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336796 target RNA into GAM336796 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336796 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336796 target genes. The mRNA of each one of this plurality of GAM336796 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336796 RNA, herein designated GAM RNA, and which when bound by GAM336796 RNA causes inhibition of translation of the GAM336796 target mRNA into a corresponding GAM336796 target protein.

The mechanism of the translational inhibition exerted by GAM336796 RNA, herein designated GAM RNA, on one or more GAM336796 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336796 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336796 RNA, herein designated GAM RNA, of

GAM336796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336796 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336796 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336796 RNA correlate with, and may be deduced from, the identity of the GAM336796 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336797 7297 TTCATTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGGGTTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTCAGGAC Messenger 336797 (GAM336797) oligonucleotides modulates expression of respective target

ATGGGTATCT genes whose function and utility is known in the art.

GGTGTACATG GAM336797 is a novel bioinformatically detectable regulatory, non protein

GGAGTTTGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336797 was detected

GGCCTCTATT is described with additional reference to Figs. 9-15.

GTAGGAGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGGAAATGT encoded by the human genome.

GTATTGTTGG GAM336797 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAGGTCCTGA GAM336797 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GGGAGGAAGT GAM336797 precursor RNA does not encode a protein. A nucleotide sequence identical or

TTGGGATGAA highly similar to the nucleotide sequence of GAM336797 precursor RNA is designated SEQ

ID:7297, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7297 is located from position 46014999 to position 46015128 relative to chromosome 19 on the `+` strand.

GAM336797 precursor RNA folds onto itself, forming GAM336797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336797 precursor RNA, designated SEQ ID NO: 7297, and a schematic representation of a predicted secondary folding of GAM336797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336797 folded precursor RNA yielding a GAM336797 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336797 RNA, hereby incorporated herein.

GAM336797 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336797 target RNA, herein designated GAM TARGET RNA.

GAM336797 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336797 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336797 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336797 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336797 RNA, herein designated GAM RNA, to target binding sites on GAM336797 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336797 target RNA into GAM336797 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336797 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336797 target genes. The mRNA of each one of this plurality of GAM336797 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336797 RNA, herein designated GAM RNA, and which when bound by GAM336797 RNA causes inhibition of translation of the GAM336797 target mRNA into a corresponding GAM336797 target protein.

The mechanism of the translational inhibition exerted by GAM336797 RNA, herein designated GAM RNA, on one or more GAM336797 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336797 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336797 RNA, herein designated GAM RNA, of GAM336797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336797 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336797 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336797 RNA correlate with, and may be deduced from, the identity of the GAM336797 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336798 7147 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGGAG Messenger 336798 (GAM336798) oligonucleotides modulates expression of respective target

GCAGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCCG GAM336798 is a novel bioinformatically detectable regulatory, non protein

AGATGAGGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336798 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGTGTGA encoded by the human genome.

AACTCCGTCT GAM336798 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336798 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336798 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336798 precursor RNA is designated SEQ ID:7147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7147 is located from position 46038899 to position 46039000

relative to chromosome 17 on the `+` strand.

GAM336798 precursor RNA folds onto itself, forming GAM336798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336798 precursor RNA, designated SEQ ID NO: 7147, and a schematic representation of a predicted secondary folding of GAM336798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336798 folded precursor RNA yielding a GAM336798 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336798 RNA, hereby incorporated herein. Expression of GAM336798 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336798 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336798 target RNA, herein designated GAM TARGET RNA.

GAM336798 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336798 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336798 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336798 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336798 RNA, herein designated GAM RNA, to target binding sites on GAM336798 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336798 target RNA into GAM336798 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336798 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336798 target genes. The mRNA of each one of this plurality of GAM336798 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336798 RNA, herein designated GAM RNA, and which when bound by GAM336798 RNA causes inhibition of translation of the GAM336798 target mRNA into a corresponding GAM336798 target protein.

The mechanism of the translational inhibition exerted by GAM336798 RNA, herein designated GAM RNA, on one or more GAM336798 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336798 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336798 RNA, herein designated GAM RNA, of GAM336798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336798 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336798 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336798 RNA correlate with, and may be deduced from, the identity of the GAM336798 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336799 6400 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 336799 (GAM336799) oligonucleotides modulates expression of respective target

CAGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCGA GAM336799 is a novel bioinformatically detectable regulatory, non protein

GATGAGGTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336799 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGTGTGAA encoded by the human genome.

ACTCCGTCTC GAM336799 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336799 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336799 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336799 precursor RNA is designated SEQ ID:6400, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6400 is located from position 46038900 to position 46038999 relative to chromosome 17 on the `+` strand.

GAM336799 precursor RNA folds onto itself, forming GAM336799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336799 precursor RNA, designated SEQ ID NO: 6400, and a schematic representation of a predicted secondary folding of GAM336799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336799 folded precursor RNA yielding a GAM336799 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336799 RNA, hereby incorporated herein. Expression of GAM336799 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336799 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336799 target RNA, herein designated GAM TARGET RNA.

GAM336799 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336799 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336799 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336799 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336799 RNA, herein designated GAM RNA, to target binding sites on GAM336799 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336799 target RNA into GAM336799 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336799 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336799 target genes. The mRNA of each one of this plurality of GAM336799 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336799 RNA, herein designated GAM RNA, and which when bound by GAM336799 RNA causes inhibition of translation of the GAM336799 target mRNA into a corresponding GAM336799 target protein.

The mechanism of the translational inhibition exerted by GAM336799 RNA, herein designated GAM RNA, on one or more GAM336799 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336799 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336799 RNA, herein designated GAM RNA, of GAM336799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336799 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336799 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336799 RNA correlate with, and may be deduced from, the identity of the GAM336799 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336800 6002 CACTCCCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGAAGGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGTGTTAGG Messenger 336800 (GAM336800) oligonucleotides modulates expression of respective target

AAATGTGCTT genes whose function and utility is known in the art.

ACTGGGTGAA GAM336800 is a novel bioinformatically detectable regulatory, non protein
CACAACAGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336800 was detected
GTGTTCCCCA is described with additional reference to Figs. 9-15.

CCTCATGATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCCACAGTCT encoded by the human genome.

AGGGAGTG GAM336800 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336800 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336800 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336800 precursor RNA is designated SEQ ID:6002, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6002 is located from position 46120406 to position 46120503 relative to chromosome 13 on the `+` strand.

GAM336800 precursor RNA folds onto itself, forming GAM336800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336800 precursor RNA, designated SEQ ID NO: 6002, and a schematic representation of a predicted secondary folding of GAM336800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336800 folded precursor RNA yielding a GAM336800 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336800 RNA, hereby incorporated herein.

GAM336800 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336800 target RNA, herein designated GAM TARGET RNA.

GAM336800 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336800 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336800 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336800 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336800 RNA, herein designated GAM RNA, to target binding sites on GAM336800 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336800 target RNA into GAM336800 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336800 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336800 target genes. The mRNA of each one of this plurality of GAM336800 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336800 RNA, herein designated GAM RNA, and which when bound by GAM336800 RNA causes inhibition of translation of the GAM336800 target mRNA into a corresponding GAM336800 target protein.

The mechanism of the translational inhibition exerted by GAM336800 RNA, herein designated GAM RNA, on one or more GAM336800 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336800 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336800 RNA, herein designated GAM RNA, of GAM336800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336800 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336800 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336800 RNA correlate with, and may be deduced from, the identity of the GAM336800 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336801 5866 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336801 (GAM336801) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336801 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336801 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336801 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336801 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336801 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336801 precursor RNA is designated SEQ ID:5866, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5866 is located from position 46150469 to position 46150550 relative to chromosome 19 on the `-` strand.

GAM336801 precursor RNA folds onto itself, forming GAM336801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336801 precursor RNA, designated SEQ ID NO: 5866, and a schematic representation of a predicted secondary folding of GAM336801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336801 folded precursor RNA yielding a GAM336801 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336801 RNA, hereby incorporated herein.

GAM336801 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336801 target RNA, herein designated GAM TARGET RNA.

GAM336801 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336801 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336801 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336801 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336801 RNA, herein designated GAM RNA, to target binding sites on GAM336801 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336801 target RNA into GAM336801 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336801 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336801 target genes. The mRNA of each one of this plurality of GAM336801 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336801 RNA, herein designated GAM RNA, and which when bound by GAM336801 RNA causes inhibition of translation of the GAM336801 target mRNA into a corresponding GAM336801 target protein.

The mechanism of the translational inhibition exerted by GAM336801 RNA, herein designated GAM RNA, on one or more GAM336801 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336801 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336801 RNA, herein designated GAM RNA, of GAM336801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336801 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336801 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336801 RNA correlate with, and may be deduced from, the identity of the GAM336801 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336804 6766 GGCTGGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTACTTACC detected oligonucleotides of the present invention, referred to here as Genomic Address
TACTCCGTGT Messenger 336804 (GAM336804) oligonucleotides modulates expression of respective target
CTCAGTTTTA genes whose function and utility is known in the art.

CTTATCTCTA GAM336804 is a novel bioinformatically detectable regulatory, non protein
AAAGGGGTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336804 was detected
AGTAACAGCA is described with additional reference to Figs. 9-15.

CTCACTGGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGAGTGTGG encoded by the human genome.

TTATGCCTCC GAM336804 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CAGCC GAM336804 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336804 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336804 precursor RNA is designated SEQ ID:6766, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6766 is located from position 46229800 to position 46229904 relative to chromosome 11 on the `+` strand.

GAM336804 precursor RNA folds onto itself, forming GAM336804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336804 precursor RNA, designated SEQ ID NO: 6766, and a schematic representation of a predicted secondary folding of GAM336804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336804 folded precursor

RNA yielding a GAM336804 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336804 RNA, hereby incorporated herein.

GAM336804 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336804 target RNA, herein designated GAM TARGET RNA.

GAM336804 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336804 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336804 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336804 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336804 RNA, herein designated GAM RNA, to target binding sites on GAM336804 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336804 target RNA into GAM336804 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336804 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336804 target genes. The mRNA of each one of this plurality of GAM336804 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336804 RNA, herein designated GAM RNA, and which when bound by GAM336804 RNA causes inhibition of translation of the GAM336804 target mRNA into a corresponding GAM336804 target protein.

The mechanism of the translational inhibition exerted by GAM336804 RNA, herein designated GAM RNA, on one or more GAM336804 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336804 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336804 RNA, herein designated GAM RNA, of GAM336804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336804 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336804 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336804 RNA correlate with, and may be deduced from, the identity of the GAM336804 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336806 5867 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336806 (GAM336806) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336806 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336806 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336806 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336806 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336806 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336806 precursor RNA is designated SEQ ID:5867, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5867 is located from position 46270121 to position 46270202 relative to chromosome 16 on the `-` strand.

GAM336806 precursor RNA folds onto itself, forming GAM336806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336806 precursor RNA, designated SEQ ID NO: 5867, and a schematic representation of a predicted secondary folding of GAM336806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336806 folded precursor RNA yielding a GAM336806 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336806 RNA, hereby incorporated herein.

GAM336806 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336806 target RNA, herein designated GAM TARGET RNA.

GAM336806 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336806 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336806 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336806 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336806 RNA, herein designated GAM RNA, to target binding sites on GAM336806 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336806 target RNA into GAM336806 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336806 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336806 target genes. The mRNA of each one of this plurality of GAM336806 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336806 RNA, herein designated GAM RNA, and which when bound by GAM336806 RNA causes inhibition of translation of the GAM336806 target mRNA into a corresponding GAM336806 target protein.

The mechanism of the translational inhibition exerted by GAM336806 RNA, herein designated GAM RNA, on one or more GAM336806 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336806 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336806 RNA, herein designated GAM RNA, of GAM336806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336806 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336806 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336806 RNA correlate with, and may be deduced from, the identity of the GAM336806 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336807 6217 CTGCCTAGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGTGAGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCCATTCTG Messenger 336807 (GAM336807) oligonucleotides modulates expression of respective target

GCTTCAGACC genes whose function and utility is known in the art.

AGTCTGGGTT GAM336807 is a novel bioinformatically detectable regulatory, non protein

TGAAACCTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336807 was detected

ACATCCCACT is described with additional reference to Figs. 9-15.

AACTTAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

G encoded by the human genome.

GAM336807 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336807 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336807 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336807 precursor RNA is designated SEQ ID:6217, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6217 is located from position 46314585 to position 46314665 relative to chromosome 17 on the `-` strand.

GAM336807 precursor RNA folds onto itself, forming GAM336807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336807 precursor RNA, designated SEQ ID NO: 6217, and a schematic representation of a predicted secondary folding of GAM336807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336807 folded precursor RNA yielding a GAM336807 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336807 RNA, hereby incorporated herein.

GAM336807 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336807 target RNA, herein designated GAM TARGET RNA.

GAM336807 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336807 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336807 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336807 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336807 RNA, herein designated GAM RNA, to target binding sites on GAM336807 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336807 target RNA into GAM336807 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336807 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336807 target genes. The mRNA of each one of this plurality of GAM336807 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM336807 RNA, herein designated GAM RNA, and which when bound by GAM336807 RNA causes inhibition of translation of the GAM336807 target mRNA into a corresponding GAM336807 target protein.

The mechanism of the translational inhibition exerted by GAM336807 RNA, herein designated GAM RNA, on one or more GAM336807 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336807 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336807 RNA, herein designated GAM RNA, of GAM336807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336807 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336807 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336807 RNA correlate with, and may be deduced from, the identity of the GAM336807 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336809 5669 AAGGATGTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCACTGAAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTACCATACA Messenger 336809 (GAM336809) oligonucleotides modulates expression of respective target

TATGTGACCC genes whose function and utility is known in the art.

TTATTAGTTA GAM336809 is a novel bioinformatically detectable regulatory, non protein

CACATAAGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336809 was detected

ATTTTTATGG is described with additional reference to Figs. 9-15.

TGGTCTTTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCCTTATCT encoded by the human genome.

TT GAM336809 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336809 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336809 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336809 precursor RNA is designated SEQ ID:5669, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5669 is located from position 46540199 to position 46540291 relative to chromosome 14 on the `+` strand.

GAM336809 precursor RNA folds onto itself, forming GAM336809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336809 precursor RNA, designated SEQ ID NO: 5669, and a schematic representation of a predicted secondary folding of GAM336809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336809 folded precursor RNA yielding a GAM336809 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336809 RNA, hereby incorporated herein. Expression of GAM336809 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336809 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336809 target RNA, herein designated GAM TARGET RNA.

GAM336809 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336809 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336809 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336809 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336809 RNA, herein designated GAM RNA, to target binding sites on GAM336809 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336809 target RNA into GAM336809 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336809 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336809 target genes. The mRNA of each one of this plurality of GAM336809 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336809 RNA, herein designated GAM RNA, and which when bound by GAM336809 RNA causes inhibition of translation of the GAM336809 target mRNA into a corresponding GAM336809 target protein.

The mechanism of the translational inhibition exerted by GAM336809 RNA, herein designated GAM RNA, on one or more GAM336809 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336809 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336809 RNA, herein designated GAM RNA, of GAM336809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336809 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336809 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336809 RNA correlate with, and may be deduced from, the identity of the GAM336809 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336810 5797 AGGTTCACAC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGGTGCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCTGGGAC Messenger 336810 (GAM336810) oligonucleotides modulates expression of respective target

AAAAAAGAGA genes whose function and utility is known in the art.

CTTTCCTGAG GAM336810 is a novel bioinformatically detectable regulatory, non protein

GGTTGTCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336810 was detected

TTCCAGTTTC is described with additional reference to Figs. 9-15.

TCAGCCACTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACCATGTGAT encoded by the human genome.

ACCT GAM336810 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336810 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336810 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336810 precursor RNA is designated SEQ ID:5797, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5797 is located from position 46654581 to position 46654674 relative to chromosome 11 on the `-` strand.

GAM336810 precursor RNA folds onto itself, forming GAM336810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336810 precursor RNA, designated SEQ ID NO: 5797, and a schematic representation of a predicted secondary folding of GAM336810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336810 folded precursor RNA yielding a GAM336810 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336810 RNA, hereby incorporated herein.

GAM336810 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336810 target RNA, herein designated GAM TARGET RNA.

GAM336810 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336810 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336810 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336810 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336810 RNA, herein designated GAM RNA, to target binding sites on GAM336810 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336810 target RNA into GAM336810 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336810 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336810 target genes. The mRNA of each one of this plurality of GAM336810 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336810 RNA, herein designated GAM RNA, and which when bound by GAM336810 RNA causes inhibition of translation of the GAM336810 target mRNA into a corresponding GAM336810 target protein.

The mechanism of the translational inhibition exerted by GAM336810 RNA, herein designated GAM RNA, on one or more GAM336810 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336810 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336810 RNA, herein designated GAM RNA, of GAM336810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336810 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336810 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336810 RNA correlate with, and may be deduced from, the identity of the GAM336810 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336811 6855 GGTTCACACA TTGGTGCCTT Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCTGGGACA Messenger 336811 (GAM336811) oligonucleotides modulates expression of respective target

AAAAAGAGAC genes whose function and utility is known in the art.

TTTCCTGAGG GAM336811 is a novel bioinformatically detectable regulatory, non protein

GTTGTCTTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336811 was detected

TCCAGTTTCT is described with additional reference to Figs. 9-15.

CAGCCACTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCATGTGATA encoded by the human genome.

CC GAM336811 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336811 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336811 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336811 precursor RNA is designated SEQ ID:6855, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6855 is located from position 46654582 to position 46654673 relative to chromosome 11 on the `-` strand.

GAM336811 precursor RNA folds onto itself, forming GAM336811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336811 precursor RNA, designated SEQ ID NO: 6855, and a schematic representation of a predicted secondary folding of GAM336811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336811 folded precursor RNA yielding a GAM336811 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336811 RNA, hereby incorporated herein.

GAM336811 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336811 target RNA, herein designated GAM TARGET RNA.

GAM336811 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336811 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336811 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336811 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336811 RNA, herein designated GAM RNA, to target binding sites on GAM336811 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336811 target RNA into GAM336811 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336811 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336811 target genes. The mRNA of each one of this plurality of GAM336811 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336811 RNA, herein designated GAM RNA, and which when bound by GAM336811 RNA causes inhibition of translation of the GAM336811 target mRNA into a corresponding GAM336811 target protein.

The mechanism of the translational inhibition exerted by GAM336811 RNA, herein designated GAM RNA, on one or more GAM336811 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336811 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336811 RNA, herein designated GAM RNA, of GAM336811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336811 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336811 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336811 RNA correlate with, and may be deduced from, the identity of the GAM336811 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336812 6516 GCGCTGTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTGGGCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCATCCTGGG Messenger 336812 (GAM336812) oligonucleotides modulates expression of respective target
ACACAGGACA genes whose function and utility is known in the art.

TTGTAGTGGA GAM336812 is a novel bioinformatically detectable regulatory, non protein
GCATCCCAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336812 was detected
CTGAAACTTT is described with additional reference to Figs. 9-15.

GTCTCAGTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGACCCAG encoded by the human genome.

AAAGATGGGG GAM336812 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
T GAM336812 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336812 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336812 precursor RNA is designated SEQ ID:6516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6516 is located from position 46926845 to position 46926945 relative to chromosome 21 on the `+` strand.

GAM336812 precursor RNA folds onto itself, forming GAM336812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336812 precursor RNA, designated SEQ ID NO: 6516, and a schematic representation of a predicted secondary folding of GAM336812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336812 folded precursor RNA yielding a GAM336812 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336812 RNA, hereby incorporated herein.

GAM336812 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336812 target RNA, herein designated GAM TARGET RNA.

GAM336812 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336812 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336812 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336812 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336812 RNA, herein designated GAM RNA, to target binding sites on GAM336812 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336812 target RNA into GAM336812 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336812 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336812 target genes. The mRNA of each one of this plurality of GAM336812 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336812 RNA, herein designated GAM RNA, and which when bound by GAM336812 RNA causes inhibition of translation of the GAM336812 target mRNA into a corresponding GAM336812 target protein.

The mechanism of the translational inhibition exerted by GAM336812 RNA, herein designated GAM RNA, on one or more GAM336812 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336812 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336812 RNA, herein designated GAM RNA, of GAM336812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336812 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336812 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336812 RNA correlate with, and may be deduced from, the identity of the GAM336812 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336814 6491 GCAGCTGCAG AAAACACAGC CGAGTTGCTA GCTAAGGGGA AACAGACGCC GCTGTGGGAA AGCACTTGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336814 (GAM336814) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336814 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336814 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336814 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336814 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336814 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336814 precursor RNA is designated SEQ ID:6491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6491 is located from position 47053946 to position 47054014 relative to chromosome 20 on the `+` strand.

GAM336814 precursor RNA folds onto itself, forming GAM336814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336814 precursor RNA, designated SEQ ID NO: 6491, and a schematic representation of a predicted secondary folding of GAM336814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336814 folded precursor RNA yielding a GAM336814 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336814 RNA, hereby incorporated herein.

GAM336814 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336814 target RNA, herein designated GAM TARGET RNA.

GAM336814 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336814 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336814 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336814 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336814 RNA, herein designated GAM RNA, to target binding sites on GAM336814 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336814 target RNA into GAM336814 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336814 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336814 target genes. The mRNA of each one of this plurality of GAM336814 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336814 RNA, herein designated GAM RNA, and which when bound by GAM336814 RNA causes inhibition of translation of the GAM336814 target mRNA into a corresponding GAM336814 target protein.

The mechanism of the translational inhibition exerted by GAM336814 RNA, herein designated GAM RNA, on one or more GAM336814 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336814 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336814 RNA, herein designated GAM RNA, of GAM336814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336814 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336814 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336814 RNA correlate with, and may be deduced from, the identity of the GAM336814 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336815 7118 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCCCAGGAG Messenger 336815 (GAM336815) oligonucleotides modulates expression of respective target
GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGACCCA GAM336815 is a novel bioinformatically detectable regulatory, non protein
TATTCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336815 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACCCTCTCTC GAM336815 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM336815 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336815 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336815 precursor RNA is designated SEQ ID:7118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7118 is located from position 47056630 to position 47056730 relative to chromosome 10 on the `-` strand.

GAM336815 precursor RNA folds onto itself, forming GAM336815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336815 precursor RNA, designated SEQ ID NO: 7118, and a schematic representation of a predicted secondary folding of GAM336815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336815 folded precursor RNA yielding a GAM336815 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336815 RNA, hereby incorporated herein. Expression of GAM336815 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336815 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336815 target RNA, herein designated GAM TARGET RNA.

GAM336815 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336815 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336815 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336815 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336815 RNA, herein designated GAM RNA, to target binding sites on GAM336815 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336815 target RNA into GAM336815 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336815 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336815 target genes. The mRNA of each one of this plurality of GAM336815 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336815 RNA, herein designated GAM RNA, and which when bound by GAM336815 RNA causes inhibition of translation of the GAM336815 target mRNA into a corresponding GAM336815 target protein.

The mechanism of the translational inhibition exerted by GAM336815 RNA, herein designated GAM RNA, on one or more GAM336815 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336815 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336815 RNA, herein designated GAM RNA, of GAM336815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336815 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336815 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336815 RNA correlate with, and may be deduced from, the identity of the GAM336815 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336816 6208 CTGCAATGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTACTTAT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGATGAAAC Messenger 336816 (GAM336816) oligonucleotides modulates expression of respective target

TGTATCAGAC genes whose function and utility is known in the art.

TTTGTAGTGG GAM336816 is a novel bioinformatically detectable regulatory, non protein

CTGTGCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336816 was detected

TGATATCCTG is described with additional reference to Figs. 9-15.

GCCAGTAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTGCGTGCA encoded by the human genome.

G GAM336816 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336816 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336816 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336816 precursor RNA is designated SEQ

ID:6208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6208 is located from position 47073422 to position 47073512 relative to chromosome 16 on the `+` strand.

GAM336816 precursor RNA folds onto itself, forming GAM336816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336816 precursor RNA, designated SEQ ID NO: 6208, and a schematic representation of a predicted secondary folding of GAM336816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336816 folded precursor RNA yielding a GAM336816 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336816 RNA, hereby incorporated herein.

GAM336816 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336816 target RNA, herein designated GAM TARGET RNA.

GAM336816 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336816 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336816 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336816 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336816 RNA, herein designated GAM RNA, to target binding sites on GAM336816 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336816 target RNA into GAM336816 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336816 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336816 target genes. The mRNA of each one of this plurality of GAM336816 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336816 RNA, herein designated GAM RNA, and which when bound by GAM336816 RNA causes inhibition of translation of the GAM336816 target mRNA into a corresponding GAM336816 target protein.

The mechanism of the translational inhibition exerted by GAM336816 RNA, herein designated GAM RNA, on one or more GAM336816 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336816 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336816 RNA, herein designated GAM RNA, of GAM336816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336816 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336816 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336816 RNA correlate with, and may be deduced from, the identity of the GAM336816 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336817 6483 GCAATGCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTACTTATAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGAAACTG Messenger 336817 (GAM336817) oligonucleotides modulates expression of respective target

TATCAGACTT genes whose function and utility is known in the art.

TGTAGTGGCT GAM336817 is a novel bioinformatically detectable regulatory, non protein

GTGCATGTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336817 was detected

ATATCCTGGC is described with additional reference to Figs. 9-15.

CAGTAGGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCGTGC encoded by the human genome.

GAM336817 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336817 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336817 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336817 precursor RNA is designated SEQ ID:6483, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6483 is located from position 47073424 to position 47073510 relative to chromosome 16 on the `+` strand.

GAM336817 precursor RNA folds onto itself, forming GAM336817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336817 precursor RNA, designated SEQ ID NO: 6483, and a schematic representation of a predicted secondary folding of GAM336817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336817 folded precursor RNA yielding a GAM336817 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336817 RNA, hereby incorporated herein.

GAM336817 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336817 target RNA, herein designated GAM TARGET RNA.

GAM336817 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336817 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336817 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336817 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336817 RNA, herein designated GAM RNA, to target binding sites on GAM336817 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336817 target RNA into GAM336817 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336817 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336817 target genes. The mRNA of each one of this plurality of GAM336817 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336817 RNA, herein designated GAM RNA, and which when bound by GAM336817 RNA causes inhibition of translation of the GAM336817 target mRNA into a corresponding GAM336817 target protein.

The mechanism of the translational inhibition exerted by GAM336817 RNA, herein designated GAM RNA, on one or more GAM336817 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336817 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336817 RNA, herein designated GAM RNA, of GAM336817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336817 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336817 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336817 RNA correlate with, and may be deduced from, the identity of the GAM336817 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336818 6090 CCCTGGCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGGGATCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGAGGCCTCT Messenger 336818 (GAM336818) oligonucleotides modulates expression of respective target

CCAGTCCCCT genes whose function and utility is known in the art.

GAGGGTGCAC GAM336818 is a novel bioinformatically detectable regulatory, non protein
CACTGGCCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336818 was
detected
TCTCACCCAG is described with additional reference to Figs. 9-15.

GG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen
gene
encoded by the human genome.

GAM336818 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336818 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA
genes
GAM336818 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336818 precursor RNA is designated SEQ ID:6090, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6090 is located from position 47279033 to position 47279105 relative to chromosome 16 on the `+` strand.

GAM336818 precursor RNA folds onto itself, forming GAM336818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336818 precursor RNA, designated SEQ ID NO: 6090, and a schematic representation of a predicted secondary folding of GAM336818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336818 folded precursor RNA yielding a GAM336818 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336818 RNA, hereby incorporated herein. Expression of GAM336818 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336818 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336818 target RNA, herein designated GAM TARGET RNA.

GAM336818 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336818 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336818 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336818 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336818 RNA, herein designated GAM RNA, to target binding sites on GAM336818 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336818 target RNA into GAM336818 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336818 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336818 target genes. The mRNA of each one of this plurality of GAM336818 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336818 RNA, herein designated GAM RNA, and which when bound by GAM336818 RNA causes inhibition of translation of the GAM336818 target mRNA into a corresponding GAM336818 target protein.

The mechanism of the translational inhibition exerted by GAM336818 RNA, herein designated GAM RNA, on one or more GAM336818 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336818 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336818 RNA, herein designated GAM RNA, of GAM336818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336818 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336818 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336818 RNA correlate with, and may be deduced from, the identity of the GAM336818 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336819 5645 AAAAGCCATG Fig. 8 further provides a conceptual description of another novel bioinformatically
TTACAGATGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCTCCTTGG Messenger 336819 (GAM336819) oligonucleotides modulates expression of respective target
ATGGCTATTC genes whose function and utility is known in the art.

CAGTCGGTTT GAM336819 is a novel bioinformatically detectable regulatory, non protein
CCGGGGCTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336819 was detected
CTGGCCCACT is described with additional reference to Figs. 9-15.

CCATTTAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTGTAGCTG encoded by the human genome.

TGAGTGTATT GAM336819 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TT GAM336819 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336819 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336819 precursor RNA is designated SEQ ID:5645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5645 is located from position 47313354 to position 47313455 relative to chromosome 17 on the `+` strand.

GAM336819 precursor RNA folds onto itself, forming GAM336819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336819 precursor RNA, designated SEQ ID NO: 5645, and a schematic representation of a predicted secondary folding of GAM336819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336819 folded precursor RNA yielding a GAM336819 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336819 RNA, hereby incorporated herein.

GAM336819 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336819 target RNA, herein designated GAM TARGET RNA.

GAM336819 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336819 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336819 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336819 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336819 RNA, herein designated GAM RNA, to target binding sites on GAM336819 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336819 target RNA into GAM336819 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336819 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336819 target genes. The mRNA of each one of this plurality of GAM336819 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336819 RNA, herein designated GAM RNA, and which when bound by GAM336819 RNA causes inhibition of translation of the GAM336819 target mRNA into a corresponding GAM336819 target protein.

The mechanism of the translational inhibition exerted by GAM336819 RNA, herein designated GAM RNA, on one or more GAM336819 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336819 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336819 RNA, herein designated GAM RNA, of GAM336819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336819 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336819 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336819 RNA correlate with, and may be deduced from, the identity of the GAM336819 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336820 7109 TGAGGCAAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TCAGAAAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAGGCAATT Messenger 336820 (GAM336820) oligonucleotides modulates expression of respective target
TTTGCCTTGT genes whose function and utility is known in the art.

TCATTGCAAC GAM336820 is a novel bioinformatically detectable regulatory, non protein
ACTCCCTTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336820 was detected
GAGCTCTGAG is described with additional reference to Figs. 9-15.

TTTAAGCTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAGTCTGAC encoded by the human genome.

TACCTTGCTG GAM336820 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CCA GAM336820 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336820 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336820 precursor RNA is designated SEQ ID:7109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7109 is located from position 47490707 to position 47490809 relative to chromosome 15 on the `+` strand.

GAM336820 precursor RNA folds onto itself, forming GAM336820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336820 precursor RNA, designated SEQ ID NO: 7109, and a schematic representation of a predicted secondary folding of GAM336820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336820 folded precursor

RNA yielding a GAM336820 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336820 RNA, hereby incorporated herein.

GAM336820 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336820 target RNA, herein designated GAM TARGET RNA.

GAM336820 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336820 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336820 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336820 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336820 RNA, herein designated GAM RNA, to target binding sites on GAM336820 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336820 target RNA into GAM336820 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336820 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336820 target genes. The mRNA of each one of this plurality of GAM336820 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336820 RNA, herein designated GAM RNA, and which when bound by GAM336820 RNA causes inhibition of translation of the GAM336820 target mRNA into a corresponding GAM336820 target protein.

The mechanism of the translational inhibition exerted by GAM336820 RNA, herein designated GAM RNA, on one or more GAM336820 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336820 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336820 RNA, herein designated GAM RNA, of GAM336820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336820 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336820 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336820 RNA correlate with, and may be deduced from, the identity of the GAM336820 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336821 7119 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCCCAGGAG Messenger 336821 (GAM336821) oligonucleotides modulates expression of respective target

GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGACCCA GAM336821 is a novel bioinformatically detectable regulatory, non protein

TATTCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336821 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACCCTCTCTC GAM336821 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336821 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336821 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336821 precursor RNA is designated SEQ ID:7119, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7119 is located from position 47538323 to position 47538423 relative to chromosome 10 on the `+` strand.

GAM336821 precursor RNA folds onto itself, forming GAM336821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336821 precursor RNA, designated SEQ ID NO: 7119, and a schematic representation of a predicted secondary folding of GAM336821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336821 folded precursor RNA yielding a GAM336821 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336821 RNA, hereby incorporated herein. Expression of GAM336821 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336821 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336821 target RNA, herein designated GAM TARGET RNA.

GAM336821 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336821 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336821 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336821 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336821 RNA, herein designated GAM RNA, to target binding sites on GAM336821 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336821 target RNA into GAM336821 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336821 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336821 target genes. The mRNA of each one of this plurality of GAM336821 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336821 RNA, herein designated GAM RNA, and which when bound by GAM336821 RNA causes inhibition of translation of the GAM336821 target mRNA into a corresponding GAM336821 target protein.

The mechanism of the translational inhibition exerted by GAM336821 RNA, herein designated GAM RNA, on one or more GAM336821 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336821 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336821 RNA, herein designated GAM RNA, of GAM336821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336821 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336821 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336821 RNA correlate with, and may be deduced from, the identity of the GAM336821 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336822 6100 CCGTCACAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTTGCCCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGTTCATC Messenger 336822 (GAM336822) oligonucleotides modulates expression of respective target

ACTGAAGACA genes whose function and utility is known in the art.

AGCATGTGAT GAM336822 is a novel bioinformatically detectable regulatory, non protein

TTTCTCATCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336822 was detected

CATCCTCCCA is described with additional reference to Figs. 9-15.

CTTCAAGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCAGGGCAG encoded by the human genome.

TGAGG GAM336822 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336822 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336822 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336822 precursor RNA is designated SEQ

ID:6100, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6100 is located from position 47560720 to position 47560814 relative to chromosome 10 on the `+` strand.

GAM336822 precursor RNA folds onto itself, forming GAM336822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336822 precursor RNA, designated SEQ ID NO: 6100, and a schematic representation of a predicted secondary folding of GAM336822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336822 folded precursor RNA yielding a GAM336822 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336822 RNA, hereby incorporated herein.

GAM336822 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336822 target RNA, herein designated GAM TARGET RNA.

GAM336822 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336822 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336822 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336822 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336822 RNA, herein designated GAM RNA, to target binding sites on GAM336822 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336822 target RNA into GAM336822 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336822 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336822 target genes. The mRNA of each one of this plurality of GAM336822 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336822 RNA, herein designated GAM RNA, and which when bound by GAM336822 RNA causes inhibition of translation of the GAM336822 target mRNA into a corresponding GAM336822 target protein.

The mechanism of the translational inhibition exerted by GAM336822 RNA, herein designated GAM RNA, on one or more GAM336822 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336822 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336822 RNA, herein designated GAM RNA, of GAM336822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336822 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336822 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336822 RNA correlate with, and may be deduced from, the identity of the GAM336822 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336823 5791 AGGGTGTGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGGCAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGGGCGGC Messenger 336823 (GAM336823) oligonucleotides modulates expression of respective target

AGGTGTCAGG genes whose function and utility is known in the art.

CCGGCTTGGA GAM336823 is a novel bioinformatically detectable regulatory, non protein

CAATGAAACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336823 was detected

CTGACCTTGC is described with additional reference to Figs. 9-15.

TGCATTCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336823 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336823 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336823 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336823 precursor RNA is designated SEQ ID:5791, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5791 is located from position 47606004 to position 47606083 relative to chromosome X on the `-` strand.

GAM336823 precursor RNA folds onto itself, forming GAM336823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336823 precursor RNA, designated SEQ ID NO: 5791, and a schematic representation of a predicted secondary folding of GAM336823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336823 folded precursor RNA yielding a GAM336823 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336823 RNA, hereby incorporated herein.

GAM336823 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336823 target RNA, herein designated GAM TARGET RNA.

GAM336823 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336823 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336823 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336823 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336823 RNA, herein designated GAM RNA, to target binding sites on GAM336823 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336823 target RNA into GAM336823 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336823 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336823 target genes. The mRNA of each one of this plurality of GAM336823 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336823 RNA, herein designated GAM RNA, and which when bound by GAM336823 RNA causes inhibition of translation of the GAM336823 target mRNA into a corresponding GAM336823 target protein.

The mechanism of the translational inhibition exerted by GAM336823 RNA, herein designated GAM RNA, on one or more GAM336823 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336823 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336823 RNA, herein designated GAM RNA, of GAM336823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336823 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336823 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336823 RNA correlate with, and may be deduced from, the identity of the GAM336823 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336824 6647 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAGG Messenger 336824 (GAM336824) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336824 is a novel bioinformatically detectable regulatory, non protein
ACTACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336824 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM336824 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336824 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336824 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336824 precursor RNA is designated SEQ ID:6647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6647 is located from position 47747389 to position 47747476 relative to chromosome 19 on the `-` strand.

GAM336824 precursor RNA folds onto itself, forming GAM336824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336824 precursor RNA, designated SEQ ID NO: 6647, and a schematic representation of a predicted secondary folding of GAM336824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336824 folded precursor RNA yielding a GAM336824 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336824 RNA, hereby incorporated herein. Expression of GAM336824 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336824 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336824 target RNA, herein designated GAM TARGET RNA.

GAM336824 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336824 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336824 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336824 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336824 RNA, herein designated GAM RNA, to target binding sites on GAM336824 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336824 target RNA into GAM336824 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336824 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336824 target genes. The mRNA of each one of this plurality of GAM336824 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336824 RNA, herein designated GAM RNA, and which when bound by GAM336824 RNA causes inhibition of translation of the GAM336824 target mRNA into a corresponding GAM336824 target protein.

The mechanism of the translational inhibition exerted by GAM336824 RNA, herein designated GAM RNA, on one or more GAM336824 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336824 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336824 RNA, herein designated GAM RNA, of GAM336824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336824 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336824 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336824 RNA correlate with, and may be deduced from, the identity of the GAM336824 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336825 6323 GAGAATCGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGACTGAGGT Messenger 336825 (GAM336825) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

TGAGATCATG GAM336825 is a novel bioinformatically detectable regulatory, non protein
CAACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336825 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACACAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTTCATC encoded by the human genome.

TC GAM336825 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336825 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336825 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336825 precursor RNA is designated SEQ ID:6323, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6323 is located from position 47783494 to position 47783585 relative to chromosome X on the `-` strand.

GAM336825 precursor RNA folds onto itself, forming GAM336825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336825 precursor RNA, designated SEQ ID NO: 6323, and a schematic representation of a predicted secondary folding of GAM336825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336825 folded precursor RNA yielding a GAM336825 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336825 RNA, hereby incorporated herein. Expression of GAM336825 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336825 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336825 target RNA, herein designated GAM TARGET RNA.

GAM336825 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336825 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336825 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336825 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336825 RNA, herein designated GAM RNA, to target binding sites on GAM336825 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336825 target RNA into GAM336825 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336825 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336825 target genes. The mRNA of each one of this plurality of GAM336825 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336825 RNA, herein designated GAM RNA, and which when bound by GAM336825 RNA causes inhibition of translation of the GAM336825 target mRNA into a corresponding GAM336825 target protein.

The mechanism of the translational inhibition exerted by GAM336825 RNA, herein designated GAM RNA, on one or more GAM336825 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336825 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336825 RNA, herein designated GAM RNA, of GAM336825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336825 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336825 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336825 RNA correlate with, and may be deduced from, the identity of the GAM336825 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336826 6559 GCTTGAACCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGAGACTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTTGCAGTG Messenger 336826 (GAM336826) oligonucleotides modulates expression of respective target
AGCTGAGATC genes whose function and utility is known in the art.

ATGCAACTGC GAM336826 is a novel bioinformatically detectable regulatory, non protein
ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336826 was detected
GGGCAACACA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336826 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336826 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336826 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336826 precursor RNA is designated SEQ ID:6559, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6559 is located from position 47783507 to position 47783578 relative to chromosome X on the `-` strand.

GAM336826 precursor RNA folds onto itself, forming GAM336826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336826 precursor RNA, designated SEQ ID NO: 6559, and a schematic representation of a predicted secondary folding of GAM336826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336826 folded precursor

RNA yielding a GAM336826 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336826 RNA, hereby incorporated herein. Expression of GAM336826 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336826 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336826 target RNA, herein designated GAM TARGET RNA.

GAM336826 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336826 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336826 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336826 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336826 RNA, herein designated GAM RNA, to target binding sites on GAM336826 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336826 target RNA into GAM336826 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336826 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336826 target genes. The mRNA of each one of this plurality of GAM336826 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336826 RNA, herein designated GAM RNA, and which when bound by GAM336826 RNA causes inhibition of translation of the GAM336826 target mRNA into a corresponding GAM336826 target protein.

The mechanism of the translational inhibition exerted by GAM336826 RNA, herein designated GAM RNA, on one or more GAM336826 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336826 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336826 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336826 RNA, herein designated GAM RNA, of GAM336826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336826 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336826 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336826 RNA correlate with, and may be deduced from, the identity of the GAM336826 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336827 7304 TTCTCTGTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCATTCCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCTACGCCC Messenger 336827 (GAM336827) oligonucleotides modulates expression of respective target
CCAGACTGTG genes whose function and utility is known in the art.

AGGGGTGTAA GAM336827 is a novel bioinformatically detectable regulatory, non protein
GGAAGATGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336827 was detected
AGATGTTGCG is described with additional reference to Figs. 9-15.

GGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336827 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336827 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336827 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336827 precursor RNA is designated SEQ ID:7304, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7304 is located from position 47935242 to position 47935317 relative to chromosome 17 on the `+` strand.

GAM336827 precursor RNA folds onto itself, forming GAM336827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336827 precursor RNA, designated SEQ ID NO: 7304, and a schematic representation of a predicted secondary folding of GAM336827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336827 folded precursor RNA yielding a GAM336827 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336827 RNA, hereby incorporated herein.

GAM336827 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336827 target RNA, herein designated GAM TARGET RNA.

GAM336827 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336827 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336827 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336827 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336827 RNA, herein designated GAM RNA, to target binding sites on GAM336827 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336827 target RNA into GAM336827 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336827 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336827 target genes. The mRNA of each one of this plurality of GAM336827 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336827 RNA, herein designated GAM RNA, and which when bound by GAM336827 RNA causes inhibition of translation of the GAM336827 target mRNA into a corresponding GAM336827 target protein.

The mechanism of the translational inhibition exerted by GAM336827 RNA, herein

designated GAM RNA, on one or more GAM336827 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336827 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336827 RNA, herein designated GAM RNA, of GAM336827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336827 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336827 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336827 RNA correlate with, and may be deduced from, the identity of the GAM336827 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336828 7069 TCTCTGTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCATTCCCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTACGCCCC Messenger 336828 (GAM336828) oligonucleotides modulates expression of respective target

CAGACTGTGA genes whose function and utility is known in the art.

GGGGTGTAAG GAM336828 is a novel bioinformatically detectable regulatory, non protein

GAAGATGGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336828 was detected

GATGTTGCGG is described with additional reference to Figs. 9-15.

GAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336828 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336828 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336828 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336828 precursor RNA is designated SEQ ID:7069, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7069 is located from position 47935243 to position 47935316

relative to chromosome 17 on the `+` strand.

GAM336828 precursor RNA folds onto itself, forming GAM336828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336828 precursor RNA, designated SEQ ID NO: 7069, and a schematic representation of a predicted secondary folding of GAM336828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336828 folded precursor RNA yielding a GAM336828 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336828 RNA, hereby incorporated herein.

GAM336828 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336828 target RNA, herein designated GAM TARGET RNA.

GAM336828 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336828 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336828 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336828 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336828 RNA, herein designated GAM RNA, to target binding sites on GAM336828 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336828 target RNA into GAM336828 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336828 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336828 target genes. The mRNA of each one of this plurality of GAM336828 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336828 RNA, herein designated GAM RNA, and which when bound by GAM336828 RNA causes inhibition of translation of the GAM336828 target mRNA into a corresponding GAM336828 target protein.

The mechanism of the translational inhibition exerted by GAM336828 RNA, herein designated GAM RNA, on one or more GAM336828 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336828 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336828 RNA, herein designated GAM RNA, of GAM336828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336828 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336828 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336828 RNA correlate with, and may be deduced from, the identity of the GAM336828 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336829 7063 TCTCAACTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTATGTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTACAGTGG Messenger 336829 (GAM336829) oligonucleotides modulates expression of respective target

GTGTAGGGAC genes whose function and utility is known in the art.

CAGCCACACA GAM336829 is a novel bioinformatically detectable regulatory, non protein

GGGTCGGTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336829 was detected

GTTTTTCTCC is described with additional reference to Figs. 9-15.

CCGTGTGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGATGAGAGA encoded by the human genome.

TTGTAGA GAM336829 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336829 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336829 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336829 precursor RNA is designated SEQ ID:7063, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7063 is located from position 47956679 to position 47956775 relative to chromosome 19 on the `+` strand.

GAM336829 precursor RNA folds onto itself, forming GAM336829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336829 precursor RNA, designated SEQ ID NO: 7063, and a schematic representation of a predicted secondary folding of GAM336829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336829 folded precursor RNA yielding a GAM336829 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336829 RNA, hereby incorporated herein.

GAM336829 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336829 target RNA, herein designated GAM TARGET RNA.

GAM336829 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336829 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336829 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336829 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336829 RNA, herein designated GAM RNA, to target binding sites on GAM336829 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336829 target RNA into GAM336829 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336829 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336829 target genes. The mRNA of each one of this plurality of GAM336829 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336829 RNA, herein designated GAM RNA, and which when bound by GAM336829 RNA causes inhibition of translation of the GAM336829 target mRNA into a corresponding GAM336829 target protein.

The mechanism of the translational inhibition exerted by GAM336829 RNA, herein designated GAM RNA, on one or more GAM336829 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336829 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336829 RNA, herein designated GAM RNA, of GAM336829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336829 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336829 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336829 RNA correlate with, and may be deduced from, the identity of the GAM336829 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336830 6085 CCCTCAGCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGTTTTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTAGAATG Messenger 336830 (GAM336830) oligonucleotides modulates expression of respective target

GGTTTTTTAA genes whose function and utility is known in the art.

AAAAAGGATC GAM336830 is a novel bioinformatically detectable regulatory, non protein

TTTCTTAATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336830 was detected

CCAGGACTCC is described with additional reference to Figs. 9-15.

TGAGTTGGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

G encoded by the human genome.

GAM336830 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336830 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336830 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336830 precursor RNA is designated SEQ ID:6085, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6085 is located from position 47994779 to position 47994859 relative to chromosome 17 on the `+` strand.

GAM336830 precursor RNA folds onto itself, forming GAM336830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336830 precursor RNA, designated SEQ ID NO: 6085, and a schematic representation of a predicted secondary folding of GAM336830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336830 folded precursor RNA yielding a GAM336830 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336830 RNA, hereby incorporated herein.

GAM336830 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336830 target RNA, herein designated GAM TARGET RNA.

GAM336830 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336830 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336830 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336830 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336830 RNA, herein designated GAM RNA, to target binding sites on GAM336830 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336830 target RNA into GAM336830 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336830 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336830 target genes. The mRNA of each one of this plurality of GAM336830 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336830 RNA, herein designated GAM RNA, and which when bound by GAM336830 RNA causes inhibition of translation of the GAM336830 target mRNA into a corresponding GAM336830 target protein.

The mechanism of the translational inhibition exerted by GAM336830 RNA, herein designated GAM RNA, on one or more GAM336830 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336830 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336830 RNA, herein designated GAM RNA, of GAM336830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336830 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336830 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336830 RNA correlate with, and may be deduced from, the identity of the GAM336830 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336832 5982 ATTTCCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCAGCTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TACTCACCAG Messenger 336832 (GAM336832) oligonucleotides modulates expression of respective target
GGCAGATTCA genes whose function and utility is known in the art.

CACCAAGTTG GAM336832 is a novel bioinformatically detectable regulatory, non protein
GGGTTTCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336832 was detected
GGCAGTCAGG is described with additional reference to Figs. 9-15.

AAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336832 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336832 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336832 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336832 precursor RNA is designated SEQ ID:5982, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5982 is located from position 48134831 to position 48134904 relative to chromosome 17 on the `-` strand.

GAM336832 precursor RNA folds onto itself, forming GAM336832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336832 precursor RNA, designated SEQ ID NO: 5982, and a schematic representation of a predicted secondary folding of GAM336832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336832 folded precursor RNA yielding a GAM336832 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336832 RNA, hereby incorporated herein.

GAM336832 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336832 target RNA, herein designated GAM TARGET RNA.

GAM336832 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336832 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336832 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336832 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336832 RNA, herein designated GAM RNA, to target binding sites on GAM336832 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336832 target RNA into GAM336832 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336832 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336832 target genes. The mRNA of each one of this plurality of GAM336832 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336832 RNA, herein designated GAM RNA, and which when bound by GAM336832 RNA causes inhibition of translation of the GAM336832 target mRNA into a corresponding GAM336832 target protein.

The mechanism of the translational inhibition exerted by GAM336832 RNA, herein designated GAM RNA, on one or more GAM336832 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336832 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336832 RNA, herein designated GAM RNA, of GAM336832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336832 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336832 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336832

RNA correlate with, and may be deduced from, the identity of the GAM336832 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336833 6355 GAGATGGCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTAAACTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTGATGACC Messenger 336833 (GAM336833) oligonucleotides modulates expression of respective target
AGGTTTCATT genes whose function and utility is known in the art.

AGGTAAGAAG GAM336833 is a novel bioinformatically detectable regulatory, non protein
GCCCGATTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336833 was detected
GCAACGGTGG is described with additional reference to Figs. 9-15.

CCCAAATAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCAGTGGTT encoded by the human genome.

CAGACACTGT GAM336833 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTTTCAAAGC GAM336833 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CAGCAGAAGT GAM336833 precursor RNA does not encode a protein. A nucleotide sequence identical or

CTTGCCAAAT highly similar to the nucleotide sequence of GAM336833 precursor RNA is designated SEQ

T ID:6355, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6355 is located from position 48164886 to position 48165016 relative to chromosome 16 on the `-` strand.

GAM336833 precursor RNA folds onto itself, forming GAM336833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336833 precursor RNA, designated SEQ ID NO: 6355, and a schematic representation of a predicted secondary folding of GAM336833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336833 folded precursor RNA yielding a GAM336833 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336833 RNA, hereby incorporated herein.

GAM336833 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336833 target RNA, herein designated GAM TARGET RNA.

GAM336833 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336833 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336833 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336833 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336833 RNA, herein designated GAM RNA, to target binding sites on GAM336833 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336833 target RNA into GAM336833 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336833 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336833 target genes. The mRNA of each one of this plurality of GAM336833 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336833 RNA, herein designated GAM RNA, and which when bound by GAM336833 RNA causes inhibition of translation of the GAM336833 target mRNA into a corresponding GAM336833 target protein.

The mechanism of the translational inhibition exerted by GAM336833 RNA, herein designated GAM RNA, on one or more GAM336833 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336833 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336833 RNA, herein designated GAM RNA, of GAM336833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336833 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336833 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336833 RNA correlate with, and may be deduced from, the identity of the GAM336833 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336834 6569 GCTTTGATGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGTTTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
TTAGGTAAGA Messenger 336834 (GAM336834) oligonucleotides modulates expression of respective target
AGGCCCGATT genes whose function and utility is known in the art.

AAGCAACGGT GAM336834 is a novel bioinformatically detectable regulatory, non protein
GGCCCAAATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336834 was detected
ACCTCAGTGG is described with additional reference to Figs. 9-15.

TTCAGACACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTTTTTCAAA encoded by the human genome.

GC GAM336834 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336834 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336834 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336834 precursor RNA is designated SEQ ID:6569, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6569 is located from position 48164907 to position 48164998 relative to chromosome 16 on the `-` strand.

GAM336834 precursor RNA folds onto itself, forming GAM336834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336834 precursor RNA, designated SEQ ID NO: 6569, and a schematic representation of a predicted secondary folding of GAM336834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336834 folded precursor RNA yielding a GAM336834 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336834 RNA, hereby incorporated herein.

GAM336834 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336834 target RNA, herein designated GAM TARGET RNA.

GAM336834 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336834 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336834 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336834 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336834 RNA, herein designated GAM RNA, to target binding sites on GAM336834 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336834 target RNA into GAM336834 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336834 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336834 target genes. The mRNA of each one of this plurality of GAM336834 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336834 RNA, herein designated GAM RNA, and which when bound by GAM336834 RNA causes inhibition of translation of the GAM336834 target mRNA into a corresponding GAM336834 target protein.

The mechanism of the translational inhibition exerted by GAM336834 RNA, herein designated GAM RNA, on one or more GAM336834 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336834 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336834 RNA, herein designated GAM RNA, of GAM336834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336834 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336834 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336834 RNA correlate with, and may be deduced from, the identity of the GAM336834 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336835 7120 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCCCAGGAG Messenger 336835 (GAM336835) oligonucleotides modulates expression of respective target

GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGACCCA GAM336835 is a novel bioinformatically detectable regulatory, non protein

TATTCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336835 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACCCTCTCTC GAM336835 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336835 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336835 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336835 precursor RNA is designated SEQ ID:7120, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7120 is located from position 48175291 to position 48175391 relative to chromosome 10 on the `+` strand.

GAM336835 precursor RNA folds onto itself, forming GAM336835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336835 precursor RNA, designated SEQ ID NO: 7120, and a schematic representation of a predicted secondary folding of GAM336835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336835 folded precursor RNA yielding a GAM336835 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336835 RNA, hereby incorporated herein. Expression of GAM336835 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336835 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336835 target RNA, herein designated GAM TARGET RNA.

GAM336835 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336835 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336835 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336835 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336835 RNA, herein designated GAM RNA, to target binding sites on GAM336835 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336835 target RNA into GAM336835 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336835 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336835 target genes. The mRNA of each one of this plurality of GAM336835 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336835 RNA,

herein designated GAM RNA, and which when bound by GAM336835 RNA causes inhibition of translation of the GAM336835 target mRNA into a corresponding GAM336835 target protein.

The mechanism of the translational inhibition exerted by GAM336835 RNA, herein designated GAM RNA, on one or more GAM336835 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336835 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336835 RNA, herein designated GAM RNA, of GAM336835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336835 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336835 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336835 RNA correlate with, and may be deduced from, the identity of the GAM336835 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336836 7083 TCTTTTTCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGTCTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTGGCAGT Messenger 336836 (GAM336836) oligonucleotides modulates expression of respective target

CATGAATGAG genes whose function and utility is known in the art.

ACTCTGTCAG GAM336836 is a novel bioinformatically detectable regulatory, non protein

ATCTCCATGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336836 was detected

CAGGGACCTG is described with additional reference to Figs. 9-15.

ATTGACAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336836 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336836 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336836 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336836 precursor RNA is designated SEQ ID:7083, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7083 is located from position 48190562 to position 48190640 relative to chromosome 19 on the `+` strand.

GAM336836 precursor RNA folds onto itself, forming GAM336836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336836 precursor RNA, designated SEQ ID NO: 7083, and a schematic representation of a predicted secondary folding of GAM336836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336836 folded precursor RNA yielding a GAM336836 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336836 RNA, hereby incorporated herein.

GAM336836 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336836 target RNA, herein designated GAM TARGET RNA.

GAM336836 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336836 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336836 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336836 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336836 RNA, herein designated GAM RNA, to target binding sites on GAM336836 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336836 target RNA

into GAM336836 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336836 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336836 target genes. The mRNA of each one of this plurality of GAM336836 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336836 RNA, herein designated GAM RNA, and which when bound by GAM336836 RNA causes inhibition of translation of the GAM336836 target mRNA into a corresponding GAM336836 target protein.

The mechanism of the translational inhibition exerted by GAM336836 RNA, herein designated GAM RNA, on one or more GAM336836 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336836 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336836 RNA, herein designated GAM RNA, of GAM336836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336836 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336836 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336836 RNA correlate with, and may be deduced from, the identity of the GAM336836 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336837 6314 GACCATGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGAGTCTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGACTCCT Messenger 336837 (GAM336837) oligonucleotides modulates expression of respective target
CACTCAACCT genes whose function and utility is known in the art.

CGGCCATGGA GAM336837 is a novel bioinformatically detectable regulatory, non protein
CGCAGGTTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336837 was detected
GTGTGAGGGG is described with additional reference to Figs. 9-15.

GGTCCCAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTCGGTCTT encoded by the human genome.

CTATTTC GAM336837 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336837 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336837 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336837 precursor RNA is designated SEQ ID:6314, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6314 is located from position 48206347 to position 48206443 relative to chromosome 10 on the `+` strand.

GAM336837 precursor RNA folds onto itself, forming GAM336837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336837 precursor RNA, designated SEQ ID NO: 6314, and a schematic representation of a predicted secondary folding of GAM336837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336837 folded precursor RNA yielding a GAM336837 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336837 RNA, hereby incorporated herein.

GAM336837 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336837 target RNA, herein designated GAM TARGET RNA.

GAM336837 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336837 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336837 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336837 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336837 RNA, herein designated GAM RNA, to target binding sites on GAM336837 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336837 target RNA into GAM336837 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336837 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336837 target genes. The mRNA of each one of this plurality of GAM336837 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336837 RNA, herein designated GAM RNA, and which when bound by GAM336837 RNA causes inhibition of translation of the GAM336837 target mRNA into a corresponding GAM336837 target protein.

The mechanism of the translational inhibition exerted by GAM336837 RNA, herein designated GAM RNA, on one or more GAM336837 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336837 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336837 RNA, herein designated GAM RNA, of GAM336837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336837 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336837 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336837 RNA correlate with, and may be deduced from, the identity of the GAM336837 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336838 6497 GCAGGTATGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGCCTTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTATCCTG Messenger 336838 (GAM336838) oligonucleotides modulates expression of respective target

GTTCCTGCAG genes whose function and utility is known in the art.

AGCTGACTGC GAM336838 is a novel bioinformatically detectable regulatory, non protein
CATGCTTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336838 was detected
AGAGGGAAAA is described with additional reference to Figs. 9-15.

GACTTATTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTGT encoded by the human genome.

GAM336838 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336838 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336838 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336838 precursor RNA is designated SEQ ID:6497, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6497 is located from position 48246637 to position 48246721 relative to chromosome 19 on the `-` strand.

GAM336838 precursor RNA folds onto itself, forming GAM336838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336838 precursor RNA, designated SEQ ID NO: 6497, and a schematic representation of a predicted secondary folding of GAM336838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336838 folded precursor RNA yielding a GAM336838 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336838 RNA, hereby incorporated herein.

GAM336838 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336838 target RNA, herein designated GAM TARGET RNA.

GAM336838 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336838 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336838 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336838 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336838 RNA, herein designated GAM RNA, to target binding sites on GAM336838 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336838 target RNA into GAM336838 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336838 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336838 target genes. The mRNA of each one of this plurality of GAM336838 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336838 RNA, herein designated GAM RNA, and which when bound by GAM336838 RNA causes inhibition of translation of the GAM336838 target mRNA into a corresponding GAM336838 target protein.

The mechanism of the translational inhibition exerted by GAM336838 RNA, herein designated GAM RNA, on one or more GAM336838 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336838 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336838 RNA, herein designated GAM RNA, of GAM336838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336838 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336838 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336838 RNA correlate with, and may be deduced from, the identity of the GAM336838 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336840 6695 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGTGG Messenger 336840 (GAM336840) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATTGT GAM336840 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336840 was detected
TCCACCCTCA is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAAACTCC encoded by the human genome.

GAM336840 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336840 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336840 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336840 precursor RNA is designated SEQ ID:6695, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6695 is located from position 48506039 to position 48506126 relative to chromosome 17 on the `+` strand.

GAM336840 precursor RNA folds onto itself, forming GAM336840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336840 precursor RNA, designated SEQ ID NO: 6695, and a schematic representation of a predicted secondary folding of GAM336840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336840 folded precursor RNA yielding a GAM336840 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336840 RNA, hereby incorporated herein.

GAM336840 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336840 target RNA, herein designated GAM TARGET RNA.

GAM336840 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336840 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336840 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336840 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336840 RNA, herein designated GAM RNA, to target binding sites on GAM336840 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336840 target RNA into GAM336840 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336840 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336840 target genes. The mRNA of each one of this plurality of GAM336840 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336840 RNA, herein designated GAM RNA, and which when bound by GAM336840 RNA causes inhibition of translation of the GAM336840 target mRNA into a corresponding GAM336840 target protein.

The mechanism of the translational inhibition exerted by GAM336840 RNA, herein designated GAM RNA, on one or more GAM336840 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336840 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336840 RNA, herein designated GAM RNA, of GAM336840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336840 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336840 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336840 RNA correlate with, and may be deduced from, the identity of the GAM336840 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336841 7141 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCCGGGA Messenger 336841 (GAM336841) oligonucleotides modulates expression of respective target
GGTGGAGGTT genes whose function and utility is known in the art.

GCAGTGAGCC GAM336841 is a novel bioinformatically detectable regulatory, non protein
GAGATCGCGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336841 was detected
CATTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAGAGTG encoded by the human genome.

AAACACTGTC GAM336841 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCA GAM336841 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336841 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336841 precursor RNA is designated SEQ ID:7141, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7141 is located from position 48685091 to position 48685193 relative to chromosome 4 on the `+` strand.

GAM336841 precursor RNA folds onto itself, forming GAM336841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336841 precursor RNA, designated SEQ ID NO: 7141, and a schematic representation of a predicted secondary folding of GAM336841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336841 folded precursor RNA yielding a GAM336841 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336841 RNA, hereby incorporated herein. Expression of GAM336841 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336841 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336841 target RNA, herein designated GAM TARGET RNA.

GAM336841 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336841 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336841 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336841 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336841 RNA, herein designated GAM RNA, to target binding sites on GAM336841 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336841 target RNA into GAM336841 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336841 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336841 target genes. The mRNA of each one of this plurality of GAM336841 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336841 RNA, herein designated GAM RNA, and which when bound by GAM336841 RNA causes inhibition of translation of the GAM336841 target mRNA into a corresponding GAM336841 target protein.

The mechanism of the translational inhibition exerted by GAM336841 RNA, herein designated GAM RNA, on one or more GAM336841 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336841 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336841 RNA, herein designated GAM RNA, of GAM336841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336841 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336841 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336841 RNA correlate with, and may be deduced from, the identity of the GAM336841 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336842 6919 GTGGTGCATA Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTGTAATCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGATACTTG Messenger 336842 (GAM336842) oligonucleotides modulates expression of respective target

GGAGGTTGAG genes whose function and utility is known in the art.

GTGGTAGGAT GAM336842 is a novel bioinformatically detectable regulatory, non protein

TGCTTGAGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336842 was detected

CAGGAGTTTG is described with additional reference to Figs. 9-15.

AGGCTGCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGCTATGAT encoded by the human genome.

CAC GAM336842 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336842 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336842 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336842 precursor RNA is designated SEQ ID:6919, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6919 is located from position 48783661 to position 48783753 relative to chromosome 14 on the `+` strand.

GAM336842 precursor RNA folds onto itself, forming GAM336842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336842 precursor RNA, designated SEQ ID NO: 6919, and a schematic representation of a predicted secondary folding of GAM336842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336842 folded precursor RNA yielding a GAM336842 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336842 RNA, hereby incorporated herein.

GAM336842 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336842 target RNA, herein designated GAM TARGET RNA.

GAM336842 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336842 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336842 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336842 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336842 RNA, herein designated GAM RNA, to target binding sites on GAM336842 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336842 target RNA into GAM336842 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336842 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336842 target genes. The mRNA of each one of this plurality of GAM336842 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336842 RNA, herein designated GAM RNA, and which when bound by GAM336842 RNA causes inhibition of translation of the GAM336842 target mRNA into a corresponding GAM336842 target protein.

The mechanism of the translational inhibition exerted by GAM336842 RNA, herein designated GAM RNA, on one or more GAM336842 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336842 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336842 RNA, herein designated GAM RNA, of GAM336842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336842 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336842 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336842 RNA correlate with, and may be deduced from, the identity of the GAM336842 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336844 6025 CAGGCTGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CGTCGTTTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCTCTCCAT Messenger 336844 (GAM336844) oligonucleotides modulates expression of respective target

TCTTGTCTTT genes whose function and utility is known in the art.

TTAATTCTTT GAM336844 is a novel bioinformatically detectable regulatory, non protein

GTGTTATTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336844 was detected

AGATGGAGTT is described with additional reference to Figs. 9-15.

TGAGAGGGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TATGAACAAG encoded by the human genome.

CCTG GAM336844 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336844 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336844 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336844 precursor RNA is designated SEQ ID:6025, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6025 is located from position 48973458 to position 48973551 relative to chromosome 22 on the `+` strand.

GAM336844 precursor RNA folds onto itself, forming GAM336844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336844 precursor RNA, designated SEQ ID NO: 6025, and a schematic representation of a predicted secondary folding of GAM336844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336844 folded precursor RNA yielding a GAM336844 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336844 RNA, hereby incorporated herein.

GAM336844 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336844 target RNA, herein designated GAM TARGET RNA.

GAM336844 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336844 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336844 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336844 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336844 RNA, herein designated GAM RNA, to target binding sites on GAM336844 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336844 target RNA into GAM336844 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336844 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336844 target genes. The mRNA of each one of this

plurality of GAM336844 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336844 RNA, herein designated GAM RNA, and which when bound by GAM336844 RNA causes inhibition of translation of the GAM336844 target mRNA into a corresponding GAM336844 target protein.

The mechanism of the translational inhibition exerted by GAM336844 RNA, herein designated GAM RNA, on one or more GAM336844 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336844 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336844 RNA, herein designated GAM RNA, of GAM336844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336844 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336844 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336844 RNA correlate with, and may be deduced from, the identity of the GAM336844 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336845 5783 AGGCTGGTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCGTTTCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTCTCCATT Messenger 336845 (GAM336845) oligonucleotides modulates expression of respective target
CTTGTCTTTT genes whose function and utility is known in the art.

TAATTCTTTG GAM336845 is a novel bioinformatically detectable regulatory, non protein
TGTTATTTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336845 was detected
GATGGAGTTT is described with additional reference to Figs. 9-15.

GAGAGGGAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATGAACAAGC encoded by the human genome.

CT GAM336845 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336845 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336845 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336845 precursor RNA is designated SEQ ID:5783, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5783 is located from position 48973459 to position 48973550 relative to chromosome 22 on the `+` strand.

GAM336845 precursor RNA folds onto itself, forming GAM336845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336845 precursor RNA, designated SEQ ID NO: 5783, and a schematic representation of a predicted secondary folding of GAM336845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336845 folded precursor RNA yielding a GAM336845 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336845 RNA, hereby incorporated herein.

GAM336845 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336845 target RNA, herein designated GAM TARGET RNA.

GAM336845 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336845 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336845 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336845 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336845 RNA, herein designated GAM RNA, to target binding sites on GAM336845 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336845 target RNA into GAM336845 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336845 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336845 target genes. The mRNA of each one of this plurality of GAM336845 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336845 RNA, herein designated GAM RNA, and which when bound by GAM336845 RNA causes inhibition of translation of the GAM336845 target mRNA into a corresponding GAM336845 target protein.

The mechanism of the translational inhibition exerted by GAM336845 RNA, herein designated GAM RNA, on one or more GAM336845 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336845 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336845 RNA, herein designated GAM RNA, of GAM336845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336845 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336845 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336845 RNA correlate with, and may be deduced from, the identity of the GAM336845 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336846 6801 GGGCATTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTCTGGTAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GGATGGCCAT Messenger 336846 (GAM336846) oligonucleotides modulates expression of respective target
GGTGCCAGCC genes whose function and utility is known in the art.

CTCCTGGGCC GAM336846 is a novel bioinformatically detectable regulatory, non protein
TCATTGGGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336846 was detected
TCACCTATAC is described with additional reference to Figs. 9-15.

AGAAAGGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATAGACCC encoded by the human genome.

GAM336846 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336846 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336846 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336846 precursor RNA is designated SEQ ID:6801, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6801 is located from position 49032571 to position 49032658 relative to chromosome 12 on the `-` strand.

GAM336846 precursor RNA folds onto itself, forming GAM336846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336846 precursor RNA, designated SEQ ID NO: 6801, and a schematic representation of a predicted secondary folding of GAM336846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336846 folded precursor RNA yielding a GAM336846 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336846 RNA, hereby incorporated herein.

GAM336846 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336846 target RNA, herein designated GAM TARGET RNA.

GAM336846 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336846 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336846 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336846 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336846 RNA, herein designated GAM RNA, to target binding sites on GAM336846 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336846 target RNA into GAM336846 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336846 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336846 target genes. The mRNA of each one of this plurality of GAM336846 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336846 RNA, herein designated GAM RNA, and which when bound by GAM336846 RNA causes inhibition of translation of the GAM336846 target mRNA into a corresponding GAM336846 target protein.

The mechanism of the translational inhibition exerted by GAM336846 RNA, herein designated GAM RNA, on one or more GAM336846 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336846 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336846 RNA, herein designated GAM RNA, of GAM336846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336846 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336846 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336846 RNA correlate with, and may be deduced from, the identity of the GAM336846 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336847 5868 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336847 (GAM336847) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336847 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336847 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336847 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336847 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336847 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336847 precursor RNA is designated SEQ ID:5868, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5868 is located from position 49043749 to position 49043830 relative to chromosome 6 on the `+` strand.

GAM336847 precursor RNA folds onto itself, forming GAM336847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336847 precursor RNA, designated SEQ ID NO: 5868, and a schematic representation of a predicted secondary folding of GAM336847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336847 folded precursor RNA yielding a GAM336847 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336847 RNA, hereby incorporated herein.

GAM336847 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336847 target RNA, herein designated GAM TARGET RNA.

GAM336847 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336847 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336847 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336847 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336847 RNA, herein designated GAM RNA, to target binding sites on GAM336847 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336847 target RNA into GAM336847 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336847 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336847 target genes. The mRNA of each one of this plurality of GAM336847 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336847 RNA, herein designated GAM RNA, and which when bound by GAM336847 RNA causes inhibition of translation of the GAM336847 target mRNA into a corresponding GAM336847 target protein.

The mechanism of the translational inhibition exerted by GAM336847 RNA, herein designated GAM RNA, on one or more GAM336847 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336847 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336847 RNA, herein designated GAM RNA, of GAM336847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336847 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336847 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336847 RNA correlate with, and may be deduced from, the identity of the GAM336847 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336848 6973 TAGGGGCAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCAGAGAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GAATGTATGT Messenger 336848 (GAM336848) oligonucleotides modulates expression of respective target
GTGGGTTTCT genes whose function and utility is known in the art.

CAGCCTTGAG GAM336848 is a novel bioinformatically detectable regulatory, non protein
GTATAAGGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336848 was detected
TAAAGGCTCT is described with additional reference to Figs. 9-15.

GGGGATTCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCATACACC encoded by the human genome.

ACTTCCAGTT GAM336848 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAAGCGCCTA GAM336848 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336848 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336848 precursor RNA is designated SEQ ID:6973, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6973 is located from position 49044659 to position 49044768 relative to chromosome 12 on the `-` strand.

GAM336848 precursor RNA folds onto itself, forming GAM336848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336848 precursor RNA, designated SEQ ID NO: 6973, and a schematic representation of a predicted secondary folding of GAM336848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336848 folded precursor RNA yielding a GAM336848 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336848 RNA, hereby incorporated herein.

GAM336848 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336848 target RNA, herein designated GAM TARGET RNA.

GAM336848 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336848 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336848 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336848 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336848 RNA, herein designated GAM RNA, to target binding sites on GAM336848 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336848 target RNA into GAM336848 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336848 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336848 target genes. The mRNA of each one of this plurality of GAM336848 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336848 RNA, herein designated GAM RNA, and which when bound by GAM336848 RNA causes inhibition of translation of the GAM336848 target mRNA into a corresponding GAM336848 target protein.

The mechanism of the translational inhibition exerted by GAM336848 RNA, herein designated GAM RNA, on one or more GAM336848 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336848 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336848 RNA, herein designated GAM RNA, of GAM336848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336848 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336848 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336848 RNA correlate with, and may be deduced from, the identity of the GAM336848 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336849 6800 GGGCAGTGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAGAATGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTATGTGTG Messenger 336849 (GAM336849) oligonucleotides modulates expression of respective target
GGTTTCTCAG genes whose function and utility is known in the art.

CCTTGAGGTA GAM336849 is a novel bioinformatically detectable regulatory, non protein
TAAGGTCTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336849 was detected
AGGCTCTGGG is described with additional reference to Figs. 9-15.

GATTCACTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATACACCACT encoded by the human genome.

TCC GAM336849 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336849 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336849 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336849 precursor RNA is designated SEQ ID:6800, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6800 is located from position 49044673 to position 49044765 relative to chromosome 12 on the `-` strand.

GAM336849 precursor RNA folds onto itself, forming GAM336849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336849 precursor RNA, designated SEQ ID NO: 6800, and a schematic representation of a predicted secondary folding of GAM336849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336849 folded precursor RNA yielding a GAM336849 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336849 RNA, hereby incorporated herein.

GAM336849 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336849 target RNA, herein designated GAM TARGET RNA.

GAM336849 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336849 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336849 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336849 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336849 RNA, herein designated GAM RNA, to target binding sites on GAM336849 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336849 target RNA into GAM336849 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336849 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336849 target genes. The mRNA of each one of this plurality of GAM336849 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336849 RNA, herein designated GAM RNA, and which when bound by GAM336849 RNA causes inhibition of translation of the GAM336849 target mRNA into a corresponding GAM336849 target protein.

The mechanism of the translational inhibition exerted by GAM336849 RNA, herein designated GAM RNA, on one or more GAM336849 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336849 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336849 RNA, herein designated GAM RNA, of GAM336849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336849 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336849 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336849 RNA correlate with, and may be deduced from, the identity of the GAM336849 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336852 7121 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCCCAGGAG Messenger 336852 (GAM336852) oligonucleotides modulates expression of respective target

GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGACCCA GAM336852 is a novel bioinformatically detectable regulatory, non protein

TATTCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336852 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACCCTCTCTC GAM336852 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336852 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336852 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336852 precursor RNA is designated SEQ ID:7121, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7121 is located from position 49108311 to position 49108411 relative to chromosome 10 on the `-` strand.

GAM336852 precursor RNA folds onto itself, forming GAM336852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336852 precursor RNA, designated SEQ ID NO: 7121, and a schematic representation of a predicted secondary folding of GAM336852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336852 folded precursor RNA yielding a GAM336852 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336852 RNA, hereby incorporated herein. Expression of GAM336852 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336852 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336852 target RNA, herein designated GAM TARGET RNA.

GAM336852 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336852 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336852 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336852 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336852 RNA, herein designated GAM RNA, to target binding sites on GAM336852 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336852 target RNA into GAM336852 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336852 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336852 target genes. The mRNA of each one of this plurality of GAM336852 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336852 RNA, herein designated GAM RNA, and which when bound by GAM336852 RNA causes inhibition of translation of the GAM336852 target mRNA into a corresponding GAM336852 target protein.

The mechanism of the translational inhibition exerted by GAM336852 RNA, herein

designated GAM RNA, on one or more GAM336852 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336852 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336852 RNA, herein designated GAM RNA, of GAM336852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336852 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336852 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336852 RNA correlate with, and may be deduced from, the identity of the GAM336852 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336853 5998 CACGAGCAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTGTCACA detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGGCCGGA Messenger 336853 (GAM336853) oligonucleotides modulates expression of respective target

AGAGACTCTT genes whose function and utility is known in the art.

TTGCCTGGTT GAM336853 is a novel bioinformatically detectable regulatory, non protein

ACAGGCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336853 was detected

TTTTCTGCCA is described with additional reference to Figs. 9-15.

TCCTGTTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTCCCATC encoded by the human genome.

AACTCCTTTG GAM336853 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336853 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336853 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336853 precursor RNA is designated SEQ ID:5998, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:5998 is located from position 49118815 to position 49118914 relative to chromosome 20 on the `+` strand.

GAM336853 precursor RNA folds onto itself, forming GAM336853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336853 precursor RNA, designated SEQ ID NO: 5998, and a schematic representation of a predicted secondary folding of GAM336853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336853 folded precursor RNA yielding a GAM336853 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336853 RNA, hereby incorporated herein.

GAM336853 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336853 target RNA, herein designated GAM TARGET RNA.

GAM336853 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336853 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336853 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336853 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336853 RNA, herein designated GAM RNA, to target binding sites on GAM336853 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336853 target RNA into GAM336853 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336853 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336853 target genes. The mRNA of each one of this plurality of GAM336853 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336853 RNA, herein designated GAM RNA, and which when bound by GAM336853 RNA causes inhibition of translation of the GAM336853 target mRNA into a corresponding GAM336853 target protein.

The mechanism of the translational inhibition exerted by GAM336853 RNA, herein designated GAM RNA, on one or more GAM336853 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336853 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336853 RNA, herein designated GAM RNA, of GAM336853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336853 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336853 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336853 RNA correlate with, and may be deduced from, the identity of the GAM336853 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336854 6327 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAAACCCGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTGGAGGT Messenger 336854 (GAM336854) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACG GAM336854 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336854 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTC encoded by the human genome.

GAM336854 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336854 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336854 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336854 precursor RNA is designated SEQ ID:6327, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6327 is located from position 49184841 to position 49184926 relative to chromosome 19 on the `+` strand.

GAM336854 precursor RNA folds onto itself, forming GAM336854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336854 precursor RNA, designated SEQ ID NO: 6327, and a schematic representation of a predicted secondary folding of GAM336854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336854 folded precursor RNA yielding a GAM336854 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336854 RNA, hereby incorporated herein. Expression of GAM336854 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336854 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336854 target RNA, herein designated GAM TARGET RNA.

GAM336854 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336854 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336854 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336854 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336854 RNA, herein designated GAM RNA, to target binding sites on GAM336854 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336854 target RNA into GAM336854 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336854 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336854 target genes. The mRNA of each one of this plurality of GAM336854 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336854 RNA, herein designated GAM RNA, and which when bound by GAM336854 RNA causes inhibition of translation of the GAM336854 target mRNA into a corresponding GAM336854 target protein.

The mechanism of the translational inhibition exerted by GAM336854 RNA, herein designated GAM RNA, on one or more GAM336854 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336854 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336854 RNA, herein designated GAM RNA, of GAM336854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336854 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336854 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336854 RNA correlate with, and may be deduced from, the identity of the GAM336854 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336855 6485 GCACCAGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCCAGGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCTGATTAA Messenger 336855 (GAM336855) oligonucleotides modulates expression of respective target

AGTGTTAGCT genes whose function and utility is known in the art.

GGCTGACACA GAM336855 is a novel bioinformatically detectable regulatory, non protein
TTATGGTGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336855 was detected
GTGGTAGAAA is described with additional reference to Figs. 9-15.

GTGTCTCATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTAATAAGTC encoded by the human genome.

ACAGTGCTGC GAM336855 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTAATCTGTG GAM336855 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TGC GAM336855 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336855 precursor RNA is designated SEQ ID:6485, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6485 is located from position 49197664 to position 49197776 relative to chromosome 14 on the `-` strand.

GAM336855 precursor RNA folds onto itself, forming GAM336855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336855 precursor RNA, designated SEQ ID NO: 6485, and a schematic representation of a predicted secondary folding of GAM336855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336855 folded precursor RNA yielding a GAM336855 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336855 RNA, hereby incorporated herein.

GAM336855 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336855 target RNA, herein designated GAM TARGET RNA.

GAM336855 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336855 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336855 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336855 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336855 RNA, herein designated GAM RNA, to target binding sites on GAM336855 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336855 target RNA into GAM336855 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336855 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336855 target genes. The mRNA of each one of this plurality of GAM336855 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336855 RNA, herein designated GAM RNA, and which when bound by GAM336855 RNA causes inhibition of translation of the GAM336855 target mRNA into a corresponding GAM336855 target protein.

The mechanism of the translational inhibition exerted by GAM336855 RNA, herein designated GAM RNA, on one or more GAM336855 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336855 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336855 RNA, herein designated GAM RNA, of GAM336855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336855 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336855 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336855 RNA correlate with, and may be deduced from, the identity of the GAM336855 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336857 7075 TCTGTCTCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTCATCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTTTGCCAC Messenger 336857 (GAM336857) oligonucleotides modulates expression of respective target
CCAGGCTGGA genes whose function and utility is known in the art.

ATGTAGTGGT GAM336857 is a novel bioinformatically detectable regulatory, non protein
GTGATCACAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336857 was detected
CTCACTACAG is described with additional reference to Figs. 9-15.

CCTGGATTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCACACAGGA encoded by the human genome.

ATCAGAGTCA GAM336857 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GA GAM336857 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336857 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336857 precursor RNA is designated SEQ ID:7075, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7075 is located from position 49351290 to position 49351391 relative to chromosome 17 on the `-` strand.

GAM336857 precursor RNA folds onto itself, forming GAM336857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336857 precursor RNA, designated SEQ ID NO: 7075, and a schematic representation of a predicted secondary folding of GAM336857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336857 folded precursor RNA yielding a GAM336857 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336857 RNA, hereby incorporated herein.

GAM336857 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336857 target RNA, herein designated GAM TARGET RNA.

GAM336857 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336857 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336857 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336857 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336857 RNA, herein designated GAM RNA, to target binding sites on GAM336857 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336857 target RNA into GAM336857 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336857 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336857 target genes. The mRNA of each one of this plurality of GAM336857 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336857 RNA, herein designated GAM RNA, and which when bound by GAM336857 RNA causes inhibition of translation of the GAM336857 target mRNA into a corresponding GAM336857 target protein.

The mechanism of the translational inhibition exerted by GAM336857 RNA, herein designated GAM RNA, on one or more GAM336857 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336857 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336857 RNA, herein designated GAM RNA, of GAM336857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336857 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336857 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336857 RNA correlate with, and may be deduced from, the identity of the GAM336857 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336860 5869 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336860 (GAM336860) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336860 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336860 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336860 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336860 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336860 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336860 precursor RNA is designated SEQ ID:5869, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5869 is located from position 49440469 to position 49440550 relative to chromosome X on the `+` strand.

GAM336860 precursor RNA folds onto itself, forming GAM336860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336860 precursor RNA, designated SEQ ID NO: 5869, and a schematic representation of a predicted secondary folding of GAM336860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336860 folded precursor RNA yielding a GAM336860 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336860 RNA, hereby incorporated herein.

GAM336860 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336860 target RNA, herein designated GAM TARGET RNA.

GAM336860 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336860 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336860 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336860 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336860 RNA, herein designated GAM RNA, to target binding sites on GAM336860 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336860 target RNA into GAM336860 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336860 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336860 target genes. The mRNA of each one of this plurality of GAM336860 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336860 RNA, herein designated GAM RNA, and which when bound by GAM336860 RNA causes inhibition of translation of the GAM336860 target mRNA into a corresponding GAM336860 target protein.

The mechanism of the translational inhibition exerted by GAM336860 RNA, herein designated GAM RNA, on one or more GAM336860 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336860 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336860 RNA, herein designated GAM RNA, of GAM336860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336860 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336860 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336860 RNA correlate with, and may be deduced from, the identity of the GAM336860 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336861 6146 CGGGTGAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGTTATTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGGGTCTC Messenger 336861 (GAM336861) oligonucleotides modulates expression of respective target

CCTTTCAGAA genes whose function and utility is known in the art.

GGCCTTGGGG GAM336861 is a novel bioinformatically detectable regulatory, non protein

CCAAGGGGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336861 was detected

GAGCTGGAAT is described with additional reference to Figs. 9-15.

TGCCTTCCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGCGTG encoded by the human genome.

GAM336861 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336861 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336861 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336861 precursor RNA is designated SEQ ID:6146, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6146 is located from position 49549736 to position 49549821 relative to chromosome 20 on the `+` strand.

GAM336861 precursor RNA folds onto itself, forming GAM336861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336861 precursor RNA, designated SEQ ID NO: 6146, and a schematic representation of a predicted secondary folding of GAM336861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336861 folded precursor RNA yielding a GAM336861 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336861 RNA, hereby incorporated herein.

GAM336861 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336861 target RNA, herein designated GAM TARGET RNA.

GAM336861 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336861 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336861 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336861 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336861 RNA, herein designated GAM RNA, to target binding sites on GAM336861 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336861 target RNA into GAM336861 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336861 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336861 target genes. The mRNA of each one of this plurality of GAM336861 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336861 RNA, herein designated GAM RNA, and which when bound by GAM336861 RNA causes inhibition of translation of the GAM336861 target mRNA into a corresponding GAM336861 target protein.

The mechanism of the translational inhibition exerted by GAM336861 RNA, herein designated GAM RNA, on one or more GAM336861 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336861 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336861 RNA, herein designated GAM RNA, of GAM336861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336861 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336861 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336861 RNA correlate with, and may be deduced from, the identity of the GAM336861 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336862 6843 GGTGAGGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTTATTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGGTCTCCC Messenger 336862 (GAM336862) oligonucleotides modulates expression of respective target

TTTCAGAAGG genes whose function and utility is known in the art.

CCTTGGGGCC GAM336862 is a novel bioinformatically detectable regulatory, non protein

AAGGGGAGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336862 was detected

GCTGGAATTG is described with additional reference to Figs. 9-15.

CCTTCCACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336862 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336862 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336862 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336862 precursor RNA is designated SEQ ID:6843, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6843 is located from position 49549738 to position 49549816 relative to chromosome 20 on the `+` strand.

GAM336862 precursor RNA folds onto itself, forming GAM336862 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336862 precursor RNA, designated SEQ ID NO: 6843, and a schematic representation of a predicted secondary folding of GAM336862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336862 folded precursor RNA yielding a GAM336862 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336862 RNA, hereby incorporated herein.

GAM336862 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336862 target RNA, herein designated GAM TARGET RNA.

GAM336862 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336862 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336862 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336862 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336862 RNA, herein designated GAM RNA, to target binding sites on GAM336862 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336862 target RNA into GAM336862 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336862 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336862 target genes. The mRNA of each one of this plurality of GAM336862 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336862 RNA,

herein designated GAM RNA, and which when bound by GAM336862 RNA causes inhibition of translation of the GAM336862 target mRNA into a corresponding GAM336862 target protein.

The mechanism of the translational inhibition exerted by GAM336862 RNA, herein designated GAM RNA, on one or more GAM336862 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336862 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336862 RNA, herein designated GAM RNA, of GAM336862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336862 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336862 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336862 RNA correlate with, and may be deduced from, the identity of the GAM336862 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336863 5714 AGAATCACTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACCTGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTGGAGGTT Messenger 336863 (GAM336863) oligonucleotides modulates expression of respective target

GCAGTGAGCC genes whose function and utility is known in the art.

GAAATTGTGC GAM336863 is a novel bioinformatically detectable regulatory, non protein

CACTGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336863 was detected

CAGTCTAGGT is described with additional reference to Figs. 9-15.

GACAGAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACT encoded by the human genome.

GAM336863 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336863 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336863 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336863 precursor RNA is designated SEQ ID:5714, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5714 is located from position 49602636 to position 49602719 relative to chromosome 17 on the `-` strand.

GAM336863 precursor RNA folds onto itself, forming GAM336863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336863 precursor RNA, designated SEQ ID NO: 5714, and a schematic representation of a predicted secondary folding of GAM336863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336863 folded precursor RNA yielding a GAM336863 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336863 RNA, hereby incorporated herein.

GAM336863 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336863 target RNA, herein designated GAM TARGET RNA.

GAM336863 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336863 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336863 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336863 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336863 RNA, herein designated GAM RNA, to target binding sites on GAM336863 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336863 target RNA

into GAM336863 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336863 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336863 target genes. The mRNA of each one of this plurality of GAM336863 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336863 RNA, herein designated GAM RNA, and which when bound by GAM336863 RNA causes inhibition of translation of the GAM336863 target mRNA into a corresponding GAM336863 target protein.

The mechanism of the translational inhibition exerted by GAM336863 RNA, herein designated GAM RNA, on one or more GAM336863 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336863 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336863 RNA, herein designated GAM RNA, of GAM336863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336863 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336863 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336863 RNA correlate with, and may be deduced from, the identity of the GAM336863 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336864 6757 GGCGTGAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGCATGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAATCCAGGA Messenger 336864 (GAM336864) oligonucleotides modulates expression of respective target

TAAAATCATC genes whose function and utility is known in the art.

ATCAGGGAAA GAM336864 is a novel bioinformatically detectable regulatory, non protein

CTCCTATGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336864 was detected

GCTGGAACTG is described with additional reference to Figs. 9-15.

GACAACAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTTAGATCC encoded by the human genome.

CTAGTCATGC GAM336864 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM336864 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336864 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336864 precursor RNA is designated SEQ ID:6757, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6757 is located from position 49753165 to position 49753265 relative to chromosome 18 on the `-` strand.

GAM336864 precursor RNA folds onto itself, forming GAM336864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336864 precursor RNA, designated SEQ ID NO: 6757, and a schematic representation of a predicted secondary folding of GAM336864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336864 folded precursor RNA yielding a GAM336864 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336864 RNA, hereby incorporated herein.

GAM336864 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336864 target RNA, herein designated GAM TARGET RNA.

GAM336864 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336864 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336864 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336864 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336864 RNA, herein designated GAM RNA, to target binding sites on GAM336864 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336864 target RNA into GAM336864 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336864 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336864 target genes. The mRNA of each one of this plurality of GAM336864 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336864 RNA, herein designated GAM RNA, and which when bound by GAM336864 RNA causes inhibition of translation of the GAM336864 target mRNA into a corresponding GAM336864 target protein.

The mechanism of the translational inhibition exerted by GAM336864 RNA, herein designated GAM RNA, on one or more GAM336864 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336864 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336864 RNA, herein designated GAM RNA, of GAM336864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336864 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336864 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336864 RNA correlate with, and may be deduced from, the identity of the GAM336864 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336866 6870 GTCAGCACCG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGTAGCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAATTAACAT Messenger 336866 (GAM336866) oligonucleotides modulates expression of respective target

TCTTGTCAGC genes whose function and utility is known in the art.

AGAGAATGAA GAM336866 is a novel bioinformatically detectable regulatory, non protein
GCAGGAATAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336866 was
detected
AATTAAAACT is described with additional reference to Figs. 9-15.

TTGCCCTTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
AATAGCTGAT encoded by the human genome.

GAM336866 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336866 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336866 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336866 precursor RNA is designated SEQ ID:6870, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6870 is located from position 50086828 to position 50086917 relative to chromosome 20 on the `+` strand.

GAM336866 precursor RNA folds onto itself, forming GAM336866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336866 precursor RNA, designated SEQ ID NO: 6870, and a schematic representation of a predicted secondary folding of GAM336866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336866 folded precursor RNA yielding a GAM336866 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336866 RNA, hereby incorporated herein.

GAM336866 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336866 target RNA, herein designated GAM TARGET RNA.

GAM336866 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336866 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336866 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336866 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336866 RNA, herein designated GAM RNA, to target binding sites on GAM336866 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336866 target RNA into GAM336866 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336866 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336866 target genes. The mRNA of each one of this plurality of GAM336866 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336866 RNA, herein designated GAM RNA, and which when bound by GAM336866 RNA causes inhibition of translation of the GAM336866 target mRNA into a corresponding GAM336866 target protein.

The mechanism of the translational inhibition exerted by GAM336866 RNA, herein designated GAM RNA, on one or more GAM336866 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336866 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336866 RNA, herein designated GAM RNA, of GAM336866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336866 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336866 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336866 RNA correlate with, and may be deduced from, the identity of the GAM336866 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336867 6809 GGGGACATAA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCGTAGGTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCGTGCCAAC Messenger 336867 (GAM336867) oligonucleotides modulates expression of respective target
AGGAAACCCC genes whose function and utility is known in the art.

AGGAAGTCTG GAM336867 is a novel bioinformatically detectable regulatory, non protein
GCTTCAGAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336867 was detected
CATTCCCTTT is described with additional reference to Figs. 9-15.

AGCTCTGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCACACTGTC encoded by the human genome.

TTGTAGTTCA GAM336867 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTCTTC GAM336867 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336867 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336867 precursor RNA is designated SEQ ID:6809, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6809 is located from position 50178453 to position 50178558 relative to chromosome 16 on the `+` strand.

GAM336867 precursor RNA folds onto itself, forming GAM336867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336867 precursor RNA, designated SEQ ID NO: 6809, and a schematic representation of a predicted secondary folding of GAM336867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336867 folded precursor RNA yielding a GAM336867 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336867 RNA, hereby incorporated herein.

GAM336867 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM336867 target RNA, herein designated GAM TARGET RNA.

GAM336867 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336867 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336867 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336867 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336867 RNA, herein designated GAM RNA, to target binding sites on GAM336867 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336867 target RNA into GAM336867 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336867 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336867 target genes. The mRNA of each one of this plurality of GAM336867 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336867 RNA, herein designated GAM RNA, and which when bound by GAM336867 RNA causes inhibition of translation of the GAM336867 target mRNA into a corresponding GAM336867 target protein.

The mechanism of the translational inhibition exerted by GAM336867 RNA, herein designated GAM RNA, on one or more GAM336867 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336867 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336867 RNA, herein designated GAM RNA, of GAM336867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336867 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336867 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336867 RNA correlate with, and may be deduced from, the identity of the GAM336867 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336868 6640 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 336868 (GAM336868) oligonucleotides modulates expression of respective target
TTGTGGTGAG genes whose function and utility is known in the art.

CCAAGATCGT GAM336868 is a novel bioinformatically detectable regulatory, non protein
GACATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336868 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGATTCC encoded by the human genome.

GAM336868 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336868 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336868 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336868 precursor RNA is designated SEQ ID:6640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6640 is located from position 50244509 to position 50244596 relative to chromosome 12 on the `+` strand.

GAM336868 precursor RNA folds onto itself, forming GAM336868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336868 precursor RNA, designated SEQ ID NO: 6640, and a schematic representation of a predicted secondary folding of GAM336868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336868 folded precursor RNA yielding a GAM336868 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336868 RNA, hereby incorporated herein. Expression of GAM336868 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336868 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336868 target RNA, herein designated GAM TARGET RNA.

GAM336868 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336868 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336868 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336868 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336868 RNA, herein designated GAM RNA, to target binding sites on GAM336868 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336868 target RNA into GAM336868 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336868 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336868 target genes. The mRNA of each one of this plurality of GAM336868 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336868 RNA, herein designated GAM RNA, and which when bound by GAM336868 RNA causes inhibition of translation of the GAM336868 target mRNA into a corresponding GAM336868 target protein.

The mechanism of the translational inhibition exerted by GAM336868 RNA, herein designated GAM RNA, on one or more GAM336868 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336868 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336868 RNA, herein designated GAM RNA, of GAM336868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336868 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336868 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336868 RNA correlate with, and may be deduced from, the identity of the GAM336868 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336869 7002 TCACTTGAAC CCGGGAGGCG GAGGTTGCAG TGAGCTGAGG TCGTGCCACT GCACTCCAGC CTGGGCAACA AGAGTGA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336869 (GAM336869) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336869 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336869 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336869 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336869 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336869 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336869 precursor RNA is designated SEQ ID:7002, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7002 is located from position 50257437 to position 50257513 relative to chromosome 19 on the `-` strand.

GAM336869 precursor RNA folds onto itself, forming GAM336869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336869 precursor RNA, designated SEQ ID NO: 7002, and a schematic representation of a predicted secondary folding of GAM336869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336869 folded precursor RNA yielding a GAM336869 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336869 RNA, hereby incorporated herein. Expression of GAM336869 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336869 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336869 target RNA, herein designated GAM TARGET RNA.

GAM336869 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336869 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336869 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336869 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336869 RNA, herein designated GAM RNA, to target binding sites on GAM336869 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336869 target RNA into GAM336869 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336869 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336869 target genes. The mRNA of each one of this plurality of GAM336869 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336869 RNA, herein designated GAM RNA, and which when bound by GAM336869 RNA causes inhibition of translation of the GAM336869 target mRNA into a corresponding GAM336869 target protein.

The mechanism of the translational inhibition exerted by GAM336869 RNA, herein designated GAM RNA, on one or more GAM336869 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336869 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336869 RNA, herein designated GAM RNA, of GAM336869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336869 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336869 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336869 RNA correlate with, and may be deduced from, the identity of the GAM336869 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336870 6630 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 336870 (GAM336870) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATTGC GAM336870 is a novel bioinformatically detectable regulatory, non protein

ACTATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336870 was detected

TCCAGTCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM336870 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336870 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336870 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336870 precursor RNA is designated SEQ

ID:6630, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6630 is located from position 50356669 to position 50356756 relative to chromosome 12 on the `+` strand.

GAM336870 precursor RNA folds onto itself, forming GAM336870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336870 precursor RNA, designated SEQ ID NO: 6630, and a schematic representation of a predicted secondary folding of GAM336870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336870 folded precursor RNA yielding a GAM336870 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336870 RNA, hereby incorporated herein.

GAM336870 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336870 target RNA, herein designated GAM TARGET RNA.

GAM336870 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336870 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336870 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336870 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336870 RNA, herein designated GAM RNA, to target binding sites on GAM336870 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336870 target RNA into GAM336870 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336870 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336870 target genes. The mRNA of each one of this plurality of GAM336870 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336870 RNA, herein designated GAM RNA, and which when bound by GAM336870 RNA causes inhibition of translation of the GAM336870 target mRNA into a corresponding GAM336870 target protein.

The mechanism of the translational inhibition exerted by GAM336870 RNA, herein designated GAM RNA, on one or more GAM336870 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336870 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336870 RNA, herein designated GAM RNA, of GAM336870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336870 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336870 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336870 RNA correlate with, and may be deduced from, the identity of the GAM336870 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336871 7228 TGGCTCACAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGTAATCCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CGCTACTCAG Messenger 336871 (GAM336871) oligonucleotides modulates expression of respective target

GAGGTTTAGG genes whose function and utility is known in the art.

CAGGAGAATC GAM336871 is a novel bioinformatically detectable regulatory, non protein

ACTTGAACCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336871 was detected

GAGAGGCAGA is described with additional reference to Figs. 9-15.

GGTTACAGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGAGTCA encoded by the human genome.

GAM336871 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336871 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336871 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336871 precursor RNA is designated SEQ ID:7228, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7228 is located from position 50415753 to position 50415840 relative to chromosome 12 on the `+` strand.

GAM336871 precursor RNA folds onto itself, forming GAM336871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336871 precursor RNA, designated SEQ ID NO: 7228, and a schematic representation of a predicted secondary folding of GAM336871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336871 folded precursor RNA yielding a GAM336871 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336871 RNA, hereby incorporated herein.

GAM336871 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336871 target RNA, herein designated GAM TARGET RNA.

GAM336871 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336871 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336871 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336871 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336871 RNA, herein designated GAM RNA, to target binding sites on GAM336871 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336871 target RNA into GAM336871 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336871 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336871 target genes. The mRNA of each one of this plurality of GAM336871 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336871 RNA, herein designated GAM RNA, and which when bound by GAM336871 RNA causes inhibition of translation of the GAM336871 target mRNA into a corresponding GAM336871 target protein.

The mechanism of the translational inhibition exerted by GAM336871 RNA, herein designated GAM RNA, on one or more GAM336871 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336871 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336871 RNA, herein designated GAM RNA, of GAM336871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336871 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336871 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336871 RNA correlate with, and may be deduced from, the identity of the GAM336871 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336872 6853 GGTGGTTATG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTGTAGTCT Messenger 336872 (GAM336872) oligonucleotides modulates expression of respective target

CATCTGCTTT genes whose function and utility is known in the art.

GGAGTTGAGG GAM336872 is a novel bioinformatically detectable regulatory, non protein
CTGCAGTGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336872 was detected
CTATGATCGT is described with additional reference to Figs. 9-15.

GCCACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336872 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336872 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336872 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336872 precursor RNA is designated SEQ ID:6853, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6853 is located from position 50638127 to position 50638202 relative to chromosome 12 on the `+` strand.

GAM336872 precursor RNA folds onto itself, forming GAM336872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336872 precursor RNA, designated SEQ ID NO: 6853, and a schematic representation of a predicted secondary folding of GAM336872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336872 folded precursor RNA yielding a GAM336872 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336872 RNA, hereby incorporated herein.

GAM336872 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336872 target RNA, herein designated GAM TARGET RNA.

GAM336872 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336872 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336872 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336872 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336872 RNA, herein designated GAM RNA, to target binding sites on GAM336872 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336872 target RNA into GAM336872 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336872 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336872 target genes. The mRNA of each one of this plurality of GAM336872 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336872 RNA, herein designated GAM RNA, and which when bound by GAM336872 RNA causes inhibition of translation of the GAM336872 target mRNA into a corresponding GAM336872 target protein.

The mechanism of the translational inhibition exerted by GAM336872 RNA, herein designated GAM RNA, on one or more GAM336872 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336872 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336872 RNA, herein designated GAM RNA, of GAM336872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336872 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336872 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336872 RNA correlate with, and may be deduced from, the identity of the GAM336872 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336873 7334 TTGGGCTACT Fig. 8 further provides a conceptual description of another novel bioinformatically
TATAGGAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAATAAACT Messenger 336873 (GAM336873) oligonucleotides modulates expression of respective target
CTGTGATGTG genes whose function and utility is known in the art.

CCAGCACCAG GAM336873 is a novel bioinformatically detectable regulatory, non protein
CACAGGCTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336873 was detected
TGTAGTTTCC is described with additional reference to Figs. 9-15.

TCCCAACTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGCTCAG encoded by the human genome.

GAM336873 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336873 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336873 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336873 precursor RNA is designated SEQ ID:7334, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7334 is located from position 50704929 to position 50705016 relative to chromosome 8 on the `+` strand.

GAM336873 precursor RNA folds onto itself, forming GAM336873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336873 precursor RNA, designated SEQ ID NO: 7334, and a schematic representation of a predicted secondary folding of GAM336873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336873 folded precursor RNA yielding a GAM336873 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336873 RNA, hereby incorporated herein.

GAM336873 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336873 target RNA, herein designated GAM TARGET RNA.

GAM336873 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336873 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336873 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336873 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336873 RNA, herein designated GAM RNA, to target binding sites on GAM336873 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336873 target RNA into GAM336873 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336873 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336873 target genes. The mRNA of each one of this plurality of GAM336873 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336873 RNA, herein designated GAM RNA, and which when bound by GAM336873 RNA causes inhibition of translation of the GAM336873 target mRNA into a corresponding GAM336873 target protein.

The mechanism of the translational inhibition exerted by GAM336873 RNA, herein designated GAM RNA, on one or more GAM336873 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336873 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336873 RNA, herein designated GAM RNA, of GAM336873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336873 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336873 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336873 RNA correlate with, and may be deduced from, the identity of the GAM336873 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336874 6768 GGCTTCCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCATATATT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCAGATTCA Messenger 336874 (GAM336874) oligonucleotides modulates expression of respective target
AAGGAACAAA genes whose function and utility is known in the art.

GTGGCCCCAG GAM336874 is a novel bioinformatically detectable regulatory, non protein
TCAGCCTTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336874 was detected
CCAGAAACCT is described with additional reference to Figs. 9-15.

GTGAGTGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGCTGGAAG encoded by the human genome.

CC GAM336874 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336874 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336874 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336874 precursor RNA is designated SEQ ID:6768, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6768 is located from position 50706273 to position 50706364 relative to chromosome 10 on the `-` strand.

GAM336874 precursor RNA folds onto itself, forming GAM336874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336874 precursor RNA, designated SEQ ID NO: 6768, and a schematic representation of a predicted secondary folding of GAM336874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336874 folded precursor RNA yielding a GAM336874 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336874 RNA, hereby incorporated herein.

GAM336874 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336874 target RNA, herein designated GAM TARGET RNA.

GAM336874 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336874 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336874 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336874 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336874 RNA, herein designated GAM RNA, to target binding sites on GAM336874 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336874 target RNA into GAM336874 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336874 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336874 target genes. The mRNA of each one of this plurality of GAM336874 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336874 RNA, herein designated GAM RNA, and which when bound by GAM336874 RNA causes inhibition of translation of the GAM336874 target mRNA into a corresponding GAM336874 target protein.

The mechanism of the translational inhibition exerted by GAM336874 RNA, herein designated GAM RNA, on one or more GAM336874 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336874 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336874 RNA, herein designated GAM RNA, of GAM336874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336874 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336874 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336874 RNA correlate with, and may be deduced from, the identity of the GAM336874 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336875 6538 GCTCTTCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TACCATGCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCTAGCCCC Messenger 336875 (GAM336875) oligonucleotides modulates expression of respective target
ACAGAAATCC genes whose function and utility is known in the art.

ACTAGTCTGG GAM336875 is a novel bioinformatically detectable regulatory, non protein
GCTTTCTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336875 was detected
CGATTGGCTG is described with additional reference to Figs. 9-15.

AGGCAGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGTGAGGCA encoded by the human genome.

CCTGGGCTGT GAM336875 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCAGGAGC GAM336875 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336875 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336875 precursor RNA is designated SEQ ID:6538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6538 is located from position 50833625 to position 50833732 relative to chromosome 10 on the `-` strand.

GAM336875 precursor RNA folds onto itself, forming GAM336875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336875 precursor RNA, designated SEQ ID NO: 6538, and a schematic representation of a predicted secondary folding of GAM336875 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336875 folded precursor RNA yielding a GAM336875 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336875 RNA, hereby incorporated herein.

GAM336875 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336875 target RNA, herein designated GAM TARGET RNA.

GAM336875 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336875 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336875 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336875 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336875 RNA, herein designated GAM RNA, to target binding sites on GAM336875 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336875 target RNA into GAM336875 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336875 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336875 target genes. The mRNA of each one of this plurality of GAM336875 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336875 RNA, herein designated GAM RNA, and which when bound by GAM336875 RNA causes inhibition of translation of the GAM336875 target mRNA into a corresponding GAM336875 target protein.

The mechanism of the translational inhibition exerted by GAM336875 RNA, herein designated GAM RNA, on one or more GAM336875 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336875 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336875 RNA, herein designated GAM RNA, of GAM336875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336875 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336875 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336875 RNA correlate with, and may be deduced from, the identity of the GAM336875 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336876 5984 CAAATCAGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCATATTAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCTCATAGG Messenger 336876 (GAM336876) oligonucleotides modulates expression of respective target

AATGTGAACC genes whose function and utility is known in the art.

GTGTTGTGAC GAM336876 is a novel bioinformatically detectable regulatory, non protein

CATGCGAGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336876 was detected

ATCTAGGTTG is described with additional reference to Figs. 9-15.

CATGCTCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGAGAATCT encoded by the human genome.

AATATCTGAT GAM336876 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GATCTG GAM336876 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336876 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336876 precursor RNA is designated SEQ ID:5984, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5984 is located from position 50911119 to position 50911224 relative to chromosome 12 on the `+` strand.

GAM336876 precursor RNA folds onto itself, forming GAM336876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336876 precursor RNA, designated SEQ ID NO: 5984, and a schematic representation of a predicted secondary folding of GAM336876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336876 folded precursor RNA yielding a GAM336876 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336876 RNA, hereby incorporated herein.

GAM336876 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336876 target RNA, herein designated GAM TARGET RNA.

GAM336876 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336876 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336876 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336876 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336876 RNA, herein designated GAM RNA, to target binding sites on GAM336876 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336876 target RNA into GAM336876 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336876 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336876 target genes. The mRNA of each one of this plurality of GAM336876 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336876 RNA, herein designated GAM RNA, and which when bound by GAM336876 RNA causes inhibition of translation of the GAM336876 target mRNA into a corresponding GAM336876 target protein.

The mechanism of the translational inhibition exerted by GAM336876 RNA, herein designated GAM RNA, on one or more GAM336876 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336876 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336876 RNA, herein designated GAM RNA, of GAM336876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336876 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336876 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336876 RNA correlate with, and may be deduced from, the identity of the GAM336876 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336877 5955 ATCAGTGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

TATTAGATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCATAGGAAT Messenger 336877 (GAM336877) oligonucleotides modulates expression of respective target

GTGAACCGTG genes whose function and utility is known in the art.

TTGTGACCAT GAM336877 is a novel bioinformatically detectable regulatory, non protein

GCGAGGGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336877 was detected

TAGGTTGCAT is described with additional reference to Figs. 9-15.

GCTCTTCATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAATCTAAT encoded by the human genome.

ATCTGAT GAM336877 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336877 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336877 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336877 precursor RNA is designated SEQ ID:5955, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5955 is located from position 50911122 to position 50911218 relative to chromosome 12 on the `+` strand.

GAM336877 precursor RNA folds onto itself, forming GAM336877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336877 precursor RNA, designated SEQ ID NO: 5955, and a schematic representation of a predicted secondary folding of GAM336877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336877 folded precursor RNA yielding a GAM336877 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336877 RNA, hereby incorporated herein.

GAM336877 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336877 target RNA, herein designated GAM TARGET RNA.

GAM336877 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336877 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336877 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336877 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336877 RNA, herein designated GAM RNA, to target binding sites on GAM336877 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336877 target RNA into GAM336877 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336877 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336877 target genes. The mRNA of each one of this plurality of GAM336877 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336877 RNA, herein designated GAM RNA, and which when bound by GAM336877 RNA causes inhibition of translation of the GAM336877 target mRNA into a corresponding GAM336877 target protein.

The mechanism of the translational inhibition exerted by GAM336877 RNA, herein designated GAM RNA, on one or more GAM336877 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336877 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336877 RNA, herein designated GAM RNA, of GAM336877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336877 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336877 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336877 RNA correlate with, and may be deduced from, the identity of the GAM336877 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336878 6971 TAGGAGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCCAGGAGT Messenger 336878 (GAM336878) oligonucleotides modulates expression of respective target

TGAAGGCTAC genes whose function and utility is known in the art.

AGTGAGCTTT GAM336878 is a novel bioinformatically detectable regulatory, non protein

GATCACATCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336878 was detected

CTGCACTCTA is described with additional reference to Figs. 9-15.

GCCTGAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAGCAAGA encoded by the human genome.

CCTCATCTCT GAM336878 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TA GAM336878 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336878 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336878 precursor RNA is designated SEQ ID:6971, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6971 is located from position 51269225 to position 51269326 relative to chromosome 13 on the `+` strand.

GAM336878 precursor RNA folds onto itself, forming GAM336878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336878 precursor RNA, designated SEQ ID NO: 6971, and a schematic representation of a predicted secondary folding of GAM336878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336878 folded precursor RNA yielding a GAM336878 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336878 RNA, hereby incorporated herein.

GAM336878 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336878 target RNA, herein designated GAM TARGET RNA.

GAM336878 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336878 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336878 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336878 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336878 RNA, herein designated GAM RNA, to target binding sites on GAM336878 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336878 target RNA into GAM336878 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336878 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336878 target genes. The mRNA of each one of this plurality of GAM336878 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336878 RNA, herein designated GAM RNA, and which when bound by GAM336878 RNA causes inhibition of translation of the GAM336878 target mRNA into a corresponding GAM336878 target protein.

The mechanism of the translational inhibition exerted by GAM336878 RNA, herein designated GAM RNA, on one or more GAM336878 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336878 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336878 RNA, herein designated GAM RNA, of GAM336878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336878 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336878 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336878 RNA correlate with, and may be deduced from, the identity of the GAM336878 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336879 7048 TCGCTCTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCCCAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGAGTGCAG Messenger 336879 (GAM336879) oligonucleotides modulates expression of respective target

TGGCATGATC genes whose function and utility is known in the art.

TCGGCTCACT GCAACCTCTG CCTCCTGGGT

GAM336879 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336879 was detected is described with additional reference to Figs. 9-15.

TCAAGCGA

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336879 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336879 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336879 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336879 precursor RNA is designated SEQ ID:7048, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7048 is located from position 51538284 to position 51538361 relative to chromosome 10 on the `-` strand.

GAM336879 precursor RNA folds onto itself, forming GAM336879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336879 precursor RNA, designated SEQ ID NO: 7048, and a schematic representation of a predicted secondary folding of GAM336879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336879 folded precursor RNA yielding a GAM336879 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM336879 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336879 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM336879 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336879 target RNA, herein designated GAM TARGET RNA.

GAM336879 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336879 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336879 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336879 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336879 RNA, herein designated GAM RNA, to target binding sites on GAM336879 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336879 target RNA into GAM336879 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336879 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336879 target genes. The mRNA of each one of this plurality of GAM336879 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336879 RNA, herein designated GAM RNA, and which when bound by GAM336879 RNA causes inhibition of translation of the GAM336879 target mRNA into a corresponding GAM336879 target protein.

The mechanism of the translational inhibition exerted by GAM336879 RNA, herein designated GAM RNA, on one or more GAM336879 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336879 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336879 RNA, herein designated GAM RNA, of GAM336879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336879 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336879 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336879 RNA correlate with, and may be deduced from, the identity of the GAM336879 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336880 6382 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATAACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGA Messenger 336880 (GAM336880) oligonucleotides modulates expression of respective target

CGGAGGTTGT genes whose function and utility is known in the art.

TGTGAGCCGA GAM336880 is a novel bioinformatically detectable regulatory, non protein

GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336880 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGAGCGAAAC encoded by the human genome.

TCCGTCTC GAM336880 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336880 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336880 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336880 precursor RNA is designated SEQ ID:6382, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6382 is located from position 51698913 to position 51699010 relative to chromosome 10 on the `-` strand.

GAM336880 precursor RNA folds onto itself, forming GAM336880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336880 precursor RNA, designated SEQ ID NO: 6382, and a schematic representation of a predicted secondary folding of GAM336880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336880 folded precursor RNA yielding a GAM336880 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336880 RNA, hereby incorporated herein. Expression of GAM336880 RNA was experimentally validated in HeLa cells using the methods

described with reference to Figs.22 to 24.

GAM336880 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336880 target RNA, herein designated GAM TARGET RNA.

GAM336880 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336880 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336880 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336880 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336880 RNA, herein designated GAM RNA, to target binding sites on GAM336880 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336880 target RNA into GAM336880 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336880 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336880 target genes. The mRNA of each one of this plurality of GAM336880 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336880 RNA, herein designated GAM RNA, and which when bound by GAM336880 RNA causes inhibition of translation of the GAM336880 target mRNA into a corresponding GAM336880 target protein.

The mechanism of the translational inhibition exerted by GAM336880 RNA, herein designated GAM RNA, on one or more GAM336880 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336880 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336880 RNA, herein designated GAM RNA, of GAM336880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336880 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336880 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336880 RNA correlate with, and may be deduced from, the identity of the GAM336880 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336882 6887 GTCTCTCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGTAGAGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTCTATGGAA Messenger 336882 (GAM336882) oligonucleotides modulates expression of respective target
GGGGTTGTCA genes whose function and utility is known in the art.

TGGTAACAGC GAM336882 is a novel bioinformatically detectable regulatory, non protein
TTCTGTTGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336882 was detected
TTCTAGCCCT is described with additional reference to Figs. 9-15.

ACCTTTTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GACACATTCA encoded by the human genome.

TGCTAGAGGG GAM336882 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AT GAM336882 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336882 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336882 precursor RNA is designated SEQ ID:6887, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6887 is located from position 51927028 to position 51927129 relative to chromosome 19 on the `+` strand.

GAM336882 precursor RNA folds onto itself, forming GAM336882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336882 precursor RNA, designated SEQ ID NO: 6887, and a schematic representation of a predicted secondary folding of GAM336882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336882 folded precursor RNA yielding a GAM336882 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336882 RNA, hereby incorporated herein.

GAM336882 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336882 target RNA, herein designated GAM TARGET RNA.

GAM336882 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336882 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336882 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336882 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336882 RNA, herein designated GAM RNA, to target binding sites on GAM336882 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336882 target RNA into GAM336882 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336882 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336882 target genes. The mRNA of each one of this plurality of GAM336882 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336882 RNA, herein designated GAM RNA, and which when bound by GAM336882 RNA causes inhibition of translation of the GAM336882 target mRNA into a corresponding GAM336882 target protein.

The mechanism of the translational inhibition exerted by GAM336882 RNA, herein designated GAM RNA, on one or more GAM336882 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336882 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336882 RNA, herein designated GAM RNA, of GAM336882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336882 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336882 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336882 RNA correlate with, and may be deduced from, the identity of the GAM336882 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336883 6013 CAGATAACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACACACCCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGGCTGGGC Messenger 336883 (GAM336883) oligonucleotides modulates expression of respective target

ACACAGTTCC genes whose function and utility is known in the art.

TTATTTGGGT GAM336883 is a novel bioinformatically detectable regulatory, non protein

TTTGTGGTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336883 was detected

TCCCAGGTGG is described with additional reference to Figs. 9-15.

TAGCTGGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTG encoded by the human genome.

GAM336883 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336883 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336883 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336883 precursor RNA is designated SEQ ID:6013, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6013 is located from position 51938752 to position 51938835 relative to chromosome 12 on the `+` strand.

GAM336883 precursor RNA folds onto itself, forming GAM336883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336883 precursor RNA, designated SEQ ID NO: 6013, and a schematic representation of a predicted secondary folding of GAM336883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336883 folded precursor RNA yielding a GAM336883 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336883 RNA, hereby incorporated herein.

GAM336883 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336883 target RNA, herein designated GAM TARGET RNA.

GAM336883 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336883 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336883 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336883 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336883 RNA, herein designated GAM RNA, to target binding sites on GAM336883 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336883 target RNA into GAM336883 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336883 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336883 target genes. The mRNA of each one of this plurality of GAM336883 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336883 RNA, herein designated GAM RNA, and which when bound by GAM336883 RNA causes inhibition of translation of the GAM336883 target mRNA into a corresponding GAM336883 target protein.

The mechanism of the translational inhibition exerted by GAM336883 RNA, herein designated GAM RNA, on one or more GAM336883 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336883 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336883 RNA, herein designated GAM RNA, of GAM336883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336883 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336883 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336883 RNA correlate with, and may be deduced from, the identity of the GAM336883 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336886 6371 GAGGCAAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCGGGAGG Messenger 336886 (GAM336886) oligonucleotides modulates expression of respective target

CGAAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM336886 is a novel bioinformatically detectable regulatory, non protein

GATGGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336886 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAGA encoded by the human genome.

CTGTGTCTC GAM336886 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336886 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336886 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336886 precursor RNA is designated SEQ

ID:6371, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6371 is located from position 52749150 to position 52749248 relative to chromosome 20 on the `+` strand.

GAM336886 precursor RNA folds onto itself, forming GAM336886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336886 precursor RNA, designated SEQ ID NO: 6371, and a schematic representation of a predicted secondary folding of GAM336886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336886 folded precursor RNA yielding a GAM336886 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336886 RNA, hereby incorporated herein. Expression of GAM336886 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336886 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336886 target RNA, herein designated GAM TARGET RNA.

GAM336886 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336886 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336886 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336886 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336886 RNA, herein designated GAM RNA, to target binding sites on GAM336886 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336886 target RNA

into GAM336886 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336886 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336886 target genes. The mRNA of each one of this plurality of GAM336886 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336886 RNA, herein designated GAM RNA, and which when bound by GAM336886 RNA causes inhibition of translation of the GAM336886 target mRNA into a corresponding GAM336886 target protein.

The mechanism of the translational inhibition exerted by GAM336886 RNA, herein designated GAM RNA, on one or more GAM336886 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336886 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336886 RNA, herein designated GAM RNA, of GAM336886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336886 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336886 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336886 RNA correlate with, and may be deduced from, the identity of the GAM336886 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336887 6429 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 336887 (GAM336887) oligonucleotides modulates expression of respective target

CGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGGTGA GAM336887 is a novel bioinformatically detectable regulatory, non protein

GATGGCGCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336887 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGATTGAGA encoded by the human genome.

CTGTCTC GAM336887 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336887 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336887 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336887 precursor RNA is designated SEQ ID:6429, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6429 is located from position 52879973 to position 52880069 relative to chromosome 19 on the `+` strand.

GAM336887 precursor RNA folds onto itself, forming GAM336887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336887 precursor RNA, designated SEQ ID NO: 6429, and a schematic representation of a predicted secondary folding of GAM336887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336887 folded precursor RNA yielding a GAM336887 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336887 RNA, hereby incorporated herein. Expression of GAM336887 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336887 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336887 target RNA, herein designated GAM TARGET RNA.

GAM336887 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336887 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336887 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336887 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336887 RNA, herein designated GAM RNA, to target binding sites on GAM336887 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336887 target RNA into GAM336887 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336887 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336887 target genes. The mRNA of each one of this plurality of GAM336887 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336887 RNA, herein designated GAM RNA, and which when bound by GAM336887 RNA causes inhibition of translation of the GAM336887 target mRNA into a corresponding GAM336887 target protein.

The mechanism of the translational inhibition exerted by GAM336887 RNA, herein designated GAM RNA, on one or more GAM336887 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336887 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336887 RNA, herein designated GAM RNA, of GAM336887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336887 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336887 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336887 RNA correlate with, and may be deduced from, the identity of the GAM336887 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336888 6450 GAGGTAAAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGGGCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTCCTTATG Messenger 336888 (GAM336888) oligonucleotides modulates expression of respective target
CAAAGAGAGC genes whose function and utility is known in the art.

TGTCTCTTTA GAM336888 is a novel bioinformatically detectable regulatory, non protein
GTAGGAACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336888 was detected
TGGATTGGCT is described with additional reference to Figs. 9-15.

CATTTTGCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
T encoded by the human genome.

GAM336888 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336888 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336888 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336888 precursor RNA is designated SEQ ID:6450, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6450 is located from position 53047643 to position 53047723 relative to chromosome 10 on the `+` strand.

GAM336888 precursor RNA folds onto itself, forming GAM336888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336888 precursor RNA, designated SEQ ID NO: 6450, and a schematic representation of a predicted secondary folding of GAM336888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336888 folded precursor RNA yielding a GAM336888 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336888 RNA, hereby incorporated herein.

GAM336888 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336888 target RNA, herein designated GAM TARGET RNA.

GAM336888 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336888 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336888 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336888 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336888 RNA, herein designated GAM RNA, to target binding sites on GAM336888 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336888 target RNA into GAM336888 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336888 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336888 target genes. The mRNA of each one of this plurality of GAM336888 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336888 RNA, herein designated GAM RNA, and which when bound by GAM336888 RNA causes inhibition of translation of the GAM336888 target mRNA into a corresponding GAM336888 target protein.

The mechanism of the translational inhibition exerted by GAM336888 RNA, herein designated GAM RNA, on one or more GAM336888 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336888 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336888 RNA, herein designated GAM RNA, of GAM336888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336888 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336888 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336888

RNA correlate with, and may be deduced from, the identity of the GAM336888 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336889 5971 ATGCTCAAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
ATACTGATGT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACCAGGCAG Messenger 336889 (GAM336889) oligonucleotides modulates expression of respective target
AATTCAGATA genes whose function and utility is known in the art.

ATGGTGACCA GAM336889 is a novel bioinformatically detectable regulatory, non protein
GAGATCCTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336889 was detected
CTGAGCAACC is described with additional reference to Figs. 9-15.

TGGTGACATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGATACCAGA encoded by the human genome.

CAT GAM336889 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336889 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336889 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336889 precursor RNA is designated SEQ ID:5971, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5971 is located from position 53301337 to position 53301429 relative to chromosome 14 on the `+` strand.

GAM336889 precursor RNA folds onto itself, forming GAM336889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336889 precursor RNA, designated SEQ ID NO: 5971, and a schematic representation of a predicted secondary folding of GAM336889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336889 folded precursor RNA yielding a GAM336889 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336889 RNA, hereby incorporated herein.

GAM336889 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336889 target RNA, herein designated GAM TARGET RNA.

GAM336889 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336889 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336889 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336889 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336889 RNA, herein designated GAM RNA, to target binding sites on GAM336889 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336889 target RNA into GAM336889 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336889 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336889 target genes. The mRNA of each one of this plurality of GAM336889 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336889 RNA, herein designated GAM RNA, and which when bound by GAM336889 RNA causes inhibition of translation of the GAM336889 target mRNA into a corresponding GAM336889 target protein.

The mechanism of the translational inhibition exerted by GAM336889 RNA, herein designated GAM RNA, on one or more GAM336889 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336889 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336889 RNA, herein designated GAM RNA, of GAM336889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336889 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336889 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336889 RNA correlate with, and may be deduced from, the identity of the GAM336889 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336892 7093 TGAGAAGTCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCCTGATGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGCTGTGCA Messenger 336892 (GAM336892) oligonucleotides modulates expression of respective target
GAGTGGGGGT genes whose function and utility is known in the art.

GAGGAGGCCA GAM336892 is a novel bioinformatically detectable regulatory, non protein
ACTTACTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336892 was detected
TCCTGAACTG is described with additional reference to Figs. 9-15.

GGCAGTGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTATGACAT encoded by the human genome.

GGCCA GAM336892 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336892 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336892 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336892 precursor RNA is designated SEQ ID:7093, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7093 is located from position 53823632 to position 53823726 relative to chromosome 12 on the `-` strand.

GAM336892 precursor RNA folds onto itself, forming GAM336892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336892 precursor RNA, designated SEQ ID NO: 7093, and a schematic representation of a predicted secondary folding of GAM336892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336892 folded precursor RNA yielding a GAM336892 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336892 RNA, hereby incorporated herein.

GAM336892 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336892 target RNA, herein designated GAM TARGET RNA.

GAM336892 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336892 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336892 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336892 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336892 RNA, herein designated GAM RNA, to target binding sites on GAM336892 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336892 target RNA into GAM336892 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336892 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336892 target genes. The mRNA of each one of this plurality of GAM336892 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336892 RNA, herein designated GAM RNA, and which when bound by GAM336892 RNA causes inhibition of translation of the GAM336892 target mRNA into a corresponding GAM336892 target protein.

The mechanism of the translational inhibition exerted by GAM336892 RNA, herein designated GAM RNA, on one or more GAM336892 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336892 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336892 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336892 RNA, herein designated GAM RNA, of GAM336892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336892 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336892 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336892 RNA correlate with, and may be deduced from, the identity of the GAM336892 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336893 6872 GTCAGTCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGGCAGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCAGAGTGG Messenger 336893 (GAM336893) oligonucleotides modulates expression of respective target

GGGTGAGGAG genes whose function and utility is known in the art.

GCCAACTTAC GAM336893 is a novel bioinformatically detectable regulatory, non protein

TGCTTCCTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336893 was detected

ACTGGGCAGT is described with additional reference to Figs. 9-15.

GCCTTCTATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACATGGC encoded by the human genome.

GAM336893 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336893 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336893 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336893 precursor RNA is designated SEQ ID:6872, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6872 is located from position 53823634 to position 53823720 relative to chromosome 12 on the `-` strand.

GAM336893 precursor RNA folds onto itself, forming GAM336893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336893 precursor RNA, designated SEQ ID NO: 6872, and a schematic representation of a predicted secondary folding of GAM336893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336893 folded precursor RNA yielding a GAM336893 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336893 RNA, hereby incorporated herein.

GAM336893 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336893 target RNA, herein designated GAM TARGET RNA.

GAM336893 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336893 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336893 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336893 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336893 RNA, herein designated GAM RNA, to target binding sites on GAM336893 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336893 target RNA into GAM336893 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336893 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336893 target genes. The mRNA of each one of this plurality of GAM336893 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336893 RNA, herein designated GAM RNA, and which when bound by GAM336893 RNA causes inhibition of translation of the GAM336893 target mRNA into a corresponding GAM336893 target protein.

The mechanism of the translational inhibition exerted by GAM336893 RNA, herein

designated GAM RNA, on one or more GAM336893 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336893 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336893 RNA, herein designated GAM RNA, of GAM336893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336893 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336893 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336893 RNA correlate with, and may be deduced from, the identity of the GAM336893 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336894 5690 ACATATGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGAAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GATTTCTCCT Messenger 336894 (GAM336894) oligonucleotides modulates expression of respective target

AATGAAAATG genes whose function and utility is known in the art.

AAGTGCTCTT GAM336894 is a novel bioinformatically detectable regulatory, non protein

TTGAGTATTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336894 was detected

CTTGTTTTAT is described with additional reference to Figs. 9-15.

TGAGATTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATCTGCCCTT encoded by the human genome.

GT GAM336894 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336894 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336894 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336894 precursor RNA is designated SEQ ID:5690, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5690 is located from position 53863297 to position 53863388

relative to chromosome 8 on the `-` strand.

GAM336894 precursor RNA folds onto itself, forming GAM336894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336894 precursor RNA, designated SEQ ID NO: 5690, and a schematic representation of a predicted secondary folding of GAM336894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336894 folded precursor RNA yielding a GAM336894 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336894 RNA, hereby incorporated herein.

GAM336894 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336894 target RNA, herein designated GAM TARGET RNA.

GAM336894 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336894 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336894 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336894 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336894 RNA, herein designated GAM RNA, to target binding sites on GAM336894 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336894 target RNA into GAM336894 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336894 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336894 target genes. The mRNA of each one of this plurality of GAM336894 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336894 RNA, herein designated GAM RNA, and which when bound by GAM336894 RNA causes inhibition of translation of the GAM336894 target mRNA into a corresponding GAM336894 target protein.

The mechanism of the translational inhibition exerted by GAM336894 RNA, herein designated GAM RNA, on one or more GAM336894 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336894 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336894 RNA, herein designated GAM RNA, of GAM336894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336894 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336894 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336894 RNA correlate with, and may be deduced from, the identity of the GAM336894 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336895 6727 GGCAGAATGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGTGATTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCTAATGAA Messenger 336895 (GAM336895) oligonucleotides modulates expression of respective target
AATGAAGTGC genes whose function and utility is known in the art.

TCTTTTGAGT GAM336895 is a novel bioinformatically detectable regulatory, non protein
ATTTCTTGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336895 was detected
TTATTGAGAT is described with additional reference to Figs. 9-15.

TCCTATCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
C encoded by the human genome.

GAM336895 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336895 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336895 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336895 precursor RNA is designated SEQ ID:6727, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6727 is located from position 53863302 to position 53863382 relative to chromosome 8 on the `-` strand.

GAM336895 precursor RNA folds onto itself, forming GAM336895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336895 precursor RNA, designated SEQ ID NO: 6727, and a schematic representation of a predicted secondary folding of GAM336895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336895 folded precursor RNA yielding a GAM336895 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336895 RNA, hereby incorporated herein.

GAM336895 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336895 target RNA, herein designated GAM TARGET RNA.

GAM336895 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336895 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336895 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336895 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336895 RNA, herein designated GAM RNA, to target

binding sites on GAM336895 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336895 target RNA into GAM336895 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336895 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336895 target genes. The mRNA of each one of this plurality of GAM336895 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336895 RNA, herein designated GAM RNA, and which when bound by GAM336895 RNA causes inhibition of translation of the GAM336895 target mRNA into a corresponding GAM336895 target protein.

The mechanism of the translational inhibition exerted by GAM336895 RNA, herein designated GAM RNA, on one or more GAM336895 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336895 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336895 RNA, herein designated GAM RNA, of GAM336895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336895 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336895 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336895 RNA correlate with, and may be deduced from, the identity of the GAM336895 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336896 5746 AGCAGGATTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAGAGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTGTGAGA Messenger 336896 (GAM336896) oligonucleotides modulates expression of respective target

AACAGGTTTT genes whose function and utility is known in the art.

GGGTTTTGCT GAM336896 is a novel bioinformatically detectable regulatory, non protein

GAAATTTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336896 was detected

TGTCAGCATT is described with additional reference to Figs. 9-15.

GCATCACTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCTTAACTG encoded by the human genome.

TT GAM336896 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336896 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336896 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336896 precursor RNA is designated SEQ ID:5746, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5746 is located from position 54032470 to position 54032561 relative to chromosome 15 on the `-` strand.

GAM336896 precursor RNA folds onto itself, forming GAM336896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336896 precursor RNA, designated SEQ ID NO: 5746, and a schematic representation of a predicted secondary folding of GAM336896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336896 folded precursor RNA yielding a GAM336896 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336896 RNA, hereby incorporated herein.

GAM336896 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336896 target RNA, herein designated GAM TARGET RNA.

GAM336896 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336896 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336896 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336896 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336896 RNA, herein designated GAM RNA, to target binding sites on GAM336896 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336896 target RNA into GAM336896 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336896 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336896 target genes. The mRNA of each one of this plurality of GAM336896 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336896 RNA, herein designated GAM RNA, and which when bound by GAM336896 RNA causes inhibition of translation of the GAM336896 target mRNA into a corresponding GAM336896 target protein.

The mechanism of the translational inhibition exerted by GAM336896 RNA, herein designated GAM RNA, on one or more GAM336896 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336896 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336896 RNA, herein designated GAM RNA, of GAM336896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336896 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336896 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336896 RNA correlate with, and may be deduced from, the identity of the GAM336896 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336897 6517 GCGGGCTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTCTCAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTTGGGTTT Messenger 336897 (GAM336897) oligonucleotides modulates expression of respective target
TCTTAGTGAA genes whose function and utility is known in the art.

ATAAGCAGCA GAM336897 is a novel bioinformatically detectable regulatory, non protein
ACAAACGACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336897 was detected
ACAAAACCGC is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336897 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336897 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336897 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336897 precursor RNA is designated SEQ ID:6517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6517 is located from position 54122958 to position 54123027 relative to chromosome 12 on the `-` strand.

GAM336897 precursor RNA folds onto itself, forming GAM336897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336897 precursor RNA, designated SEQ ID NO: 6517, and a schematic representation of a predicted secondary folding of GAM336897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336897 folded precursor RNA yielding a GAM336897 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336897 RNA, hereby incorporated herein.

GAM336897 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336897 target RNA, herein designated GAM TARGET RNA.

GAM336897 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336897 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336897 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336897 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336897 RNA, herein designated GAM RNA, to target binding sites on GAM336897 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336897 target RNA into GAM336897 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336897 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336897 target genes. The mRNA of each one of this plurality of GAM336897 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336897 RNA, herein designated GAM RNA, and which when bound by GAM336897 RNA causes inhibition of translation of the GAM336897 target mRNA into a corresponding GAM336897 target protein.

The mechanism of the translational inhibition exerted by GAM336897 RNA, herein designated GAM RNA, on one or more GAM336897 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336897 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336897 RNA, herein designated GAM RNA, of GAM336897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336897 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336897 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336897 RNA correlate with, and may be deduced from, the identity of the GAM336897 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336898 6653 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 336898 (GAM336898) oligonucleotides modulates expression of respective target
TTGCGGTGAG genes whose function and utility is known in the art.

CCAAGATCGT GAM336898 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336898 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAAACTCC encoded by the human genome.

GAM336898 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336898 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336898 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336898 precursor RNA is designated SEQ ID:6653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6653 is located from position 54260659 to position 54260747 relative to chromosome 12 on the `-` strand.

GAM336898 precursor RNA folds onto itself, forming GAM336898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336898 precursor RNA, designated SEQ ID NO: 6653, and a schematic representation of a predicted secondary folding of GAM336898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336898 folded precursor RNA yielding a GAM336898 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336898 RNA, hereby incorporated herein.

GAM336898 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336898 target RNA, herein designated GAM TARGET RNA.

GAM336898 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336898 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336898 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336898 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336898 RNA, herein designated GAM RNA, to target binding sites on GAM336898 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336898 target RNA into GAM336898 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336898 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336898 target genes. The mRNA of each one of this plurality of GAM336898 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336898 RNA, herein designated GAM RNA, and which when bound by GAM336898 RNA causes inhibition of translation of the GAM336898 target mRNA into a corresponding GAM336898 target protein.

The mechanism of the translational inhibition exerted by GAM336898 RNA, herein designated GAM RNA, on one or more GAM336898 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336898 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336898 RNA, herein designated GAM RNA, of GAM336898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336898 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336898 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336898 RNA correlate with, and may be deduced from, the identity of the GAM336898 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336901 5870 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336901 (GAM336901) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336901 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336901 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336901 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336901 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336901 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336901 precursor RNA is designated SEQ ID:5870, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5870 is located from position 55006289 to position 55006370 relative to chromosome 16 on the `+` strand.

GAM336901 precursor RNA folds onto itself, forming GAM336901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336901 precursor RNA, designated SEQ ID NO: 5870, and a schematic representation of a predicted secondary folding of GAM336901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336901 folded precursor

RNA yielding a GAM336901 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336901 RNA, hereby incorporated herein.

GAM336901 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336901 target RNA, herein designated GAM TARGET RNA.

GAM336901 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336901 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336901 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336901 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336901 RNA, herein designated GAM RNA, to target binding sites on GAM336901 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336901 target RNA into GAM336901 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336901 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336901 target genes. The mRNA of each one of this plurality of GAM336901 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336901 RNA, herein designated GAM RNA, and which when bound by GAM336901 RNA causes inhibition of translation of the GAM336901 target mRNA into a corresponding GAM336901 target protein.

The mechanism of the translational inhibition exerted by GAM336901 RNA, herein designated GAM RNA, on one or more GAM336901 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336901 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336901 RNA, herein designated GAM RNA, of GAM336901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336901 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336901 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336901 RNA correlate with, and may be deduced from, the identity of the GAM336901 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336903 7102 TGAGACGGAG TTTCGCTCTT GTCCCCCAGG CTTTAGTGCA ATGGCGCGAT CTCGGCTCAC CGCAGCCTCC GCCACCTGGG TTCAAACGAT TCTCCTGCCT CA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336903 (GAM336903) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336903 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336903 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336903 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336903 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336903 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336903 precursor RNA is designated SEQ ID:7102, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7102 is located from position 55618701 to position 55618802 relative to chromosome 20 on the `+` strand.

GAM336903 precursor RNA folds onto itself, forming GAM336903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336903 precursor RNA, designated SEQ ID NO: 7102, and a schematic representation of a predicted secondary folding of GAM336903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336903 folded precursor RNA yielding a GAM336903 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336903 RNA, hereby incorporated herein.

GAM336903 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336903 target RNA, herein designated GAM TARGET RNA.

GAM336903 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336903 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336903 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336903 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336903 RNA, herein designated GAM RNA, to target binding sites on GAM336903 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336903 target RNA into GAM336903 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336903 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336903 target genes. The mRNA of each one of this plurality of GAM336903 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336903 RNA, herein designated GAM RNA, and which when bound by GAM336903 RNA causes inhibition of translation of the GAM336903 target mRNA into a corresponding GAM336903 target protein.

The mechanism of the translational inhibition exerted by GAM336903 RNA, herein designated GAM RNA, on one or more GAM336903 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336903 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336903 RNA, herein designated GAM RNA, of GAM336903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336903 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336903 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336903 RNA correlate with, and may be deduced from, the identity of the GAM336903 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336906 7132 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 336906 (GAM336906) oligonucleotides modulates expression of respective target

GTGGAGCTTG genes whose function and utility is known in the art.

CGGTGAGCCG GAM336906 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336906 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGTGA encoded by the human genome.

AACTCCATCT GAM336906 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM336906 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336906 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336906 precursor RNA is designated SEQ ID:7132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7132 is located from position 56423119 to position 56423220

relative to chromosome 12 on the `-` strand.

GAM336906 precursor RNA folds onto itself, forming GAM336906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336906 precursor RNA, designated SEQ ID NO: 7132, and a schematic representation of a predicted secondary folding of GAM336906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336906 folded precursor RNA yielding a GAM336906 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336906 RNA, hereby incorporated herein. Expression of GAM336906 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336906 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336906 target RNA, herein designated GAM TARGET RNA.

GAM336906 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336906 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336906 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336906 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336906 RNA, herein designated GAM RNA, to target binding sites on GAM336906 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336906 target RNA into GAM336906 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336906 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336906 target genes. The mRNA of each one of this plurality of GAM336906 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336906 RNA, herein designated GAM RNA, and which when bound by GAM336906 RNA causes inhibition of translation of the GAM336906 target mRNA into a corresponding GAM336906 target protein.

The mechanism of the translational inhibition exerted by GAM336906 RNA, herein designated GAM RNA, on one or more GAM336906 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336906 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336906 RNA, herein designated GAM RNA, of GAM336906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336906 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336906 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336906 RNA correlate with, and may be deduced from, the identity of the GAM336906 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336907 6613 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 336907 (GAM336907) oligonucleotides modulates expression of respective target

TTGCGGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM336907 is a novel bioinformatically detectable regulatory, non protein

GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336907 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAAACTCC encoded by the human genome.

GAM336907 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336907 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336907 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336907 precursor RNA is designated SEQ ID:6613, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6613 is located from position 56423125 to position 56423213 relative to chromosome 12 on the `-` strand.

GAM336907 precursor RNA folds onto itself, forming GAM336907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336907 precursor RNA, designated SEQ ID NO: 6613, and a schematic representation of a predicted secondary folding of GAM336907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336907 folded precursor RNA yielding a GAM336907 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336907 RNA, hereby incorporated herein. Expression of GAM336907 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336907 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336907 target RNA, herein designated GAM TARGET RNA.

GAM336907 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336907 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336907 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336907 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336907 RNA, herein designated GAM RNA, to target binding sites on GAM336907 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336907 target RNA into GAM336907 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336907 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336907 target genes. The mRNA of each one of this plurality of GAM336907 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336907 RNA, herein designated GAM RNA, and which when bound by GAM336907 RNA causes inhibition of translation of the GAM336907 target mRNA into a corresponding GAM336907 target protein.

The mechanism of the translational inhibition exerted by GAM336907 RNA, herein designated GAM RNA, on one or more GAM336907 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336907 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336907 RNA, herein designated GAM RNA, of GAM336907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336907 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336907 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336907 RNA correlate with, and may be deduced from, the identity of the GAM336907 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336908 5871 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336908 (GAM336908) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336908 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336908 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336908 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336908 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336908 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336908 precursor RNA is designated SEQ ID:5871, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5871 is located from position 56590496 to position 56590577 relative to chromosome 2 on the `-` strand.

GAM336908 precursor RNA folds onto itself, forming GAM336908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336908 precursor RNA, designated SEQ ID NO: 5871, and a schematic representation of a predicted secondary folding of GAM336908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336908 folded precursor RNA yielding a GAM336908 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336908 RNA, hereby incorporated herein.

GAM336908 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336908 target RNA, herein designated GAM TARGET RNA.

GAM336908 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336908 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336908 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336908 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336908 RNA, herein designated GAM RNA, to target binding sites on GAM336908 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336908 target RNA into GAM336908 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336908 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336908 target genes. The mRNA of each one of this plurality of GAM336908 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336908 RNA, herein designated GAM RNA, and which when bound by GAM336908 RNA causes inhibition of translation of the GAM336908 target mRNA into a corresponding GAM336908 target protein.

The mechanism of the translational inhibition exerted by GAM336908 RNA, herein designated GAM RNA, on one or more GAM336908 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336908 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336908 RNA, herein designated GAM RNA, of GAM336908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336908 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336908 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336908 RNA correlate with, and may be deduced from, the identity of the GAM336908 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336909 6715 GGAGGTGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGTGTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTGGCATCT Messenger 336909 (GAM336909) oligonucleotides modulates expression of respective target
AGTGGCTGCT genes whose function and utility is known in the art.

AAACATCCTA GAM336909 is a novel bioinformatically detectable regulatory, non protein
CACTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336909 was detected
is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336909 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336909 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336909 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336909 precursor RNA is designated SEQ ID:6715, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6715 is located from position 56700933 to position 56700988 relative to chromosome 12 on the `+` strand.

GAM336909 precursor RNA folds onto itself, forming GAM336909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336909 precursor RNA, designated SEQ ID NO: 6715, and a schematic representation of a predicted secondary folding of GAM336909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336909 folded precursor RNA yielding a GAM336909 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336909 RNA, hereby incorporated herein.

GAM336909 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336909 target RNA, herein designated GAM TARGET RNA.

GAM336909 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336909 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336909 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336909 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336909 RNA, herein designated GAM RNA, to target binding sites on GAM336909 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336909 target RNA into GAM336909 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336909 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336909 target genes. The mRNA of each one of this plurality of GAM336909 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336909 RNA, herein designated GAM RNA, and which when bound by GAM336909 RNA causes inhibition of translation of the GAM336909 target mRNA into a corresponding GAM336909 target protein.

The mechanism of the translational inhibition exerted by GAM336909 RNA, herein designated GAM RNA, on one or more GAM336909 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336909 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336909 RNA, herein designated GAM RNA, of GAM336909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336909 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336909 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336909 RNA correlate with, and may be deduced from, the identity of the GAM336909 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336911 6930 GTGTTAGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGTTAAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTAAGACACT Messenger 336911 (GAM336911) oligonucleotides modulates expression of respective target
TTCTAAATAG genes whose function and utility is known in the art.

AAGTCTTGTA GAM336911 is a novel bioinformatically detectable regulatory, non protein
TATGGGGCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336911 was detected
TTGAGAAAGT is described with additional reference to Figs. 9-15.

GTTTTCCCGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATGCTGGGG encoded by the human genome.

GGAAACAC GAM336911 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336911 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336911 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336911 precursor RNA is designated SEQ ID:6930, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6930 is located from position 56703572 to position 56703669 relative to chromosome 16 on the `+` strand.

GAM336911 precursor RNA folds onto itself, forming GAM336911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336911 precursor RNA, designated SEQ ID NO: 6930, and a schematic representation of a predicted secondary folding of GAM336911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336911 folded precursor RNA yielding a GAM336911 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336911 RNA, hereby incorporated herein.

GAM336911 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336911 target RNA, herein designated GAM TARGET RNA.

GAM336911 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336911 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336911 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336911 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336911 RNA, herein designated GAM RNA, to target binding sites on GAM336911 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336911 target RNA into GAM336911 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336911 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336911 target genes. The mRNA of each one of this plurality of GAM336911 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336911 RNA, herein designated GAM RNA, and which when bound by GAM336911 RNA causes inhibition of translation of the GAM336911 target mRNA into a corresponding GAM336911 target protein.

The mechanism of the translational inhibition exerted by GAM336911 RNA, herein designated GAM RNA, on one or more GAM336911 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336911 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336911 RNA, herein designated GAM RNA, of

GAM336911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336911 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336911 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336911 RNA correlate with, and may be deduced from, the identity of the GAM336911 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336913 5697 ACCTCATCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TACAAAAAAT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACGAAAATTA Messenger 336913 (GAM336913) oligonucleotides modulates expression of respective target

GCTGGGTGTG genes whose function and utility is known in the art.

GTGGCATGTA GAM336913 is a novel bioinformatically detectable regulatory, non protein

CCTGTAGTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336913 was detected

CAGCTATTTG is described with additional reference to Figs. 9-15.

AGAGACTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GT encoded by the human genome.

GAM336913 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336913 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336913 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336913 precursor RNA is designated SEQ ID:5697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5697 is located from position 56716065 to position 56716146 relative to chromosome 12 on the `-` strand.

GAM336913 precursor RNA folds onto itself, forming GAM336913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336913 precursor RNA, designated SEQ ID NO: 5697, and

a schematic representation of a predicted secondary folding of GAM336913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336913 folded precursor RNA yielding a GAM336913 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336913 RNA, hereby incorporated herein.

GAM336913 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336913 target RNA, herein designated GAM TARGET RNA.

GAM336913 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336913 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336913 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336913 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336913 RNA, herein designated GAM RNA, to target binding sites on GAM336913 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336913 target RNA into GAM336913 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336913 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336913 target genes. The mRNA of each one of this plurality of GAM336913 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336913 RNA, herein designated GAM RNA, and which when bound by GAM336913 RNA causes inhibition of translation of the GAM336913 target mRNA into a corresponding GAM336913 target protein.

The mechanism of the translational inhibition exerted by GAM336913 RNA, herein designated GAM RNA, on one or more GAM336913 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336913 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336913 RNA, herein designated GAM RNA, of GAM336913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336913 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336913 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336913 RNA correlate with, and may be deduced from, the identity of the GAM336913 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336914 6110 CCTCATCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

ACAAAAAATA detected oligonucleotides of the present invention, referred to here as Genomic Address

CGAAAATTAG Messenger 336914 (GAM336914) oligonucleotides modulates expression of respective target

CTGGGTGTGG genes whose function and utility is known in the art.

TGGCATGTAC GAM336914 is a novel bioinformatically detectable regulatory, non protein

CTGTAGTCCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336914 was detected

AGCTATTTGA is described with additional reference to Figs. 9-15.

GAGACTGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336914 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336914 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336914 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336914 precursor RNA is designated SEQ ID:6110, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6110 is located from position 56716066 to position 56716145 relative to chromosome 12 on the `-` strand.

GAM336914 precursor RNA folds onto itself, forming GAM336914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336914 precursor RNA, designated SEQ ID NO: 6110, and a schematic representation of a predicted secondary folding of GAM336914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336914 folded precursor RNA yielding a GAM336914 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336914 RNA, hereby incorporated herein.

GAM336914 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336914 target RNA, herein designated GAM TARGET RNA.

GAM336914 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336914 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336914 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336914 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336914 RNA, herein designated GAM RNA, to target binding sites on GAM336914 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336914 target RNA into GAM336914 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336914 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336914 target genes. The mRNA of each one of this plurality of GAM336914 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336914 RNA, herein designated GAM RNA, and which when bound by GAM336914 RNA causes inhibition of translation of the GAM336914 target mRNA into a corresponding GAM336914 target protein.

The mechanism of the translational inhibition exerted by GAM336914 RNA, herein designated GAM RNA, on one or more GAM336914 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336914 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336914 RNA, herein designated GAM RNA, of GAM336914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336914 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336914 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336914 RNA correlate with, and may be deduced from, the identity of the GAM336914 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336916 6302 GAATAGCGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCCCAAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCACAAAGTA Messenger 336916 (GAM336916) oligonucleotides modulates expression of respective target

TGTGATGGAG genes whose function and utility is known in the art.

CTAGAGATTC GAM336916 is a novel bioinformatically detectable regulatory, non protein

AAACCCAGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336916 was detected

CTCTCTGGCT is described with additional reference to Figs. 9-15.

CCTTCTTTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTGGGCTTG encoded by the human genome.

CTCTGGGAAA GAM336916 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

ATATGCTATT GAM336916 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

T GAM336916 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336916 precursor RNA is designated SEQ ID:6302, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6302 is located from position 56865886 to position 56865996 relative to chromosome 19 on the `-` strand.

GAM336916 precursor RNA folds onto itself, forming GAM336916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336916 precursor RNA, designated SEQ ID NO: 6302, and a schematic representation of a predicted secondary folding of GAM336916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336916 folded precursor RNA yielding a GAM336916 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336916 RNA, hereby incorporated herein.

GAM336916 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336916 target RNA, herein designated GAM TARGET RNA.

GAM336916 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336916 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336916 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336916 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336916 RNA, herein designated GAM RNA, to target binding sites on GAM336916 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336916 target RNA into GAM336916 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM336916 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336916 target genes. The mRNA of each one of this plurality of GAM336916 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336916 RNA, herein designated GAM RNA, and which when bound by GAM336916 RNA causes inhibition of translation of the GAM336916 target mRNA into a corresponding GAM336916 target protein.

The mechanism of the translational inhibition exerted by GAM336916 RNA, herein designated GAM RNA, on one or more GAM336916 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336916 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336916 RNA, herein designated GAM RNA, of GAM336916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336916 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336916 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336916 RNA correlate with, and may be deduced from, the identity of the GAM336916 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336917 6133 CCTTTGCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCCTTTAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTCAGTGT Messenger 336917 (GAM336917) oligonucleotides modulates expression of respective target

TTTGGTCTAA genes whose function and utility is known in the art.

TCTTCAAGAG GAM336917 is a novel bioinformatically detectable regulatory, non protein

GAATTTGAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336917 was detected

TTCACTTGAA is described with additional reference to Figs. 9-15.

TAAGTTAGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGTTTGAGG encoded by the human genome.

TGGGTGTAGC GAM336917 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TAGAGG GAM336917 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336917 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336917 precursor RNA is designated SEQ ID:6133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6133 is located from position 56876889 to position 56876994 relative to chromosome 15 on the `+` strand.

GAM336917 precursor RNA folds onto itself, forming GAM336917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336917 precursor RNA, designated SEQ ID NO: 6133, and a schematic representation of a predicted secondary folding of GAM336917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336917 folded precursor RNA yielding a GAM336917 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336917 RNA, hereby incorporated herein.

GAM336917 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336917 target RNA, herein designated GAM TARGET RNA.

GAM336917 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336917 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336917 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336917 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336917 RNA, herein designated GAM RNA, to target binding sites on GAM336917 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336917 target RNA into GAM336917 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336917 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336917 target genes. The mRNA of each one of this plurality of GAM336917 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336917 RNA, herein designated GAM RNA, and which when bound by GAM336917 RNA causes inhibition of translation of the GAM336917 target mRNA into a corresponding GAM336917 target protein.

The mechanism of the translational inhibition exerted by GAM336917 RNA, herein designated GAM RNA, on one or more GAM336917 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336917 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336917 RNA, herein designated GAM RNA, of GAM336917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336917 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336917 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336917 RNA correlate with, and may be deduced from, the identity of the GAM336917 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336918 6570 GCTTTGGCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAACAACTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGTGTTTTGG Messenger 336918 (GAM336918) oligonucleotides modulates expression of respective target

TCTAATCTTC genes whose function and utility is known in the art.

AAGAGGAATT GAM336918 is a novel bioinformatically detectable regulatory, non protein
TGAGGTTCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336918 was detected
TTGAATAAGT is described with additional reference to Figs. 9-15.

TAGACTAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGGTGGGT encoded by the human genome.

GTAGCTAGAG GAM336918 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GATTGAAGT GAM336918 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336918 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336918 precursor RNA is designated SEQ ID:6570, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6570 is located from position 56876894 to position 56877002 relative to chromosome 15 on the `+` strand.

GAM336918 precursor RNA folds onto itself, forming GAM336918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336918 precursor RNA, designated SEQ ID NO: 6570, and a schematic representation of a predicted secondary folding of GAM336918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336918 folded precursor RNA yielding a GAM336918 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336918 RNA, hereby incorporated herein.

GAM336918 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336918 target RNA, herein designated GAM TARGET RNA.

GAM336918 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336918 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336918 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336918 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336918 RNA, herein designated GAM RNA, to target binding sites on GAM336918 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336918 target RNA into GAM336918 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336918 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336918 target genes. The mRNA of each one of this plurality of GAM336918 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336918 RNA, herein designated GAM RNA, and which when bound by GAM336918 RNA causes inhibition of translation of the GAM336918 target mRNA into a corresponding GAM336918 target protein.

The mechanism of the translational inhibition exerted by GAM336918 RNA, herein designated GAM RNA, on one or more GAM336918 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336918 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336918 RNA, herein designated GAM RNA, of GAM336918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336918 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336918 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336918 RNA correlate with, and may be deduced from, the identity of the GAM336918 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336919 5872 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336919 (GAM336919) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336919 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336919 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336919 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336919 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336919 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336919 precursor RNA is designated SEQ ID:5872, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5872 is located from position 56896949 to position 56897030 relative to chromosome 5 on the `+` strand.

GAM336919 precursor RNA folds onto itself, forming GAM336919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336919 precursor RNA, designated SEQ ID NO: 5872, and a schematic representation of a predicted secondary folding of GAM336919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336919 folded precursor RNA yielding a GAM336919 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336919 RNA, hereby incorporated herein.

GAM336919 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336919 target RNA, herein designated GAM TARGET RNA.

GAM336919 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336919 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336919 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336919 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336919 RNA, herein designated GAM RNA, to target binding sites on GAM336919 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336919 target RNA into GAM336919 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336919 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336919 target genes. The mRNA of each one of this plurality of GAM336919 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336919 RNA, herein designated GAM RNA, and which when bound by GAM336919 RNA causes inhibition of translation of the GAM336919 target mRNA into a corresponding GAM336919 target protein.

The mechanism of the translational inhibition exerted by GAM336919 RNA, herein designated GAM RNA, on one or more GAM336919 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336919 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336919 RNA, herein designated GAM RNA, of GAM336919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336919 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336919 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336919 RNA correlate with, and may be deduced from, the identity of the GAM336919 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336920 7247 TGGGTGCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically
TAATCCCAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TACTTGGGAG Messenger 336920 (GAM336920) oligonucleotides modulates expression of respective target
GTTGAGGCAG genes whose function and utility is known in the art.

GAGAATCACT GAM336920 is a novel bioinformatically detectable regulatory, non protein
TGAACCCAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336920 was detected
AGGTGGAGGT is described with additional reference to Figs. 9-15.

TGCAGTGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCA encoded by the human genome.

GAM336920 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336920 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336920 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336920 precursor RNA is designated SEQ ID:7247, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7247 is located from position 56913348 to position 56913430 relative to chromosome 16 on the `+` strand.

GAM336920 precursor RNA folds onto itself, forming GAM336920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336920 precursor RNA, designated SEQ ID NO: 7247, and a schematic representation of a predicted secondary folding of GAM336920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336920 folded precursor RNA yielding a GAM336920 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336920 RNA, hereby incorporated herein.

GAM336920 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336920 target RNA, herein designated GAM TARGET RNA.

GAM336920 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336920 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336920 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336920 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336920 RNA, herein designated GAM RNA, to target binding sites on GAM336920 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336920 target RNA into GAM336920 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336920 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336920 target genes. The mRNA of each one of this plurality of GAM336920 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336920 RNA, herein designated GAM RNA, and which when bound by GAM336920 RNA causes inhibition of translation of the GAM336920 target mRNA into a corresponding GAM336920 target protein.

The mechanism of the translational inhibition exerted by GAM336920 RNA, herein designated GAM RNA, on one or more GAM336920 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336920 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336920 RNA, herein designated GAM RNA, of GAM336920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336920 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336920 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336920 RNA correlate with, and may be deduced from, the identity of the GAM336920 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336921 7105 TGAGATGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGACTGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCCCAGGAG Messenger 336921 (GAM336921) oligonucleotides modulates expression of respective target
GTTGAGGTTG genes whose function and utility is known in the art.

CAGTGAACCA GAM336921 is a novel bioinformatically detectable regulatory, non protein
TGATCATGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336921 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACCTTGTTTC GAM336921 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM336921 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336921 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336921 precursor RNA is designated SEQ ID:7105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7105 is located from position 57181803 to position 57181903 relative to chromosome 17 on the `+` strand.

GAM336921 precursor RNA folds onto itself, forming GAM336921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336921 precursor RNA, designated SEQ ID NO: 7105, and a schematic representation of a predicted secondary folding of GAM336921 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336921 folded precursor RNA yielding a GAM336921 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336921 RNA, hereby incorporated herein.

GAM336921 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336921 target RNA, herein designated GAM TARGET RNA.

GAM336921 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336921 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336921 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336921 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336921 RNA, herein designated GAM RNA, to target binding sites on GAM336921 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336921 target RNA into GAM336921 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336921 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336921 target genes. The mRNA of each one of this plurality of GAM336921 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336921 RNA, herein designated GAM RNA, and which when bound by GAM336921 RNA causes inhibition of translation of the GAM336921 target mRNA into a corresponding GAM336921 target protein.

The mechanism of the translational inhibition exerted by GAM336921 RNA, herein designated GAM RNA, on one or more GAM336921 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336921 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336921 RNA, herein designated GAM RNA, of GAM336921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336921 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336921 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336921 RNA correlate with, and may be deduced from, the identity of the GAM336921 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336922 6599 GGACTGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTGAGGTTG Messenger 336922 (GAM336922) oligonucleotides modulates expression of respective target

CAGTGAACCA genes whose function and utility is known in the art.

TGATCATGTC GAM336922 is a novel bioinformatically detectable regulatory, non protein

ACTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336922 was detected

AGCCTGGGTA is described with additional reference to Figs. 9-15.

ACAGAGTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACC encoded by the human genome.

GAM336922 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336922 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336922 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336922 precursor RNA is designated SEQ ID:6599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6599 is located from position 57181813 to position 57181895 relative to chromosome 17 on the `+` strand.

GAM336922 precursor RNA folds onto itself, forming GAM336922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336922 precursor RNA, designated SEQ ID NO: 6599, and a schematic representation of a predicted secondary folding of GAM336922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336922 folded precursor RNA yielding a GAM336922 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336922 RNA, hereby incorporated herein.

GAM336922 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336922 target RNA, herein designated GAM TARGET RNA.

GAM336922 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336922 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336922 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336922 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336922 RNA, herein designated GAM RNA, to target binding sites on GAM336922 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336922 target RNA into GAM336922 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336922 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336922 target genes. The mRNA of each one of this plurality of GAM336922 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336922 RNA, herein designated GAM RNA, and which when bound by GAM336922 RNA causes inhibition of translation of the GAM336922 target mRNA into a corresponding GAM336922 target protein.

The mechanism of the translational inhibition exerted by GAM336922 RNA, herein designated GAM RNA, on one or more GAM336922 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336922 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336922 RNA, herein designated GAM RNA, of GAM336922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336922 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336922 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336922 RNA correlate with, and may be deduced from, the identity of the GAM336922 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336923 6458 GAGGTGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCAGAATT Messenger 336923 (GAM336923) oligonucleotides modulates expression of respective target

TCAAGGCTGC genes whose function and utility is known in the art.

AGTGAGCTAT GAM336923 is a novel bioinformatically detectable regulatory, non protein

GATTAAGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336923 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGTGAGA encoded by the human genome.

CCTCCAACTT GAM336923 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

T GAM336923 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336923 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM336923 precursor RNA is designated SEQ ID:6458, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6458 is located from position 57192272 to position 57192372 relative to chromosome 4 on the `+` strand.

GAM336923 precursor RNA folds onto itself, forming GAM336923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336923 precursor RNA, designated SEQ ID NO: 6458, and a schematic representation of a predicted secondary folding of GAM336923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336923 folded precursor RNA yielding a GAM336923 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336923 RNA, hereby incorporated herein. Expression of GAM336923 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336923 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336923 target RNA, herein designated GAM TARGET RNA.

GAM336923 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336923 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336923 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336923 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336923 RNA, herein designated GAM RNA, to target binding sites on GAM336923 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336923 target RNA into GAM336923 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336923 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336923 target genes. The mRNA of each one of this plurality of GAM336923 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336923 RNA, herein designated GAM RNA, and which when bound by GAM336923 RNA causes inhibition of translation of the GAM336923 target mRNA into a corresponding GAM336923 target protein.

The mechanism of the translational inhibition exerted by GAM336923 RNA, herein designated GAM RNA, on one or more GAM336923 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336923 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336923 RNA, herein designated GAM RNA, of GAM336923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336923 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336923 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336923 RNA correlate with, and may be deduced from, the identity of the GAM336923 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336924 5873 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336924 (GAM336924) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336924 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336924 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336924 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336924 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336924 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336924 precursor RNA is designated SEQ ID:5873, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5873 is located from position 57442342 to position 57442423 relative to chromosome 8 on the `+` strand.

GAM336924 precursor RNA folds onto itself, forming GAM336924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336924 precursor RNA, designated SEQ ID NO: 5873, and a schematic representation of a predicted secondary folding of GAM336924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336924 folded precursor RNA yielding a GAM336924 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336924 RNA, hereby incorporated herein.

GAM336924 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336924 target RNA, herein designated GAM TARGET RNA.

GAM336924 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336924 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336924 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336924 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336924 RNA, herein designated GAM RNA, to target binding sites on GAM336924 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336924 target RNA into GAM336924 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336924 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336924 target genes. The mRNA of each one of this plurality of GAM336924 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336924 RNA, herein designated GAM RNA, and which when bound by GAM336924 RNA causes inhibition of translation of the GAM336924 target mRNA into a corresponding GAM336924 target protein.

The mechanism of the translational inhibition exerted by GAM336924 RNA, herein designated GAM RNA, on one or more GAM336924 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336924 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336924 RNA, herein designated GAM RNA, of GAM336924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336924 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336924 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336924 RNA correlate with, and may be deduced from, the identity of the GAM336924 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336925 6784 GGGAGACTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGAACCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGGCGGAG Messenger 336925 (GAM336925) oligonucleotides modulates expression of respective target

GGTGCAGTGA genes whose function and utility is known in the art.

GTCGACATCA GAM336925 is a novel bioinformatically detectable regulatory, non protein
TGCCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336925 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGACCC encoded by the human genome.

GAM336925 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336925 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336925 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336925 precursor RNA is designated SEQ ID:6784, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6784 is located from position 57533860 to position 57533947 relative to chromosome 12 on the `+` strand.

GAM336925 precursor RNA folds onto itself, forming GAM336925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336925 precursor RNA, designated SEQ ID NO: 6784, and a schematic representation of a predicted secondary folding of GAM336925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336925 folded precursor RNA yielding a GAM336925 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336925 RNA, hereby incorporated herein. Expression of GAM336925 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336925 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336925 target RNA, herein designated GAM TARGET RNA.

GAM336925 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336925 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336925 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336925 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336925 RNA, herein designated GAM RNA, to target binding sites on GAM336925 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336925 target RNA into GAM336925 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336925 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336925 target genes. The mRNA of each one of this plurality of GAM336925 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336925 RNA, herein designated GAM RNA, and which when bound by GAM336925 RNA causes inhibition of translation of the GAM336925 target mRNA into a corresponding GAM336925 target protein.

The mechanism of the translational inhibition exerted by GAM336925 RNA, herein designated GAM RNA, on one or more GAM336925 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336925 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336925 RNA, herein designated GAM RNA, of GAM336925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336925 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336925 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336925 RNA correlate with, and may be deduced from, the identity of the GAM336925 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336926 6268 CTTGCTTGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCAGGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGGTGCA Messenger 336926 (GAM336926) oligonucleotides modulates expression of respective target
GTGAGTCGAC genes whose function and utility is known in the art.

ATCATGCCAC GAM336926 is a novel bioinformatically detectable regulatory, non protein
TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336926 was detected
CCTGGGCAAC is described with additional reference to Figs. 9-15.

AGAGCAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336926 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336926 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336926 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336926 precursor RNA is designated SEQ ID:6268, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6268 is located from position 57533866 to position 57533943 relative to chromosome 12 on the `+` strand.

GAM336926 precursor RNA folds onto itself, forming GAM336926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336926 precursor RNA, designated SEQ ID NO: 6268, and a schematic representation of a predicted secondary folding of GAM336926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336926 folded precursor RNA yielding a GAM336926 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336926 RNA, hereby incorporated herein. Expression of GAM336926 RNA was experimentally validated in HeLa cells using the methods

described with reference to Figs.22 to 24.

GAM336926 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336926 target RNA, herein designated GAM TARGET RNA.

GAM336926 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336926 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336926 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336926 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336926 RNA, herein designated GAM RNA, to target binding sites on GAM336926 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336926 target RNA into GAM336926 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336926 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336926 target genes. The mRNA of each one of this plurality of GAM336926 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336926 RNA, herein designated GAM RNA, and which when bound by GAM336926 RNA causes inhibition of translation of the GAM336926 target mRNA into a corresponding GAM336926 target protein.

The mechanism of the translational inhibition exerted by GAM336926 RNA, herein designated GAM RNA, on one or more GAM336926 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336926 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336926 RNA, herein designated GAM RNA, of GAM336926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336926 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336926 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336926 RNA correlate with, and may be deduced from, the identity of the GAM336926 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336927 7300 TTCCATTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCATTGCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AAGATCTCTG Messenger 336927 (GAM336927) oligonucleotides modulates expression of respective target
CTGATGCTCC genes whose function and utility is known in the art.

TGGAGAATGA GAM336927 is a novel bioinformatically detectable regulatory, non protein
CTTTGGGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336927 was detected
TTTAGAAAGA is described with additional reference to Figs. 9-15.

ATATTGCCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCCGTCTCGG encoded by the human genome.

CAAGGAGATG GAM336927 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ATGGGA GAM336927 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336927 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336927 precursor RNA is designated SEQ ID:7300, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7300 is located from position 57662274 to position 57662379 relative to chromosome 20 on the `+` strand.

GAM336927 precursor RNA folds onto itself, forming GAM336927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336927 precursor RNA, designated SEQ ID NO: 7300, and a schematic representation of a predicted secondary folding of GAM336927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336927 folded precursor RNA yielding a GAM336927 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336927 RNA, hereby incorporated herein.

GAM336927 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336927 target RNA, herein designated GAM TARGET RNA.

GAM336927 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336927 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336927 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336927 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336927 RNA, herein designated GAM RNA, to target binding sites on GAM336927 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336927 target RNA into GAM336927 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336927 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336927 target genes. The mRNA of each one of this plurality of GAM336927 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336927 RNA, herein designated GAM RNA, and which when bound by GAM336927 RNA causes inhibition of translation of the GAM336927 target mRNA into a corresponding GAM336927 target protein.

The mechanism of the translational inhibition exerted by GAM336927 RNA, herein designated GAM RNA, on one or more GAM336927 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336927 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336927 RNA, herein designated GAM RNA, of GAM336927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336927 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336927 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336927 RNA correlate with, and may be deduced from, the identity of the GAM336927 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336931 6649 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 336931 (GAM336931) oligonucleotides modulates expression of respective target

TGGTGGTGAG genes whose function and utility is known in the art.

CCGAGATTGT GAM336931 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336931 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAAACTCC encoded by the human genome.

GAM336931 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336931 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336931 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336931 precursor RNA is designated SEQ ID:6649, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6649 is located from position 57796024 to position 57796113 relative to chromosome 19 on the `+` strand.

GAM336931 precursor RNA folds onto itself, forming GAM336931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336931 precursor RNA, designated SEQ ID NO: 6649, and a schematic representation of a predicted secondary folding of GAM336931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336931 folded precursor RNA yielding a GAM336931 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336931 RNA, hereby incorporated herein. Expression of GAM336931 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336931 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336931 target RNA, herein designated GAM TARGET RNA.

GAM336931 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336931 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336931 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336931 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336931 RNA, herein designated GAM RNA, to target binding sites on GAM336931 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336931 target RNA into GAM336931 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336931 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336931 target genes. The mRNA of each one of this plurality of GAM336931 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336931 RNA, herein designated GAM RNA, and which when bound by GAM336931 RNA causes inhibition of

translation of the GAM336931 target mRNA into a corresponding GAM336931 target protein.

The mechanism of the translational inhibition exerted by GAM336931 RNA, herein designated GAM RNA, on one or more GAM336931 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336931 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336931 RNA, herein designated GAM RNA, of GAM336931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336931 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336931 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336931 RNA correlate with, and may be deduced from, the identity of the GAM336931 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336932 6175 CTCTCTTTGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTACAGACTT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTCAGGCT Messenger 336932 (GAM336932) oligonucleotides modulates expression of respective target
GGCTGGAGAG genes whose function and utility is known in the art.

TAAATCAGGT GAM336932 is a novel bioinformatically detectable regulatory, non protein
CTAAAAGAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336932 was detected
CTCCTTCATA is described with additional reference to Figs. 9-15.

ACAGGCTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATACTCCCA encoded by the human genome.

GCAATCTGAA GAM336932 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCCGGAGAGA GAM336932 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

G GAM336932 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336932 precursor RNA is designated SEQ ID:6175, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6175 is located from position 58065317 to position 58065427 relative to chromosome 14 on the `+` strand.

GAM336932 precursor RNA folds onto itself, forming GAM336932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336932 precursor RNA, designated SEQ ID NO: 6175, and a schematic representation of a predicted secondary folding of GAM336932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336932 folded precursor RNA yielding a GAM336932 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336932 RNA, hereby incorporated herein.

GAM336932 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336932 target RNA, herein designated GAM TARGET RNA.

GAM336932 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336932 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336932 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336932 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336932 RNA, herein designated GAM RNA, to target binding sites on GAM336932 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336932 target RNA

into GAM336932 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336932 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336932 target genes. The mRNA of each one of this plurality of GAM336932 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336932 RNA, herein designated GAM RNA, and which when bound by GAM336932 RNA causes inhibition of translation of the GAM336932 target mRNA into a corresponding GAM336932 target protein.

The mechanism of the translational inhibition exerted by GAM336932 RNA, herein designated GAM RNA, on one or more GAM336932 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336932 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336932 RNA, herein designated GAM RNA, of GAM336932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336932 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336932 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336932 RNA correlate with, and may be deduced from, the identity of the GAM336932 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336933 6290 GAAGAACTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGATCTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAATCTGTG Messenger 336933 (GAM336933) oligonucleotides modulates expression of respective target

GACCCTACAT genes whose function and utility is known in the art.

TGGCACTTAG GAM336933 is a novel bioinformatically detectable regulatory, non protein

TGTGTACCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336933 was detected

AGGGCTAACG is described with additional reference to Figs. 9-15.

TCCCAAATAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTCATTCAG encoded by the human genome.

TGCTTT GAM336933 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336933 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336933 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336933 precursor RNA is designated SEQ ID:6290, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6290 is located from position 58083077 to position 58083172 relative to chromosome 17 on the `+` strand.

GAM336933 precursor RNA folds onto itself, forming GAM336933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336933 precursor RNA, designated SEQ ID NO: 6290, and a schematic representation of a predicted secondary folding of GAM336933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336933 folded precursor RNA yielding a GAM336933 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336933 RNA, hereby incorporated herein. Expression of GAM336933 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336933 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336933 target RNA, herein designated GAM TARGET RNA.

GAM336933 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336933 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336933 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336933 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336933 RNA, herein designated GAM RNA, to target binding sites on GAM336933 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336933 target RNA into GAM336933 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336933 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336933 target genes. The mRNA of each one of this plurality of GAM336933 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336933 RNA, herein designated GAM RNA, and which when bound by GAM336933 RNA causes inhibition of translation of the GAM336933 target mRNA into a corresponding GAM336933 target protein.

The mechanism of the translational inhibition exerted by GAM336933 RNA, herein designated GAM RNA, on one or more GAM336933 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336933 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336933 RNA, herein designated GAM RNA, of GAM336933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336933 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336933 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336933 RNA correlate with, and may be deduced from, the identity of the GAM336933 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336934 7170 TGAGGCCGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCTAGAG Messenger 336934 (GAM336934) oligonucleotides modulates expression of respective target
GCAGGTTGCA genes whose function and utility is known in the art.

GTGAGCCCAG GAM336934 is a novel bioinformatically detectable regulatory, non protein
ATTGCATCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336934 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAGAGGGA encoded by the human genome.

GACTCCATCT GAM336934 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336934 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336934 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336934 precursor RNA is designated SEQ ID:7170, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7170 is located from position 58103929 to position 58104030 relative to chromosome 17 on the `+` strand.

GAM336934 precursor RNA folds onto itself, forming GAM336934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336934 precursor RNA, designated SEQ ID NO: 7170, and a schematic representation of a predicted secondary folding of GAM336934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336934 folded precursor RNA yielding a GAM336934 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336934 RNA, hereby incorporated herein. Expression of GAM336934 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336934 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336934 target RNA, herein designated GAM TARGET RNA.

GAM336934 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336934 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336934 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336934 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336934 RNA, herein designated GAM RNA, to target binding sites on GAM336934 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336934 target RNA into GAM336934 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336934 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336934 target genes. The mRNA of each one of this plurality of GAM336934 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336934 RNA, herein designated GAM RNA, and which when bound by GAM336934 RNA causes inhibition of translation of the GAM336934 target mRNA into a corresponding GAM336934 target protein.

The mechanism of the translational inhibition exerted by GAM336934 RNA, herein designated GAM RNA, on one or more GAM336934 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336934 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336934 RNA, herein designated GAM RNA, of GAM336934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336934 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336934 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336934 RNA correlate with, and may be deduced from, the identity of the GAM336934 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336937 5956 ATCATCAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTAGATTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CATAAGGAGC Messenger 336937 (GAM336937) oligonucleotides modulates expression of respective target
ACACAACCTA genes whose function and utility is known in the art.

GATTGCTAGC GAM336937 is a novel bioinformatically detectable regulatory, non protein
AGGCACAGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336937 was detected
CACAATAGGG is described with additional reference to Figs. 9-15.

TTCGTTCTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTGAGAATG encoded by the human genome.

GCATGCCGCT GAM336937 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCTGAT GAM336937 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336937 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336937 precursor RNA is designated SEQ ID:5956, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5956 is located from position 58596055 to position 58596160 relative to chromosome 17 on the `+` strand.

GAM336937 precursor RNA folds onto itself, forming GAM336937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336937 precursor RNA, designated SEQ ID NO: 5956, and a schematic representation of a predicted secondary folding of GAM336937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336937 folded precursor RNA yielding a GAM336937 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336937 RNA, hereby incorporated herein.

GAM336937 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336937 target RNA, herein designated GAM TARGET RNA.

GAM336937 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336937 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336937 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336937 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336937 RNA, herein designated GAM RNA, to target binding sites on GAM336937 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336937 target RNA into GAM336937 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336937 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336937 target genes. The mRNA of each one of this plurality of GAM336937 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336937 RNA, herein designated GAM RNA, and which when bound by GAM336937 RNA causes inhibition of translation of the GAM336937 target mRNA into a corresponding GAM336937 target protein.

The mechanism of the translational inhibition exerted by GAM336937 RNA, herein designated GAM RNA, on one or more GAM336937 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336937 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336937 RNA, herein designated GAM RNA, of

GAM336937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336937 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336937 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336937 RNA correlate with, and may be deduced from, the identity of the GAM336937 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336938 6742 GGCATTAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTCATAAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCACACAAC Messenger 336938 (GAM336938) oligonucleotides modulates expression of respective target

CTAGATTGCT genes whose function and utility is known in the art.

AGCAGGCACA GAM336938 is a novel bioinformatically detectable regulatory, non protein

GTTCACAATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336938 was detected

GGGTTCGTTC is described with additional reference to Figs. 9-15.

TCCTGTGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGGCATGCC encoded by the human genome.

GAM336938 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336938 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336938 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336938 precursor RNA is designated SEQ ID:6742, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6742 is located from position 58596062 to position 58596151 relative to chromosome 17 on the `+` strand.

GAM336938 precursor RNA folds onto itself, forming GAM336938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336938 precursor RNA, designated SEQ ID NO: 6742, and

a schematic representation of a predicted secondary folding of GAM336938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336938 folded precursor RNA yielding a GAM336938 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336938 RNA, hereby incorporated herein.

GAM336938 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336938 target RNA, herein designated GAM TARGET RNA.

GAM336938 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336938 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336938 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336938 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336938 RNA, herein designated GAM RNA, to target binding sites on GAM336938 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336938 target RNA into GAM336938 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336938 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336938 target genes. The mRNA of each one of this plurality of GAM336938 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336938 RNA, herein designated GAM RNA, and which when bound by GAM336938 RNA causes inhibition of translation of the GAM336938 target mRNA into a corresponding GAM336938 target protein.

The mechanism of the translational inhibition exerted by GAM336938 RNA, herein designated GAM RNA, on one or more GAM336938 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336938 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336938 RNA, herein designated GAM RNA, of GAM336938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336938 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336938 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336938 RNA correlate with, and may be deduced from, the identity of the GAM336938 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336939 6885 GTCTAGGTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GATAATTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTCATTTCT Messenger 336939 (GAM336939) oligonucleotides modulates expression of respective target

TTCATGGACA genes whose function and utility is known in the art.

TGGTGACTCT GAM336939 is a novel bioinformatically detectable regulatory, non protein

TTTCTTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336939 was detected

TCCTTAAGGA is described with additional reference to Figs. 9-15.

GAAAAGCCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGACACTACA encoded by the human genome.

AAATCTTTGA GAM336939 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGTTTGAAGT GAM336939 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GGGAACTAGG GAM336939 precursor RNA does not encode a protein. A nucleotide sequence identical or

AGATTCAGGC highly similar to the nucleotide sequence of GAM336939 precursor RNA is designated SEQ

ID:6885, and is provided hereinbelow with reference to the sequence listing part.
Nucleotide sequence SEQ ID:6885 is located from position 58665635 to position 58665764 relative to chromosome 12 on the `+` strand.

GAM336939 precursor RNA folds onto itself, forming GAM336939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336939 precursor RNA, designated SEQ ID NO: 6885, and a schematic representation of a predicted secondary folding of GAM336939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336939 folded precursor RNA yielding a GAM336939 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336939 RNA, hereby incorporated herein.

GAM336939 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336939 target RNA, herein designated GAM TARGET RNA.

GAM336939 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336939 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336939 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336939 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336939 RNA, herein designated GAM RNA, to target binding sites on GAM336939 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336939 target RNA into GAM336939 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336939 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336939 target genes. The mRNA of each one of this

plurality of GAM336939 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336939 RNA, herein designated GAM RNA, and which when bound by GAM336939 RNA causes inhibition of translation of the GAM336939 target mRNA into a corresponding GAM336939 target protein.

The mechanism of the translational inhibition exerted by GAM336939 RNA, herein designated GAM RNA, on one or more GAM336939 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336939 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336939 RNA, herein designated GAM RNA, of GAM336939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336939 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336939 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336939 RNA correlate with, and may be deduced from, the identity of the GAM336939 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336941 5874 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336941 (GAM336941) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336941 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336941 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336941 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336941 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336941 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336941 precursor RNA is designated SEQ ID:5874, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5874 is located from position 59119812 to position 59119893 relative to chromosome 4 on the `-` strand.

GAM336941 precursor RNA folds onto itself, forming GAM336941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336941 precursor RNA, designated SEQ ID NO: 5874, and a schematic representation of a predicted secondary folding of GAM336941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336941 folded precursor RNA yielding a GAM336941 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336941 RNA, hereby incorporated herein.

GAM336941 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336941 target RNA, herein designated GAM TARGET RNA.

GAM336941 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336941 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336941 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336941 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336941 RNA, herein designated GAM RNA, to target binding sites on GAM336941 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336941 target RNA into GAM336941 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336941 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336941 target genes. The mRNA of each one of this plurality of GAM336941 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336941 RNA, herein designated GAM RNA, and which when bound by GAM336941 RNA causes inhibition of translation of the GAM336941 target mRNA into a corresponding GAM336941 target protein.

The mechanism of the translational inhibition exerted by GAM336941 RNA, herein designated GAM RNA, on one or more GAM336941 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336941 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336941 RNA, herein designated GAM RNA, of GAM336941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336941 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336941 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336941 RNA correlate with, and may be deduced from, the identity of the GAM336941 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336942 7242 TGGGGTACTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAGTCAAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTTGGCTGT Messenger 336942 (GAM336942) oligonucleotides modulates expression of respective target
CAGCCCTGAG genes whose function and utility is known in the art.

TCTGCCTCAA GAM336942 is a novel bioinformatically detectable regulatory, non protein
CCTCCAAGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336942 was detected
TCATAGCCAC is described with additional reference to Figs. 9-15.

GGCTTCACCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGTGCCTC encoded by the human genome.

A GAM336942 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336942 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336942 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336942 precursor RNA is designated SEQ ID:7242, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7242 is located from position 59207699 to position 59207789 relative to chromosome 11 on the `+` strand.

GAM336942 precursor RNA folds onto itself, forming GAM336942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336942 precursor RNA, designated SEQ ID NO: 7242, and a schematic representation of a predicted secondary folding of GAM336942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336942 folded precursor RNA yielding a GAM336942 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336942 RNA, hereby incorporated herein.

GAM336942 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336942 target RNA, herein designated GAM TARGET RNA.

GAM336942 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336942 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336942 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336942 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336942 RNA, herein designated GAM RNA, to target binding sites on GAM336942 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336942 target RNA into GAM336942 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336942 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336942 target genes. The mRNA of each one of this plurality of GAM336942 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336942 RNA, herein designated GAM RNA, and which when bound by GAM336942 RNA causes inhibition of translation of the GAM336942 target mRNA into a corresponding GAM336942 target protein.

The mechanism of the translational inhibition exerted by GAM336942 RNA, herein designated GAM RNA, on one or more GAM336942 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336942 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336942 RNA, herein designated GAM RNA, of GAM336942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336942 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336942 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336942 RNA correlate with, and may be deduced from, the identity of the GAM336942 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336945 6236 CTGTAATTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCACTTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GATGCCGAGT Messenger 336945 (GAM336945) oligonucleotides modulates expression of respective target

TGAGAGGATC genes whose function and utility is known in the art.

ACTTGAAGCC GAM336945 is a novel bioinformatically detectable regulatory, non protein
GGGAATTTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336945 was detected
GGCTGCAGTG is described with additional reference to Figs. 9-15.

AGCTATGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATGCCGGTGT encoded by the human genome.

ACTTCAGTCT GAM336945 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGGCAACAG GAM336945 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336945 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336945 precursor RNA is designated SEQ ID:6236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6236 is located from position 59990343 to position 59990451 relative to chromosome 18 on the `+` strand.

GAM336945 precursor RNA folds onto itself, forming GAM336945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336945 precursor RNA, designated SEQ ID NO: 6236, and a schematic representation of a predicted secondary folding of GAM336945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336945 folded precursor RNA yielding a GAM336945 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336945 RNA, hereby incorporated herein.

GAM336945 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336945 target RNA, herein designated GAM TARGET RNA.

GAM336945 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336945 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM336945 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336945 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336945 RNA, herein designated GAM RNA, to target binding sites on GAM336945 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336945 target RNA into GAM336945 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336945 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336945 target genes. The mRNA of each one of this plurality of GAM336945 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336945 RNA, herein designated GAM RNA, and which when bound by GAM336945 RNA causes inhibition of translation of the GAM336945 target mRNA into a corresponding GAM336945 target protein.

The mechanism of the translational inhibition exerted by GAM336945 RNA, herein designated GAM RNA, on one or more GAM336945 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336945 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336945 RNA, herein designated GAM RNA, of GAM336945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336945 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336945 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336945 RNA correlate with, and may be deduced from, the identity of the GAM336945 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336946 5823 AGTTCCCACG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCATGGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTAGTTTTT Messenger 336946 (GAM336946) oligonucleotides modulates expression of respective target
CCCACATTCC genes whose function and utility is known in the art.

TCTTAGGAGC GAM336946 is a novel bioinformatically detectable regulatory, non protein
TGTGCCTAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336946 was detected
ATGCTGCGCT is described with additional reference to Figs. 9-15.

AGCAACCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTATTGTGAA encoded by the human genome.

GGAACT GAM336946 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336946 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336946 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336946 precursor RNA is designated SEQ ID:5823, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5823 is located from position 60087508 to position 60087603 relative to chromosome 20 on the `+` strand.

GAM336946 precursor RNA folds onto itself, forming GAM336946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336946 precursor RNA, designated SEQ ID NO: 5823, and a schematic representation of a predicted secondary folding of GAM336946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336946 folded precursor RNA yielding a GAM336946 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336946 RNA, hereby incorporated herein.

GAM336946 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336946 target RNA, herein designated GAM TARGET RNA.

GAM336946 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336946 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336946 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336946 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336946 RNA, herein designated GAM RNA, to target binding sites on GAM336946 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336946 target RNA into GAM336946 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336946 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336946 target genes. The mRNA of each one of this plurality of GAM336946 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336946 RNA, herein designated GAM RNA, and which when bound by GAM336946 RNA causes inhibition of translation of the GAM336946 target mRNA into a corresponding GAM336946 target protein.

The mechanism of the translational inhibition exerted by GAM336946 RNA, herein designated GAM RNA, on one or more GAM336946 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336946 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336946 RNA, herein designated GAM RNA, of GAM336946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336946 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336946 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336946 RNA correlate with, and may be deduced from, the identity of the GAM336946 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336947 7045 TCCTTCAGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATGATGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGTGGTCT Messenger 336947 (GAM336947) oligonucleotides modulates expression of respective target
TGTTCAGGAA genes whose function and utility is known in the art.

TTTACAAACT GAM336947 is a novel bioinformatically detectable regulatory, non protein
AGAGGAAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336947 was detected
TTATCTCACC is described with additional reference to Figs. 9-15.

AAGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336947 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336947 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336947 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336947 precursor RNA is designated SEQ ID:7045, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7045 is located from position 60363185 to position 60363260 relative to chromosome 15 on the `+` strand.

GAM336947 precursor RNA folds onto itself, forming GAM336947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336947 precursor RNA, designated SEQ ID NO: 7045, and a schematic representation of a predicted secondary folding of GAM336947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336947 folded precursor

RNA yielding a GAM336947 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336947 RNA, hereby incorporated herein.

GAM336947 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336947 target RNA, herein designated GAM TARGET RNA.

GAM336947 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336947 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336947 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336947 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336947 RNA, herein designated GAM RNA, to target binding sites on GAM336947 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336947 target RNA into GAM336947 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336947 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336947 target genes. The mRNA of each one of this plurality of GAM336947 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336947 RNA, herein designated GAM RNA, and which when bound by GAM336947 RNA causes inhibition of translation of the GAM336947 target mRNA into a corresponding GAM336947 target protein.

The mechanism of the translational inhibition exerted by GAM336947 RNA, herein designated GAM RNA, on one or more GAM336947 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336947 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336947 RNA, herein designated GAM RNA, of GAM336947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336947 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336947 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336947 RNA correlate with, and may be deduced from, the identity of the GAM336947 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336950 5875 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336950 (GAM336950) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336950 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336950 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336950 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336950 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336950 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336950 precursor RNA is designated SEQ ID:5875, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5875 is located from position 60746489 to position 60746570 relative to chromosome 17 on the `-` strand.

GAM336950 precursor RNA folds onto itself, forming GAM336950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336950 precursor RNA, designated SEQ ID NO: 5875, and a schematic representation of a predicted secondary folding of GAM336950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336950 folded precursor RNA yielding a GAM336950 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336950 RNA, hereby incorporated herein.

GAM336950 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336950 target RNA, herein designated GAM TARGET RNA.

GAM336950 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336950 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336950 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336950 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336950 RNA, herein designated GAM RNA, to target binding sites on GAM336950 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336950 target RNA into GAM336950 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336950 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336950 target genes. The mRNA of each one of this plurality of GAM336950 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336950 RNA, herein designated GAM RNA, and which when bound by GAM336950 RNA causes inhibition of translation of the GAM336950 target mRNA into a corresponding GAM336950 target protein.

The mechanism of the translational inhibition exerted by GAM336950 RNA, herein designated GAM RNA, on one or more GAM336950 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336950 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336950 RNA, herein designated GAM RNA, of GAM336950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336950 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336950 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336950 RNA correlate with, and may be deduced from, the identity of the GAM336950 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336951 6166 CTCCCCCGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGTCAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTTGAAGCT Messenger 336951 (GAM336951) oligonucleotides modulates expression of respective target

GCGGTCTGTC genes whose function and utility is known in the art.

TATGCTGGTC GAM336951 is a novel bioinformatically detectable regulatory, non protein

GTACCCTCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336951 was detected

AGCCTAAGAT is described with additional reference to Figs. 9-15.

GACACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCAGGAAATG encoded by the human genome.

AACACCCTCG GAM336951 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAGGGGG GAM336951 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336951 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336951 precursor RNA is designated SEQ ID:6166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6166 is located from position 60952390 to position 60952496 relative to chromosome 11 on the `+` strand.

GAM336951 precursor RNA folds onto itself, forming GAM336951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336951 precursor RNA, designated SEQ ID NO: 6166, and a schematic representation of a predicted secondary folding of GAM336951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336951 folded precursor RNA yielding a GAM336951 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336951 RNA, hereby incorporated herein.

GAM336951 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336951 target RNA, herein designated GAM TARGET RNA.

GAM336951 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336951 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336951 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336951 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336951 RNA, herein designated GAM RNA, to target binding sites on GAM336951 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336951 target RNA into GAM336951 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336951 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336951 target genes. The mRNA of each one of this

plurality of GAM336951 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336951 RNA, herein designated GAM RNA, and which when bound by GAM336951 RNA causes inhibition of translation of the GAM336951 target mRNA into a corresponding GAM336951 target protein.

The mechanism of the translational inhibition exerted by GAM336951 RNA, herein designated GAM RNA, on one or more GAM336951 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336951 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336951 RNA, herein designated GAM RNA, of GAM336951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336951 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336951 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336951 RNA correlate with, and may be deduced from, the identity of the GAM336951 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336956 7186 TGAGTAAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTGGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTTTGAGAG Messenger 336956 (GAM336956) oligonucleotides modulates expression of respective target

ACATCGTAAT genes whose function and utility is known in the art.

GGCTGTCCAC GAM336956 is a novel bioinformatically detectable regulatory, non protein

CACAGTCTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336956 was detected

CTCCGTCCCC is described with additional reference to Figs. 9-15.

ACCTCCCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GATTCA encoded by the human genome.

GAM336956 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336956 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336956 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336956 precursor RNA is designated SEQ ID:7186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7186 is located from position 61750038 to position 61750123 relative to chromosome 19 on the `+` strand.

GAM336956 precursor RNA folds onto itself, forming GAM336956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336956 precursor RNA, designated SEQ ID NO: 7186, and a schematic representation of a predicted secondary folding of GAM336956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336956 folded precursor RNA yielding a GAM336956 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336956 RNA, hereby incorporated herein.

GAM336956 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336956 target RNA, herein designated GAM TARGET RNA.

GAM336956 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336956 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336956 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336956 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336956 RNA, herein designated GAM RNA, to target binding sites on GAM336956 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336956 target RNA into GAM336956 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336956 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336956 target genes. The mRNA of each one of this plurality of GAM336956 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336956 RNA, herein designated GAM RNA, and which when bound by GAM336956 RNA causes inhibition of translation of the GAM336956 target mRNA into a corresponding GAM336956 target protein.

The mechanism of the translational inhibition exerted by GAM336956 RNA, herein designated GAM RNA, on one or more GAM336956 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336956 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336956 RNA, herein designated GAM RNA, of GAM336956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336956 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336956 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336956 RNA correlate with, and may be deduced from, the identity of the GAM336956 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336957 5660 AAGACGGCAA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATATTCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGAAGGAGG Messenger 336957 (GAM336957) oligonucleotides modulates expression of respective target
TATAATGGGG genes whose function and utility is known in the art.

AAACACATTT GAM336957 is a novel bioinformatically detectable regulatory, non protein
ATTTTCCCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336957 was detected
TTTAAACTTC is described with additional reference to Figs. 9-15.

CCTGCTGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGTCTTTGC encoded by the human genome.

CTTCTT GAM336957 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336957 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336957 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336957 precursor RNA is designated SEQ ID:5660, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5660 is located from position 61814814 to position 61814909 relative to chromosome 11 on the `-` strand.

GAM336957 precursor RNA folds onto itself, forming GAM336957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336957 precursor RNA, designated SEQ ID NO: 5660, and a schematic representation of a predicted secondary folding of GAM336957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336957 folded precursor RNA yielding a GAM336957 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336957 RNA, hereby incorporated herein.

GAM336957 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336957 target RNA, herein designated GAM TARGET RNA.

GAM336957 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336957 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336957 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336957 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336957 RNA, herein designated GAM RNA, to target binding sites on GAM336957 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336957 target RNA into GAM336957 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336957 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336957 target genes. The mRNA of each one of this plurality of GAM336957 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336957 RNA, herein designated GAM RNA, and which when bound by GAM336957 RNA causes inhibition of translation of the GAM336957 target mRNA into a corresponding GAM336957 target protein.

The mechanism of the translational inhibition exerted by GAM336957 RNA, herein designated GAM RNA, on one or more GAM336957 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336957 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336957 RNA, herein designated GAM RNA, of GAM336957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336957 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336957 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336957 RNA correlate with, and may be deduced from, the identity of the GAM336957 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336958 6283 GAAATCCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTTGCAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGCCAGCCT Messenger 336958 (GAM336958) oligonucleotides modulates expression of respective target
GTGTGATCAA genes whose function and utility is known in the art.

TCCTGCGGTT GAM336958 is a novel bioinformatically detectable regulatory, non protein
AGGAAGGTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336958 was detected
AGTTTTGCTT is described with additional reference to Figs. 9-15.

TCCCATCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TC encoded by the human genome.

GAM336958 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336958 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336958 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336958 precursor RNA is designated SEQ ID:6283, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6283 is located from position 61985320 to position 61985401 relative to chromosome 11 on the `-` strand.

GAM336958 precursor RNA folds onto itself, forming GAM336958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336958 precursor RNA, designated SEQ ID NO: 6283, and a schematic representation of a predicted secondary folding of GAM336958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336958 folded precursor RNA yielding a GAM336958 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336958 RNA, hereby incorporated herein.

GAM336958 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336958 target RNA, herein designated GAM TARGET RNA.

GAM336958 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336958 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336958 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336958 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336958 RNA, herein designated GAM RNA, to target binding sites on GAM336958 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336958 target RNA into GAM336958 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336958 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336958 target genes. The mRNA of each one of this plurality of GAM336958 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336958 RNA, herein designated GAM RNA, and which when bound by GAM336958 RNA causes inhibition of translation of the GAM336958 target mRNA into a corresponding GAM336958 target protein.

The mechanism of the translational inhibition exerted by GAM336958 RNA, herein designated GAM RNA, on one or more GAM336958 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336958 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336958 RNA, herein designated GAM RNA, of GAM336958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336958 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336958 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336958 RNA correlate with, and may be deduced from, the identity of the GAM336958 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336959 5876 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336959 (GAM336959) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336959 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336959 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336959 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336959 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336959 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336959 precursor RNA is designated SEQ ID:5876, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5876 is located from position 62004748 to position 62004829 relative to chromosome X on the `+` strand.

GAM336959 precursor RNA folds onto itself, forming GAM336959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336959 precursor RNA, designated SEQ ID NO: 5876, and a schematic representation of a predicted secondary folding of GAM336959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336959 folded precursor RNA yielding a GAM336959 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336959 RNA, hereby incorporated herein.

GAM336959 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336959 target RNA, herein designated GAM TARGET RNA.

GAM336959 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336959 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336959 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336959 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336959 RNA, herein designated GAM RNA, to target binding sites on GAM336959 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336959 target RNA into GAM336959 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336959 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336959 target genes. The mRNA of each one of this plurality of GAM336959 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336959 RNA, herein designated GAM RNA, and which when bound by GAM336959 RNA causes inhibition of translation of the GAM336959 target mRNA into a corresponding GAM336959 target protein.

The mechanism of the translational inhibition exerted by GAM336959 RNA, herein designated GAM RNA, on one or more GAM336959 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336959 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336959 RNA, herein designated GAM RNA, of GAM336959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM336959 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336959 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336959 RNA correlate with, and may be deduced from, the identity of the GAM336959 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336961 5948 ATAAGCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTAATTGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAATTCACA Messenger 336961 (GAM336961) oligonucleotides modulates expression of respective target
TGTGGTTGTA genes whose function and utility is known in the art.

TGCAGCTTTA GAM336961 is a novel bioinformatically detectable regulatory, non protein
CTGGGAGACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336961 was detected
GAAGTGTATC is described with additional reference to Figs. 9-15.

TGCATGTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTGCTGTGA encoded by the human genome.

TGGACACTTG GAM336961 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TAAGTTTGT GAM336961 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336961 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336961 precursor RNA is designated SEQ ID:5948, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5948 is located from position 62131101 to position 62131209 relative to chromosome 9 on the `-` strand.

GAM336961 precursor RNA folds onto itself, forming GAM336961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336961 precursor RNA, designated SEQ ID NO: 5948, and a schematic representation of a predicted secondary folding of GAM336961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336961 folded precursor RNA yielding a GAM336961 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336961 RNA, hereby incorporated herein.

GAM336961 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336961 target RNA, herein designated GAM TARGET RNA.

GAM336961 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336961 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336961 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336961 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336961 RNA, herein designated GAM RNA, to target binding sites on GAM336961 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336961 target RNA into GAM336961 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336961 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336961 target genes. The mRNA of each one of this plurality of GAM336961 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336961 RNA, herein designated GAM RNA, and which when bound by GAM336961 RNA causes inhibition of translation of the GAM336961 target mRNA into a corresponding GAM336961 target protein.

The mechanism of the translational inhibition exerted by GAM336961 RNA, herein designated GAM RNA, on one or more GAM336961 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336961 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336961 RNA, herein designated GAM RNA, of GAM336961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336961 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336961 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336961 RNA correlate with, and may be deduced from, the identity of the GAM336961 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336962 6960 TACATGTGTT ACACTCAGTG TGTAAATAAC TGTGAAGAGG CAATTGTCAG ATAGCAAATT GGGCACCTGC TGTGTACGGT ATATTGCACT GGGGCTGACG GGTGTG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 336962 (GAM336962) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM336962 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336962 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM336962 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336962 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM336962 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336962 precursor RNA is designated SEQ ID:6960, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6960 is located from position 62164421 to position 62164526 relative to chromosome 20 on the `-` strand.

GAM336962 precursor RNA folds onto itself, forming GAM336962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336962 precursor RNA, designated SEQ ID NO: 6960, and a schematic representation of a predicted secondary folding of GAM336962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336962 folded precursor RNA yielding a GAM336962 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336962 RNA, hereby incorporated herein.

GAM336962 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336962 target RNA, herein designated GAM TARGET RNA.

GAM336962 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336962 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336962 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336962 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336962 RNA, herein designated GAM RNA, to target binding sites on GAM336962 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336962 target RNA into GAM336962 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336962 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336962 target genes. The mRNA of each one of this plurality of GAM336962 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336962 RNA, herein designated GAM RNA, and which when bound by GAM336962 RNA causes inhibition of translation of the GAM336962 target mRNA into a corresponding GAM336962 target protein.

The mechanism of the translational inhibition exerted by GAM336962 RNA, herein

designated GAM RNA, on one or more GAM336962 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336962 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336962 RNA, herein designated GAM RNA, of GAM336962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336962 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336962 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336962 RNA correlate with, and may be deduced from, the identity of the GAM336962 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336963 7286 TTAGCCTCCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGATGTCCTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGCTAGTTT Messenger 336963 (GAM336963) oligonucleotides modulates expression of respective target
TAGCTGTTTT genes whose function and utility is known in the art.

CAGGTGTTGA GAM336963 is a novel bioinformatically detectable regulatory, non protein
TAAAAGCTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336963 was detected
AGGAGCTGGC is described with additional reference to Figs. 9-15.

AGGAGGAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGGAAGC encoded by the human genome.

TAG GAM336963 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336963 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336963 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336963 precursor RNA is designated SEQ ID:7286, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7286 is located from position 62264330 to position 62264422

relative to chromosome 8 on the `-` strand.

GAM336963 precursor RNA folds onto itself, forming GAM336963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336963 precursor RNA, designated SEQ ID NO: 7286, and a schematic representation of a predicted secondary folding of GAM336963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336963 folded precursor RNA yielding a GAM336963 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336963 RNA, hereby incorporated herein.

GAM336963 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336963 target RNA, herein designated GAM TARGET RNA.

GAM336963 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336963 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336963 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336963 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336963 RNA, herein designated GAM RNA, to target binding sites on GAM336963 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336963 target RNA into GAM336963 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336963 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336963 target genes. The mRNA of each one of this plurality of GAM336963 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336963 RNA, herein designated GAM RNA, and which when bound by GAM336963 RNA causes inhibition of translation of the GAM336963 target mRNA into a corresponding GAM336963 target protein.

The mechanism of the translational inhibition exerted by GAM336963 RNA, herein designated GAM RNA, on one or more GAM336963 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336963 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336963 RNA, herein designated GAM RNA, of GAM336963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336963 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336963 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336963 RNA correlate with, and may be deduced from, the identity of the GAM336963 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336964 5877 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336964 (GAM336964) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336964 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336964 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336964 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336964 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336964 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336964 precursor RNA is designated SEQ ID:5877, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5877 is located from position 62270288 to position 62270369 relative to chromosome 5 on the `+` strand.

GAM336964 precursor RNA folds onto itself, forming GAM336964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336964 precursor RNA, designated SEQ ID NO: 5877, and a schematic representation of a predicted secondary folding of GAM336964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336964 folded precursor RNA yielding a GAM336964 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336964 RNA, hereby incorporated herein.

GAM336964 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336964 target RNA, herein designated GAM TARGET RNA.

GAM336964 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336964 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336964 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336964 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336964 RNA, herein designated GAM RNA, to target

binding sites on GAM336964 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336964 target RNA into GAM336964 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336964 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336964 target genes. The mRNA of each one of this plurality of GAM336964 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336964 RNA, herein designated GAM RNA, and which when bound by GAM336964 RNA causes inhibition of translation of the GAM336964 target mRNA into a corresponding GAM336964 target protein.

The mechanism of the translational inhibition exerted by GAM336964 RNA, herein designated GAM RNA, on one or more GAM336964 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336964 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336964 RNA, herein designated GAM RNA, of GAM336964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336964 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336964 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336964 RNA correlate with, and may be deduced from, the identity of the GAM336964 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336965 6277 CTTTTTCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTGAACGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGACTTGACA Messenger 336965 (GAM336965) oligonucleotides modulates expression of respective target

GAGGTACATA genes whose function and utility is known in the art.

GGAGGCTACT GAM336965 is a novel bioinformatically detectable regulatory, non protein

TGTTCTCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336965 was detected

TTGGCTGCTT is described with additional reference to Figs. 9-15.

GTATTTGCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCTGGAAGGT encoded by the human genome.

TATTGTTTTC GAM336965 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAGGATCTTA GAM336965 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AG GAM336965 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336965 precursor RNA is designated SEQ ID:6277, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6277 is located from position 62330677 to position 62330788 relative to chromosome 14 on the `+` strand.

GAM336965 precursor RNA folds onto itself, forming GAM336965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336965 precursor RNA, designated SEQ ID NO: 6277, and a schematic representation of a predicted secondary folding of GAM336965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336965 folded precursor RNA yielding a GAM336965 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336965 RNA, hereby incorporated herein.

GAM336965 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336965 target RNA, herein designated GAM TARGET RNA.

GAM336965 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336965 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336965 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336965 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336965 RNA, herein designated GAM RNA, to target binding sites on GAM336965 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336965 target RNA into GAM336965 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336965 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336965 target genes. The mRNA of each one of this plurality of GAM336965 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336965 RNA, herein designated GAM RNA, and which when bound by GAM336965 RNA causes inhibition of translation of the GAM336965 target mRNA into a corresponding GAM336965 target protein.

The mechanism of the translational inhibition exerted by GAM336965 RNA, herein designated GAM RNA, on one or more GAM336965 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336965 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336965 RNA, herein designated GAM RNA, of GAM336965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336965 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336965 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336965 RNA correlate with, and may be deduced from, the identity of the GAM336965 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336966 7038 TCCTCCAGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AACGGTGACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGACAGAGGT Messenger 336966 (GAM336966) oligonucleotides modulates expression of respective target
ACATAGGAGG genes whose function and utility is known in the art.

CTACTTGTTC GAM336966 is a novel bioinformatically detectable regulatory, non protein
TCTTGTTGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336966 was detected
TGCTTGTATT is described with additional reference to Figs. 9-15.

TGCTTTCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGTTATTG encoded by the human genome.

TTTTCAAGGA GAM336966 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336966 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336966 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336966 precursor RNA is designated SEQ ID:7038, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7038 is located from position 62330682 to position 62330781 relative to chromosome 14 on the `+` strand.

GAM336966 precursor RNA folds onto itself, forming GAM336966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336966 precursor RNA, designated SEQ ID NO: 7038, and a schematic representation of a predicted secondary folding of GAM336966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336966 folded precursor RNA yielding a GAM336966 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336966 RNA, hereby incorporated herein.

GAM336966 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336966 target RNA, herein designated GAM TARGET RNA.

GAM336966 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336966 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336966 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336966 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336966 RNA, herein designated GAM RNA, to target binding sites on GAM336966 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336966 target RNA into GAM336966 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336966 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336966 target genes. The mRNA of each one of this plurality of GAM336966 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336966 RNA, herein designated GAM RNA, and which when bound by GAM336966 RNA causes inhibition of translation of the GAM336966 target mRNA into a corresponding GAM336966 target protein.

The mechanism of the translational inhibition exerted by GAM336966 RNA, herein designated GAM RNA, on one or more GAM336966 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336966 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336966 RNA, herein designated GAM RNA, of GAM336966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336966 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336966 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336966 RNA correlate with, and may be deduced from, the identity of the GAM336966 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336967 7283 TGTTTTGACT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCCGCCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTTAGGTCT Messenger 336967 (GAM336967) oligonucleotides modulates expression of respective target
GGAATGGTAG genes whose function and utility is known in the art.

AGCATTGAGT GAM336967 is a novel bioinformatically detectable regulatory, non protein
ACTGTTATCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336967 was detected
TCCACATCTC is described with additional reference to Figs. 9-15.

AGGAGAAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCAGTAGAG encoded by the human genome.

AGACA GAM336967 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM336967 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336967 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336967 precursor RNA is designated SEQ ID:7283, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7283 is located from position 62410126 to position 62410220 relative to chromosome 11 on the `+` strand.

GAM336967 precursor RNA folds onto itself, forming GAM336967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336967 precursor RNA, designated SEQ ID NO: 7283, and a schematic representation of a predicted secondary folding of GAM336967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336967 folded precursor RNA yielding a GAM336967 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336967 RNA, hereby incorporated herein.

GAM336967 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336967 target RNA, herein designated GAM TARGET RNA.

GAM336967 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336967 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336967 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336967 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336967 RNA, herein designated GAM RNA, to target binding sites on GAM336967 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336967 target RNA into GAM336967 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336967 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336967 target genes. The mRNA of each one of this plurality of GAM336967 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336967 RNA, herein designated GAM RNA, and which when bound by GAM336967 RNA causes inhibition of translation of the GAM336967 target mRNA into a corresponding GAM336967 target protein.

The mechanism of the translational inhibition exerted by GAM336967 RNA, herein designated GAM RNA, on one or more GAM336967 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336967 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336967 RNA, herein designated GAM RNA, of GAM336967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336967 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336967 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336967 RNA correlate with, and may be deduced from, the identity of the GAM336967 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336968 6168 CTCCTGTAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTAGAGCGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCTCTTGAA Messenger 336968 (GAM336968) oligonucleotides modulates expression of respective target
CCCTAATTTT genes whose function and utility is known in the art.

TAGGTCTCAA GAM336968 is a novel bioinformatically detectable regulatory, non protein
AGAGTGGGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336968 was detected
TCAGAGATAA is described with additional reference to Figs. 9-15.

AGAGGTTTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAGGGACAG encoded by the human genome.

GGCGAGGAG GAM336968 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM336968 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336968 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336968 precursor RNA is designated SEQ ID:6168, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6168 is located from position 62447485 to position 62447583 relative to chromosome 9 on the `+` strand.

GAM336968 precursor RNA folds onto itself, forming GAM336968 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336968 precursor RNA, designated SEQ ID NO: 6168, and a schematic representation of a predicted secondary folding of GAM336968 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336968 folded precursor RNA yielding a GAM336968 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336968 RNA, hereby incorporated herein.

GAM336968 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336968 target RNA, herein designated GAM TARGET RNA.

GAM336968 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336968 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336968 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336968 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336968 RNA, herein designated GAM RNA, to target binding sites on GAM336968 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336968 target RNA into GAM336968 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336968 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336968 target genes. The mRNA of each one of this plurality of GAM336968 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336968 RNA, herein designated GAM RNA, and which when bound by GAM336968 RNA causes inhibition of translation of the GAM336968 target mRNA into a corresponding GAM336968 target protein.

The mechanism of the translational inhibition exerted by GAM336968 RNA, herein designated GAM RNA, on one or more GAM336968 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336968 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336968 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336968 RNA, herein designated GAM RNA, of GAM336968 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336968 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336968 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336968 RNA correlate with, and may be deduced from, the identity of the GAM336968 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336969 5878 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 336969 (GAM336969) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336969 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336969 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336969 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336969 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336969 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336969 precursor RNA is designated SEQ ID:5878, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5878 is located from position 62677320 to position 62677401 relative to chromosome 12 on the `-` strand.

GAM336969 precursor RNA folds onto itself, forming GAM336969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336969 precursor RNA, designated SEQ ID NO: 5878, and a schematic representation of a predicted secondary folding of GAM336969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336969 folded precursor RNA yielding a GAM336969 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336969 RNA, hereby incorporated herein.

GAM336969 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336969 target RNA, herein designated GAM TARGET RNA.

GAM336969 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336969 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336969 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336969 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336969 RNA, herein designated GAM RNA, to target binding sites on GAM336969 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336969 target RNA into GAM336969 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336969 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336969 target genes. The mRNA of each one of this plurality of GAM336969 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336969 RNA, herein designated GAM RNA, and which when bound by GAM336969 RNA causes inhibition of translation of the GAM336969 target mRNA into a corresponding GAM336969 target protein.

The mechanism of the translational inhibition exerted by GAM336969 RNA, herein designated GAM RNA, on one or more GAM336969 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336969 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336969 RNA, herein designated GAM RNA, of GAM336969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336969 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336969 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336969 RNA correlate with, and may be deduced from, the identity of the GAM336969 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336970 5782 AGGCTGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGTGACTCG detected oligonucleotides of the present invention, referred to here as Genomic Address

TACTTGTAAT Messenger 336970 (GAM336970) oligonucleotides modulates expression of respective target

CCTAGTGCTT genes whose function and utility is known in the art.

TGAGAGGCTG GAM336970 is a novel bioinformatically detectable regulatory, non protein

AGGCAGGAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336970 was detected

ATTGCTTGAG is described with additional reference to Figs. 9-15.

ACCAGGAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACCAGC encoded by the human genome.

CT GAM336970 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336970 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336970 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336970 precursor RNA is designated SEQ

ID:5782, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5782 is located from position 62689480 to position 62689571 relative to chromosome 12 on the `+` strand.

GAM336970 precursor RNA folds onto itself, forming GAM336970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336970 precursor RNA, designated SEQ ID NO: 5782, and a schematic representation of a predicted secondary folding of GAM336970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336970 folded precursor RNA yielding a GAM336970 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336970 RNA, hereby incorporated herein.

GAM336970 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336970 target RNA, herein designated GAM TARGET RNA.

GAM336970 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336970 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336970 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336970 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336970 RNA, herein designated GAM RNA, to target binding sites on GAM336970 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336970 target RNA into GAM336970 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336970 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336970 target genes. The mRNA of each one of this plurality of GAM336970 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336970 RNA, herein designated GAM RNA, and which when bound by GAM336970 RNA causes inhibition of translation of the GAM336970 target mRNA into a corresponding GAM336970 target protein.

The mechanism of the translational inhibition exerted by GAM336970 RNA, herein designated GAM RNA, on one or more GAM336970 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336970 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336970 RNA, herein designated GAM RNA, of GAM336970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336970 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336970 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336970 RNA correlate with, and may be deduced from, the identity of the GAM336970 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336971 6764 GGCTGGGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTGACTCGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACTTGTAATC Messenger 336971 (GAM336971) oligonucleotides modulates expression of respective target

CTAGTGCTTT genes whose function and utility is known in the art.

GAGAGGCTGA GAM336971 is a novel bioinformatically detectable regulatory, non protein

GGCAGGAGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336971 was detected

TTGCTTGAGA is described with additional reference to Figs. 9-15.

CCAGGAGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACCAGCC encoded by the human genome.

GAM336971 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336971 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336971 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336971 precursor RNA is designated SEQ ID:6764, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6764 is located from position 62689481 to position 62689570 relative to chromosome 12 on the `+` strand.

GAM336971 precursor RNA folds onto itself, forming GAM336971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336971 precursor RNA, designated SEQ ID NO: 6764, and a schematic representation of a predicted secondary folding of GAM336971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336971 folded precursor RNA yielding a GAM336971 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336971 RNA, hereby incorporated herein.

GAM336971 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336971 target RNA, herein designated GAM TARGET RNA.

GAM336971 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336971 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336971 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336971 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336971 RNA, herein designated GAM RNA, to target binding sites on GAM336971 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336971 target RNA into GAM336971 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336971 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336971 target genes. The mRNA of each one of this plurality of GAM336971 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336971 RNA, herein designated GAM RNA, and which when bound by GAM336971 RNA causes inhibition of translation of the GAM336971 target mRNA into a corresponding GAM336971 target protein.

The mechanism of the translational inhibition exerted by GAM336971 RNA, herein designated GAM RNA, on one or more GAM336971 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336971 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336971 RNA, herein designated GAM RNA, of GAM336971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336971 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336971 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336971 RNA correlate with, and may be deduced from, the identity of the GAM336971 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336972 5879 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336972 (GAM336972) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336972 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336972 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM336972 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336972 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336972 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336972 precursor RNA is designated SEQ ID:5879, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5879 is located from position 62708765 to position 62708846 relative to chromosome 13 on the `-` strand.

GAM336972 precursor RNA folds onto itself, forming GAM336972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336972 precursor RNA, designated SEQ ID NO: 5879, and a schematic representation of a predicted secondary folding of GAM336972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336972 folded precursor RNA yielding a GAM336972 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336972 RNA, hereby incorporated herein.

GAM336972 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336972 target RNA, herein designated GAM TARGET RNA.

GAM336972 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336972 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336972 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336972 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336972 RNA, herein designated GAM RNA, to target binding sites on GAM336972 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336972 target RNA into GAM336972 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336972 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336972 target genes. The mRNA of each one of this plurality of GAM336972 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336972 RNA, herein designated GAM RNA, and which when bound by GAM336972 RNA causes inhibition of translation of the GAM336972 target mRNA into a corresponding GAM336972 target protein.

The mechanism of the translational inhibition exerted by GAM336972 RNA, herein designated GAM RNA, on one or more GAM336972 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336972 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336972 RNA, herein designated GAM RNA, of GAM336972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336972 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336972 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336972 RNA correlate with, and may be deduced from, the identity of the GAM336972 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336974 7190 TGATGCGCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGTATCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CGTCTGGATC Messenger 336974 (GAM336974) oligonucleotides modulates expression of respective target
GCCACTTCAC genes whose function and utility is known in the art.

GTTTTAGCCA GAM336974 is a novel bioinformatically detectable regulatory, non protein
CAAGTGACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336974 was detected
AGTGGAAGAT is described with additional reference to Figs. 9-15.

CCAGAGTCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGGCTCG encoded by the human genome.

TCA GAM336974 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336974 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336974 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336974 precursor RNA is designated SEQ ID:7190, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7190 is located from position 62725558 to position 62725650 relative to chromosome 11 on the `-` strand.

GAM336974 precursor RNA folds onto itself, forming GAM336974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336974 precursor RNA, designated SEQ ID NO: 7190, and a schematic representation of a predicted secondary folding of GAM336974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336974 folded precursor RNA yielding a GAM336974 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336974 RNA, hereby incorporated herein.

GAM336974 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336974 target RNA, herein designated GAM TARGET RNA.

GAM336974 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336974 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336974 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336974 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336974 RNA, herein designated GAM RNA, to target binding sites on GAM336974 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336974 target RNA into GAM336974 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336974 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336974 target genes. The mRNA of each one of this plurality of GAM336974 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336974 RNA, herein designated GAM RNA, and which when bound by GAM336974 RNA causes inhibition of translation of the GAM336974 target mRNA into a corresponding GAM336974 target protein.

The mechanism of the translational inhibition exerted by GAM336974 RNA, herein designated GAM RNA, on one or more GAM336974 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336974 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336974 RNA, herein designated GAM RNA, of GAM336974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336974 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336974 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336974 RNA correlate with, and may be deduced from, the identity of the GAM336974 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336975 7178 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGGAG Messenger 336975 (GAM336975) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

CGGTGAGCCG GAM336975 is a novel bioinformatically detectable regulatory, non protein
AGATTGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336975 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGA encoded by the human genome.

AACTCCGTCT GAM336975 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM336975 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336975 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336975 precursor RNA is designated SEQ ID:7178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7178 is located from position 62729661 to position 62729762 relative to chromosome 11 on the `+` strand.

GAM336975 precursor RNA folds onto itself, forming GAM336975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336975 precursor RNA, designated SEQ ID NO: 7178, and a schematic representation of a predicted secondary folding of GAM336975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336975 folded precursor RNA yielding a GAM336975 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336975 RNA, hereby incorporated herein. Expression of GAM336975 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM336975 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336975 target RNA, herein designated GAM TARGET RNA.

GAM336975 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336975 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336975 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336975 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336975 RNA, herein designated GAM RNA, to target binding sites on GAM336975 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336975 target RNA into GAM336975 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336975 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336975 target genes. The mRNA of each one of this plurality of GAM336975 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336975 RNA, herein designated GAM RNA, and which when bound by GAM336975 RNA causes inhibition of translation of the GAM336975 target mRNA into a corresponding GAM336975 target protein.

The mechanism of the translational inhibition exerted by GAM336975 RNA, herein designated GAM RNA, on one or more GAM336975 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336975 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336975 RNA, herein designated GAM RNA, of GAM336975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336975 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336975 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336975 RNA correlate with, and may be deduced from, the identity of the GAM336975 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336976 6122 CCTGGTCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGAGTGATT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGAGGCTGGG Messenger 336976 (GAM336976) oligonucleotides modulates expression of respective target

CATGGTGGCT genes whose function and utility is known in the art.

TATGCCTGTA GAM336976 is a novel bioinformatically detectable regulatory, non protein

ATCCCAGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336976 was detected

TTTGGGAGGC is described with additional reference to Figs. 9-15.

CAAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336976 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336976 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336976 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336976 precursor RNA is designated SEQ ID:6122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6122 is located from position 62755250 to position 62755324 relative to chromosome 11 on the `+` strand.

GAM336976 precursor RNA folds onto itself, forming GAM336976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336976 precursor RNA, designated SEQ ID NO: 6122, and a schematic representation of a predicted secondary folding of GAM336976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336976 folded precursor RNA yielding a GAM336976 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336976 RNA, hereby incorporated herein.

GAM336976 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336976 target RNA, herein designated GAM TARGET RNA.

GAM336976 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336976 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336976 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336976 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336976 RNA, herein designated GAM RNA, to target binding sites on GAM336976 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336976 target RNA into GAM336976 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336976 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336976 target genes. The mRNA of each one of this plurality of GAM336976 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336976 RNA, herein designated GAM RNA, and which when bound by GAM336976 RNA causes inhibition of translation of the GAM336976 target mRNA into a corresponding GAM336976 target protein.

The mechanism of the translational inhibition exerted by GAM336976 RNA, herein designated GAM RNA, on one or more GAM336976 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336976 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336976 RNA, herein designated GAM RNA, of GAM336976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336976 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336976 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336976 RNA correlate with, and may be deduced from, the identity of the GAM336976 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336978 6587 GGACATCAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATAAATAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGCTCTAA Messenger 336978 (GAM336978) oligonucleotides modulates expression of respective target

TTGCCAAGAA genes whose function and utility is known in the art.

TTCACATGTG GAM336978 is a novel bioinformatically detectable regulatory, non protein

GTTGTATGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336978 was detected

GCTTTACTGG is described with additional reference to Figs. 9-15.

GAGACTGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTATCTGCA encoded by the human genome.

TGTGATTCTG GAM336978 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTGTGATGGA GAM336978 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

CACTTGTAAG GAM336978 precursor RNA does not encode a protein. A nucleotide sequence identical or

TTTGTGCC highly similar to the nucleotide sequence of GAM336978 precursor RNA is designated SEQ

ID:6587, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6587 is located from position 62875338 to position 62875465

relative to chromosome 9 on the `-` strand.

GAM336978 precursor RNA folds onto itself, forming GAM336978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336978 precursor RNA, designated SEQ ID NO: 6587, and a schematic representation of a predicted secondary folding of GAM336978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336978 folded precursor RNA yielding a GAM336978 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336978 RNA, hereby incorporated herein.

GAM336978 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336978 target RNA, herein designated GAM TARGET RNA.

GAM336978 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336978 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336978 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336978 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336978 RNA, herein designated GAM RNA, to target binding sites on GAM336978 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336978 target RNA into GAM336978 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336978 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM336978 target genes. The mRNA of each one of this plurality of GAM336978 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336978 RNA, herein designated GAM RNA, and which when bound by GAM336978 RNA causes inhibition of translation of the GAM336978 target mRNA into a corresponding GAM336978 target protein.

The mechanism of the translational inhibition exerted by GAM336978 RNA, herein designated GAM RNA, on one or more GAM336978 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336978 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336978 RNA, herein designated GAM RNA, of GAM336978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336978 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336978 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336978 RNA correlate with, and may be deduced from, the identity of the GAM336978 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336979 5949 ATAAGCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTAATTGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAATTCACA Messenger 336979 (GAM336979) oligonucleotides modulates expression of respective target
TGTGGTTGTA genes whose function and utility is known in the art.

TGCAGCTTTA GAM336979 is a novel bioinformatically detectable regulatory, non protein
CTGGGAGACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336979 was detected
GAAGTGTATC is described with additional reference to Figs. 9-15.

TGCATGTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTGCTGTGA encoded by the human genome.

TGGACACTTG GAM336979 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TAAGTTTGT GAM336979 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336979 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336979 precursor RNA is designated SEQ ID:5949, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5949 is located from position 62875341 to position 62875449 relative to chromosome 9 on the `-` strand.

GAM336979 precursor RNA folds onto itself, forming GAM336979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336979 precursor RNA, designated SEQ ID NO: 5949, and a schematic representation of a predicted secondary folding of GAM336979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336979 folded precursor RNA yielding a GAM336979 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336979 RNA, hereby incorporated herein.

GAM336979 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336979 target RNA, herein designated GAM TARGET RNA.

GAM336979 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336979 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336979 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336979 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336979 RNA, herein designated GAM RNA, to target binding sites on GAM336979 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336979 target RNA into GAM336979 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336979 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336979 target genes. The mRNA of each one of this plurality of GAM336979 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336979 RNA, herein designated GAM RNA, and which when bound by GAM336979 RNA causes inhibition of translation of the GAM336979 target mRNA into a corresponding GAM336979 target protein.

The mechanism of the translational inhibition exerted by GAM336979 RNA, herein designated GAM RNA, on one or more GAM336979 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336979 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336979 RNA, herein designated GAM RNA, of GAM336979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336979 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336979 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336979 RNA correlate with, and may be deduced from, the identity of the GAM336979 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336980 6301 GAATAAATAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTGCTCTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCCAAGAA Messenger 336980 (GAM336980) oligonucleotides modulates expression of respective target

TTCACATGTG genes whose function and utility is known in the art.

GTTGTATGCA GAM336980 is a novel bioinformatically detectable regulatory, non protein

GCTTTACTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336980 was detected

GAGACTGAAG is described with additional reference to Figs. 9-15.

TGTATCTGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTGATTCTG encoded by the human genome.

CTGTGATGGA GAM336980 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CACTTGTAAG GAM336980 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TTT GAM336980 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336980 precursor RNA is designated SEQ ID:6301, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6301 is located from position 62875343 to position 62875455 relative to chromosome 9 on the `-` strand.

GAM336980 precursor RNA folds onto itself, forming GAM336980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336980 precursor RNA, designated SEQ ID NO: 6301, and a schematic representation of a predicted secondary folding of GAM336980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336980 folded precursor RNA yielding a GAM336980 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336980 RNA, hereby incorporated herein.

GAM336980 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336980 target RNA, herein designated GAM TARGET RNA.

GAM336980 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336980 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336980 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336980 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336980 RNA, herein designated GAM RNA, to target binding sites on GAM336980 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336980 target RNA into GAM336980 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336980 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336980 target genes. The mRNA of each one of this plurality of GAM336980 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336980 RNA, herein designated GAM RNA, and which when bound by GAM336980 RNA causes inhibition of translation of the GAM336980 target mRNA into a corresponding GAM336980 target protein.

The mechanism of the translational inhibition exerted by GAM336980 RNA, herein designated GAM RNA, on one or more GAM336980 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336980 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336980 RNA, herein designated GAM RNA, of GAM336980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336980 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336980 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336980 RNA correlate with, and may be deduced from, the identity of the GAM336980 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336981 5947 ATAAGCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTAATTGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAATTCACA Messenger 336981 (GAM336981) oligonucleotides modulates expression of respective target
TGTGGTTGTA genes whose function and utility is known in the art.

TGCAGCTTTA GAM336981 is a novel bioinformatically detectable regulatory, non protein
CTGGGAGACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336981 was detected
GAAGTGTATC is described with additional reference to Figs. 9-15.

TGCATGTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTGCTGTGA encoded by the human genome.

TGGACACTTG GAM336981 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
T GAM336981 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336981 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336981 precursor RNA is designated SEQ ID:5947, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5947 is located from position 62875349 to position 62875449 relative to chromosome 9 on the `-` strand.

GAM336981 precursor RNA folds onto itself, forming GAM336981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336981 precursor RNA, designated SEQ ID NO: 5947, and a schematic representation of a predicted secondary folding of GAM336981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336981 folded precursor RNA yielding a GAM336981 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336981 RNA, hereby incorporated herein.

GAM336981 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336981 target RNA, herein designated GAM TARGET RNA.

GAM336981 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336981 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336981 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336981 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336981 RNA, herein designated GAM RNA, to target binding sites on GAM336981 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336981 target RNA into GAM336981 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336981 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336981 target genes. The mRNA of each one of this plurality of GAM336981 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336981 RNA, herein designated GAM RNA, and which when bound by GAM336981 RNA causes inhibition of translation of the GAM336981 target mRNA into a corresponding GAM336981 target protein.

The mechanism of the translational inhibition exerted by GAM336981 RNA, herein designated GAM RNA, on one or more GAM336981 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336981 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336981 RNA, herein designated GAM RNA, of GAM336981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336981 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336981 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336981 RNA correlate with, and may be deduced from, the identity of the GAM336981 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336983 6933 GTGTTTGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TAGAGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGAAATTA Messenger 336983 (GAM336983) oligonucleotides modulates expression of respective target
TAAGCACTGG genes whose function and utility is known in the art.

GGTACTCCTA GAM336983 is a novel bioinformatically detectable regulatory, non protein
TGTGTCTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336983 was detected
ACTCTATGCC is described with additional reference to Figs. 9-15.

AAGTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336983 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336983 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336983 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336983 precursor RNA is designated SEQ ID:6933, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6933 is located from position 62901709 to position 62901784 relative to chromosome 11 on the `+` strand.

GAM336983 precursor RNA folds onto itself, forming GAM336983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336983 precursor RNA, designated SEQ ID NO: 6933, and a schematic representation of a predicted secondary folding of GAM336983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336983 folded precursor RNA yielding a GAM336983 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336983 RNA, hereby incorporated herein.

GAM336983 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336983 target RNA, herein designated GAM TARGET RNA.

GAM336983 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336983 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336983 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336983 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336983 RNA, herein designated GAM RNA, to target binding sites on GAM336983 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336983 target RNA into GAM336983 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336983 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336983 target genes. The mRNA of each one of this plurality of GAM336983 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336983 RNA, herein designated GAM RNA, and which when bound by GAM336983 RNA causes inhibition of translation of the GAM336983 target mRNA into a corresponding GAM336983 target protein.

The mechanism of the translational inhibition exerted by GAM336983 RNA, herein designated GAM RNA, on one or more GAM336983 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336983 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336983 RNA, herein designated GAM RNA, of GAM336983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336983 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336983 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336983 RNA correlate with, and may be deduced from, the identity of the GAM336983 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336984 6045 CCAAGTAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GCAAACTGTA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTTGATGCT Messenger 336984 (GAM336984) oligonucleotides modulates expression of respective target
AGAACACTAT genes whose function and utility is known in the art.

TCTTTGAGAG GAM336984 is a novel bioinformatically detectable regulatory, non protein
GGTATGTGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336984 was detected
ATACTCGAAA is described with additional reference to Figs. 9-15.

TGCAGTCATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTCACGGCT encoded by the human genome.

TGG GAM336984 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336984 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336984 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336984 precursor RNA is designated SEQ ID:6045, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6045 is located from position 62916210 to position 62916302 relative to chromosome 14 on the `+` strand.

GAM336984 precursor RNA folds onto itself, forming GAM336984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336984 precursor RNA, designated SEQ ID NO: 6045, and a schematic representation of a predicted secondary folding of GAM336984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336984 folded precursor RNA yielding a GAM336984 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336984 RNA, hereby incorporated herein.

GAM336984 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336984 target RNA, herein designated GAM TARGET RNA.

GAM336984 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336984 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336984 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336984 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336984 RNA, herein designated GAM RNA, to target binding sites on GAM336984 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336984 target RNA into GAM336984 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336984 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336984 target genes. The mRNA of each one of this plurality of GAM336984 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336984 RNA, herein designated GAM RNA, and which when bound by GAM336984 RNA causes inhibition of translation of the GAM336984 target mRNA into a corresponding GAM336984 target protein.

The mechanism of the translational inhibition exerted by GAM336984 RNA, herein designated GAM RNA, on one or more GAM336984 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336984 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336984 RNA, herein designated GAM RNA, of GAM336984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336984 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336984 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336984 RNA correlate with, and may be deduced from, the identity of the GAM336984 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336989 6004 CACTGCCAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGGCAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGCTCAGGA Messenger 336989 (GAM336989) oligonucleotides modulates expression of respective target

GAGTCTTCGC genes whose function and utility is known in the art.

CTCTTGTACC GAM336989 is a novel bioinformatically detectable regulatory, non protein

CTCCTTGGGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336989 was detected

CTCTCCAAAA is described with additional reference to Figs. 9-15.

CCAGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM336989 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336989 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336989 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336989 precursor RNA is designated SEQ ID:6004, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6004 is located from position 63216696 to position 63216771 relative to chromosome 19 on the `-` strand.

GAM336989 precursor RNA folds onto itself, forming GAM336989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336989 precursor RNA, designated SEQ ID NO: 6004, and a schematic representation of a predicted secondary folding of GAM336989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336989 folded precursor RNA yielding a GAM336989 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336989 RNA, hereby incorporated herein.

GAM336989 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336989 target RNA, herein designated GAM TARGET RNA.

GAM336989 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336989 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336989 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336989 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336989 RNA, herein designated GAM RNA, to target binding sites on GAM336989 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336989 target RNA into GAM336989 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336989 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336989 target genes. The mRNA of each one of this plurality of GAM336989 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336989 RNA, herein designated GAM RNA, and which when bound by GAM336989 RNA causes inhibition of translation of the GAM336989 target mRNA into a corresponding GAM336989 target protein.

The mechanism of the translational inhibition exerted by GAM336989 RNA, herein designated GAM RNA, on one or more GAM336989 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336989 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336989 RNA, herein designated GAM RNA, of GAM336989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336989 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336989 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336989 RNA correlate with, and may be deduced from, the identity of the GAM336989 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336990 6269 CTTGGCTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTTTCCACG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGATGGTG Messenger 336990 (GAM336990) oligonucleotides modulates expression of respective target

TCATATTGCT genes whose function and utility is known in the art.

GGGTCCAGCA GAM336990 is a novel bioinformatically detectable regulatory, non protein

CCCAGTTATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336990 was detected

GTGGCCCAAT is described with additional reference to Figs. 9-15.

TTCCTATACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGCCTAG encoded by the human genome.

GAM336990 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336990 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336990 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336990 precursor RNA is designated SEQ ID:6269, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6269 is located from position 63236493 to position 63236580 relative to chromosome 7 on the `+` strand.

GAM336990 precursor RNA folds onto itself, forming GAM336990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336990 precursor RNA, designated SEQ ID NO: 6269, and a schematic representation of a predicted secondary folding of GAM336990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336990 folded precursor RNA yielding a GAM336990 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336990 RNA, hereby incorporated herein.

GAM336990 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336990 target RNA, herein designated GAM TARGET RNA.

GAM336990 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336990 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336990 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336990 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336990 RNA, herein designated GAM RNA, to target binding sites on GAM336990 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336990 target RNA into GAM336990 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336990 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336990 target genes. The mRNA of each one of this plurality of GAM336990 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336990 RNA, herein designated GAM RNA, and which when bound by GAM336990 RNA causes inhibition of translation of the GAM336990 target mRNA into a corresponding GAM336990 target protein.

The mechanism of the translational inhibition exerted by GAM336990 RNA, herein designated GAM RNA, on one or more GAM336990 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336990 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336990 RNA, herein designated GAM RNA, of GAM336990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336990 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336990 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336990 RNA correlate with, and may be deduced from, the identity of the GAM336990 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336991 5880 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 336991 (GAM336991) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM336991 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336991 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM336991 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336991 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336991 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336991 precursor RNA is designated SEQ ID:5880, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5880 is located from position 63263870 to position 63263951 relative to chromosome 11 on the `+` strand.

GAM336991 precursor RNA folds onto itself, forming GAM336991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336991 precursor RNA, designated SEQ ID NO: 5880, and a schematic representation of a predicted secondary folding of GAM336991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336991 folded precursor RNA yielding a GAM336991 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336991 RNA, hereby incorporated herein.

GAM336991 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336991 target RNA, herein designated GAM TARGET RNA.

GAM336991 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336991 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336991 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336991 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336991 RNA, herein designated GAM RNA, to target binding sites on GAM336991 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336991 target RNA into GAM336991 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336991 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336991 target genes. The mRNA of each one of this plurality of GAM336991 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336991 RNA, herein designated GAM RNA, and which when bound by GAM336991 RNA causes inhibition of translation of the GAM336991 target mRNA into a corresponding GAM336991 target protein.

The mechanism of the translational inhibition exerted by GAM336991 RNA, herein designated GAM RNA, on one or more GAM336991 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336991 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336991 RNA, herein designated GAM RNA, of GAM336991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336991 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336991 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336991 RNA correlate with, and may be deduced from, the identity of the GAM336991 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336992 7266 TGTCTATAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATGTGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTTTCTGC Messenger 336992 (GAM336992) oligonucleotides modulates expression of respective target

CCGTAAAATG genes whose function and utility is known in the art.

TTCAAATGTT GAM336992 is a novel bioinformatically detectable regulatory, non protein

TTCTCTCTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336992 was detected

AAAGCTTTGT is described with additional reference to Figs. 9-15.

TCATTGTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTGGAATT encoded by the human genome.

TTGGTTCTCA GAM336992 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGGAGTAGAC GAM336992 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

A GAM336992 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336992 precursor RNA is designated SEQ ID:7266, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7266 is located from position 63315058 to position 63315168 relative to chromosome 17 on the `-` strand.

GAM336992 precursor RNA folds onto itself, forming GAM336992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336992 precursor RNA, designated SEQ ID NO: 7266, and a schematic representation of a predicted secondary folding of GAM336992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336992 folded precursor RNA yielding a GAM336992 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM336992 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336992 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM336992 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336992 target RNA, herein designated GAM TARGET RNA.

GAM336992 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336992 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336992 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336992 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336992 RNA, herein designated GAM RNA, to target binding sites on GAM336992 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336992 target RNA into GAM336992 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336992 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336992 target genes. The mRNA of each one of this plurality of GAM336992 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336992 RNA, herein designated GAM RNA, and which when bound by GAM336992 RNA causes inhibition of translation of the GAM336992 target mRNA into a corresponding GAM336992 target protein.

The mechanism of the translational inhibition exerted by GAM336992 RNA, herein designated GAM RNA, on one or more GAM336992 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336992 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336992 RNA, herein designated GAM RNA, of GAM336992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336992 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336992 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336992 RNA correlate with, and may be deduced from, the identity of the GAM336992 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336995 6627 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGTGGAGG Messenger 336995 (GAM336995) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCAATATTGT GAM336995 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336995 was detected
TCCAGCTTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAAACTCC encoded by the human genome.

GAM336995 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336995 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336995 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336995 precursor RNA is designated SEQ ID:6627, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6627 is located from position 63490699 to position 63490787 relative to chromosome 19 on the `+` strand.

GAM336995 precursor RNA folds onto itself, forming GAM336995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336995 precursor RNA, designated SEQ ID NO: 6627, and a schematic representation of a predicted secondary folding of GAM336995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336995 folded precursor RNA yielding a GAM336995 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336995 RNA, hereby incorporated herein.

GAM336995 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336995 target RNA, herein designated GAM TARGET RNA.

GAM336995 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336995 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336995 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336995 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336995 RNA, herein designated GAM RNA, to target binding sites on GAM336995 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336995 target RNA into GAM336995 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336995 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336995 target genes. The mRNA of each one of this plurality of GAM336995 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336995 RNA, herein designated GAM RNA, and which when bound by GAM336995 RNA causes inhibition of translation of the GAM336995 target mRNA into a corresponding GAM336995 target protein.

The mechanism of the translational inhibition exerted by GAM336995 RNA, herein designated GAM RNA, on one or more GAM336995 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336995 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336995 RNA, herein designated GAM RNA, of GAM336995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336995 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336995 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336995 RNA correlate with, and may be deduced from, the identity of the GAM336995 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336996 7049 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGAAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTGCAG Messenger 336996 (GAM336996) oligonucleotides modulates expression of respective target
TGAGCCAATA genes whose function and utility is known in the art.

TTGTGCCATT GAM336996 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336996 was detected
TTGGGCAACA is described with additional reference to Figs. 9-15.

AGAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336996 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336996 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM336996 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336996 precursor RNA is designated SEQ ID:7049, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7049 is located from position 63490705 to position 63490781 relative to chromosome 19 on the `+` strand.

GAM336996 precursor RNA folds onto itself, forming GAM336996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336996 precursor RNA, designated SEQ ID NO: 7049, and a schematic representation of a predicted secondary folding of GAM336996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336996 folded precursor RNA yielding a GAM336996 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336996 RNA, hereby incorporated herein.

GAM336996 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336996 target RNA, herein designated GAM TARGET RNA.

GAM336996 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336996 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336996 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336996 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336996 RNA, herein designated GAM RNA, to target binding sites on GAM336996 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336996 target RNA into GAM336996 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336996 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336996 target genes. The mRNA of each one of this plurality of GAM336996 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336996 RNA, herein designated GAM RNA, and which when bound by GAM336996 RNA causes inhibition of translation of the GAM336996 target mRNA into a corresponding GAM336996 target protein.

The mechanism of the translational inhibition exerted by GAM336996 RNA, herein designated GAM RNA, on one or more GAM336996 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336996 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM336996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336996 RNA, herein designated GAM RNA, of GAM336996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336996 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336996 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336996 RNA correlate with, and may be deduced from, the identity of the GAM336996 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM336997 5773 AGGCATTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCAACATGT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCACTGGTC Messenger 336997 (GAM336997) oligonucleotides modulates expression of respective target
TGGCTTTTGT genes whose function and utility is known in the art.

TAGGCCCATT GAM336997 is a novel bioinformatically detectable regulatory, non protein
AATAGTGTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM336997 was detected
ATGTGACAGC is described with additional reference to Figs. 9-15.

CT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM336997 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM336997 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM336997 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336997 precursor RNA is designated SEQ ID:5773, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5773 is located from position 63567534 to position 63567605 relative to chromosome 20 on the `+` strand.

GAM336997 precursor RNA folds onto itself, forming GAM336997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM336997 precursor RNA, designated SEQ ID NO: 5773, and a schematic representation of a predicted secondary folding of GAM336997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM336997 folded precursor RNA yielding a GAM336997 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM336997 RNA, hereby incorporated herein.

GAM336997 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336997 target RNA, herein designated GAM TARGET RNA.

GAM336997 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM336997 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336997 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336997 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM336997 RNA, herein designated GAM RNA, to target binding sites on GAM336997 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336997 target RNA into GAM336997 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM336997 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336997 target genes. The mRNA of each one of this plurality of GAM336997 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336997 RNA, herein designated GAM RNA, and which when bound by GAM336997 RNA causes inhibition of translation of the GAM336997 target mRNA into a corresponding GAM336997 target protein.

The mechanism of the translational inhibition exerted by GAM336997 RNA, herein designated GAM RNA, on one or more GAM336997 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM336997 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM336997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM336997 RNA, herein designated GAM RNA, of GAM336997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM336997 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM336997 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM336997 RNA correlate with, and may be deduced from, the identity of the GAM336997 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337000 5702 ACTACTGGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTATAAATGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTTGTGTGT Messenger 337000 (GAM337000) oligonucleotides modulates expression of respective target

GTATGTATTT genes whose function and utility is known in the art.

ATAGATGTTC GAM337000 is a novel bioinformatically detectable regulatory, non protein

TTTAAGGTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337000 was detected

CCTTGAAAAC is described with additional reference to Figs. 9-15.

TCTACATTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTATGCCACA encoded by the human genome.

TAATGACATT GAM337000 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCAGTCAGTG GAM337000 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GT GAM337000 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337000 precursor RNA is designated SEQ ID:5702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5702 is located from position 63919661 to position 63919772 relative to chromosome 12 on the `+` strand.

GAM337000 precursor RNA folds onto itself, forming GAM337000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337000 precursor RNA, designated SEQ ID NO: 5702, and a schematic representation of a predicted secondary folding of GAM337000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337000 folded precursor RNA yielding a GAM337000 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337000 RNA, hereby incorporated herein.

GAM337000 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337000 target RNA, herein designated GAM TARGET RNA.

GAM337000 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337000 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337000 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337000 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337000 RNA, herein designated GAM RNA, to target binding sites on GAM337000 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337000 target RNA into GAM337000 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337000 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337000 target genes. The mRNA of each one of this plurality of GAM337000 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337000 RNA, herein designated GAM RNA, and which when bound by GAM337000 RNA causes inhibition of translation of the GAM337000 target mRNA into a corresponding GAM337000 target protein.

The mechanism of the translational inhibition exerted by GAM337000 RNA, herein designated GAM RNA, on one or more GAM337000 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337000 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337000 RNA, herein designated GAM RNA, of GAM337000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337000 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337000 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337000 RNA correlate with, and may be deduced from, the identity of the GAM337000 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337001 6115 CCTGAACCCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGCGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGCAGTGG Messenger 337001 (GAM337001) oligonucleotides modulates expression of respective target

GCCAAGATTA genes whose function and utility is known in the art.

AGCCACTGCA GAM337001 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337001 was detected

GGCAACAGG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337001 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337001 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337001 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337001 precursor RNA is designated SEQ ID:6115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6115 is located from position 63948506 to position 63948574 relative to chromosome 17 on the `+` strand.

GAM337001 precursor RNA folds onto itself, forming GAM337001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337001 precursor RNA, designated SEQ ID NO: 6115, and a schematic representation of a predicted secondary folding of GAM337001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337001 folded precursor RNA yielding a GAM337001 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337001 RNA, hereby incorporated herein. Expression of GAM337001 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337001 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337001 target RNA, herein designated GAM TARGET RNA.

GAM337001 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337001 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337001 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337001 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337001 RNA, herein designated GAM RNA, to target binding sites on GAM337001 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337001 target RNA into GAM337001 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337001 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337001 target genes. The mRNA of each one of this plurality of GAM337001 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337001 RNA, herein designated GAM RNA, and which when bound by GAM337001 RNA causes inhibition of translation of the GAM337001 target mRNA into a corresponding GAM337001 target protein.

The mechanism of the translational inhibition exerted by GAM337001 RNA, herein designated GAM RNA, on one or more GAM337001 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337001 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337001 RNA, herein designated GAM RNA, of GAM337001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337001 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337001 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337001 RNA correlate with, and may be deduced from, the identity of the GAM337001 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337003 6262 CTTGAACCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGGCAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGCGGTGA Messenger 337003 (GAM337003) oligonucleotides modulates expression of respective target

GCTGAGATTG genes whose function and utility is known in the art.

CGCCATTGCA GAM337003 is a novel bioinformatically detectable regulatory, non protein

CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337003 was detected

GGCAACAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337003 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337003 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337003 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337003 precursor RNA is designated SEQ ID:6262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6262 is located from position 64886976 to position 64887044 relative to chromosome 7 on the `-` strand.

GAM337003 precursor RNA folds onto itself, forming GAM337003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337003 precursor RNA, designated SEQ ID NO: 6262, and a schematic representation of a predicted secondary folding of GAM337003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337003 folded precursor RNA yielding a GAM337003 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337003 RNA, hereby incorporated herein. Expression of GAM337003 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337003 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337003 target RNA, herein designated GAM TARGET RNA.

GAM337003 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337003 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337003 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337003 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337003 RNA, herein designated GAM RNA, to target binding sites on GAM337003 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337003 target RNA into GAM337003 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337003 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337003 target genes. The mRNA of each one of this plurality of GAM337003 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337003 RNA, herein designated GAM RNA, and which when bound by GAM337003 RNA causes inhibition of translation of the GAM337003 target mRNA into a corresponding GAM337003 target protein.

The mechanism of the translational inhibition exerted by GAM337003 RNA, herein designated GAM RNA, on one or more GAM337003 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337003 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337003 RNA, herein designated GAM RNA, of GAM337003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337003 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337003 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337003 RNA correlate with, and may be deduced from, the identity of the GAM337003 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337004 6145 CGGGGATTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCTGTGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CGGGAAGCCC Messenger 337004 (GAM337004) oligonucleotides modulates expression of respective target
ACTAGGAGGA genes whose function and utility is known in the art.

CTCTCACTTT GAM337004 is a novel bioinformatically detectable regulatory, non protein
GCTGAGTCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337004 was detected
TCTTTCCCTT is described with additional reference to Figs. 9-15.

CTTTCTTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CACCCAATAA encoded by the human genome.

ACCCTG GAM337004 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337004 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337004 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337004 precursor RNA is designated SEQ ID:6145, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6145 is located from position 65016569 to position 65016664 relative to chromosome 17 on the `+` strand.

GAM337004 precursor RNA folds onto itself, forming GAM337004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337004 precursor RNA, designated SEQ ID NO: 6145, and a schematic representation of a predicted secondary folding of GAM337004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337004 folded precursor RNA yielding a GAM337004 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337004 RNA, hereby incorporated herein.

GAM337004 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337004 target RNA, herein designated GAM TARGET RNA.

GAM337004 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337004 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337004 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337004 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337004 RNA, herein designated GAM RNA, to target binding sites on GAM337004 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337004 target RNA into GAM337004 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337004 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337004 target genes. The mRNA of each one of this plurality of GAM337004 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337004 RNA, herein designated GAM RNA, and which when bound by GAM337004 RNA causes inhibition of translation of the GAM337004 target mRNA into a corresponding GAM337004 target protein.

The mechanism of the translational inhibition exerted by GAM337004 RNA, herein designated GAM RNA, on one or more GAM337004 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337004 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337004 RNA, herein designated GAM RNA, of GAM337004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337004 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337004 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337004 RNA correlate with, and may be deduced from, the identity of the GAM337004 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337007 7130 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337007 (GAM337007) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM337007 is a novel bioinformatically detectable regulatory, non protein
AGATCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337007 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

GCTCCTTCTC GAM337007 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337007 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337007 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337007 precursor RNA is designated SEQ ID:7130, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7130 is located from position 65030778 to position 65030878 relative to chromosome 5 on the `+` strand.

GAM337007 precursor RNA folds onto itself, forming GAM337007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337007 precursor RNA, designated SEQ ID NO: 7130, and a schematic representation of a predicted secondary folding of GAM337007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337007 folded precursor RNA yielding a GAM337007 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337007 RNA, hereby incorporated herein. Expression of GAM337007 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337007 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337007 target RNA, herein designated GAM TARGET RNA.

GAM337007 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337007 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337007 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337007 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337007 RNA, herein designated GAM RNA, to target binding sites on GAM337007 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337007 target RNA into GAM337007 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337007 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337007 target genes. The mRNA of each one of this plurality of GAM337007 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337007 RNA, herein designated GAM RNA, and which when bound by GAM337007 RNA causes inhibition of translation of the GAM337007 target mRNA into a corresponding GAM337007 target protein.

The mechanism of the translational inhibition exerted by GAM337007 RNA, herein designated GAM RNA, on one or more GAM337007 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337007 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337007 RNA, herein designated GAM RNA, of

GAM337007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337007 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337007 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337007 RNA correlate with, and may be deduced from, the identity of the GAM337007 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337008 6163 CTCATGGTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAAAGGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTACCCAGAC Messenger 337008 (GAM337008) oligonucleotides modulates expression of respective target

ATTTCAACTT genes whose function and utility is known in the art.

TGTTGTTCTT GAM337008 is a novel bioinformatically detectable regulatory, non protein

TGGCTACAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337008 was detected

GAACAGGAGA is described with additional reference to Figs. 9-15.

AATGGAGGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCTGTGGGA encoded by the human genome.

GTGTGGAGAC GAM337008 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AGTGAG GAM337008 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337008 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337008 precursor RNA is designated SEQ ID:6163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6163 is located from position 65050472 to position 65050577 relative to chromosome 9 on the `+` strand.

GAM337008 precursor RNA folds onto itself, forming GAM337008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337008 precursor RNA, designated SEQ ID NO: 6163, and a schematic representation of a predicted secondary folding of GAM337008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337008 folded precursor RNA yielding a GAM337008 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337008 RNA, hereby incorporated herein.

GAM337008 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337008 target RNA, herein designated GAM TARGET RNA.

GAM337008 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337008 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337008 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337008 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337008 RNA, herein designated GAM RNA, to target binding sites on GAM337008 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337008 target RNA into GAM337008 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337008 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337008 target genes. The mRNA of each one of this plurality of GAM337008 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337008 RNA, herein designated GAM RNA, and which when bound by GAM337008 RNA causes inhibition of translation of the GAM337008 target mRNA into a corresponding GAM337008 target protein.

The mechanism of the translational inhibition exerted by GAM337008 RNA, herein designated GAM RNA, on one or more GAM337008 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337008 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337008 RNA, herein designated GAM RNA, of GAM337008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337008 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337008 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337008 RNA correlate with, and may be deduced from, the identity of the GAM337008 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337009 5881 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337009 (GAM337009) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337009 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337009 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337009 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337009 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337009 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337009 precursor RNA is designated SEQ ID:5881, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5881 is located from position 65068010 to position 65068091 relative to chromosome 8 on the `+` strand.

GAM337009 precursor RNA folds onto itself, forming GAM337009 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337009 precursor RNA, designated SEQ ID NO: 5881, and a schematic representation of a predicted secondary folding of GAM337009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337009 folded precursor RNA yielding a GAM337009 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337009 RNA, hereby incorporated herein.

GAM337009 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337009 target RNA, herein designated GAM TARGET RNA.

GAM337009 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337009 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337009 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337009 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337009 RNA, herein designated GAM RNA, to target binding sites on GAM337009 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337009 target RNA into GAM337009 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337009 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337009 target genes. The mRNA of each one of this plurality of GAM337009 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337009 RNA,

herein designated GAM RNA, and which when bound by GAM337009 RNA causes inhibition of translation of the GAM337009 target mRNA into a corresponding GAM337009 target protein.

The mechanism of the translational inhibition exerted by GAM337009 RNA, herein designated GAM RNA, on one or more GAM337009 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337009 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337009 RNA, herein designated GAM RNA, of GAM337009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337009 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337009 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337009 RNA correlate with, and may be deduced from, the identity of the GAM337009 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337010 5882 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337010 (GAM337010) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337010 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337010 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337010 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337010 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337010 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337010 precursor RNA is designated SEQ ID:5882, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5882 is located from position 65112308 to position 65112389 relative to chromosome X on the `+` strand.

GAM337010 precursor RNA folds onto itself, forming GAM337010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337010 precursor RNA, designated SEQ ID NO: 5882, and a schematic representation of a predicted secondary folding of GAM337010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337010 folded precursor RNA yielding a GAM337010 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337010 RNA, hereby incorporated herein.

GAM337010 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337010 target RNA, herein designated GAM TARGET RNA.

GAM337010 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337010 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337010 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337010 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337010 RNA, herein designated GAM RNA, to target binding sites on GAM337010 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337010 target RNA

into GAM337010 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337010 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337010 target genes. The mRNA of each one of this plurality of GAM337010 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337010 RNA, herein designated GAM RNA, and which when bound by GAM337010 RNA causes inhibition of translation of the GAM337010 target mRNA into a corresponding GAM337010 target protein.

The mechanism of the translational inhibition exerted by GAM337010 RNA, herein designated GAM RNA, on one or more GAM337010 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337010 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337010 RNA, herein designated GAM RNA, of GAM337010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337010 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337010 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337010 RNA correlate with, and may be deduced from, the identity of the GAM337010 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337011 6481 GCAAGGTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGTTTTTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTTCCCCAC Messenger 337011 (GAM337011) oligonucleotides modulates expression of respective target

CTGTCTCTTA genes whose function and utility is known in the art.

GCCTGGGGAA GAM337011 is a novel bioinformatically detectable regulatory, non protein

TTAAATGAGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337011 was detected

AGCCTTAGAA is described with additional reference to Figs. 9-15.

TGGGTGGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGT encoded by the human genome.

GAM337011 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337011 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337011 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337011 precursor RNA is designated SEQ ID:6481, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6481 is located from position 65182638 to position 65182721 relative to chromosome X on the `+` strand.

GAM337011 precursor RNA folds onto itself, forming GAM337011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337011 precursor RNA, designated SEQ ID NO: 6481, and a schematic representation of a predicted secondary folding of GAM337011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337011 folded precursor RNA yielding a GAM337011 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337011 RNA, hereby incorporated herein.

GAM337011 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337011 target RNA, herein designated GAM TARGET RNA.

GAM337011 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337011 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337011 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337011 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337011 RNA, herein designated GAM RNA, to target binding sites on GAM337011 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337011 target RNA into GAM337011 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337011 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337011 target genes. The mRNA of each one of this plurality of GAM337011 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337011 RNA, herein designated GAM RNA, and which when bound by GAM337011 RNA causes inhibition of translation of the GAM337011 target mRNA into a corresponding GAM337011 target protein.

The mechanism of the translational inhibition exerted by GAM337011 RNA, herein designated GAM RNA, on one or more GAM337011 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337011 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337011 RNA, herein designated GAM RNA, of GAM337011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337011 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337011 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337011 RNA correlate with, and may be deduced from, the identity of the GAM337011 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337013 5883 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337013 (GAM337013) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337013 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337013 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337013 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337013 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337013 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337013 precursor RNA is designated SEQ ID:5883, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5883 is located from position 65319486 to position 65319567 relative to chromosome 15 on the `+` strand.

GAM337013 precursor RNA folds onto itself, forming GAM337013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337013 precursor RNA, designated SEQ ID NO: 5883, and a schematic representation of a predicted secondary folding of GAM337013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337013 folded precursor RNA yielding a GAM337013 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337013 RNA, hereby incorporated herein.

GAM337013 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337013 target RNA, herein designated GAM TARGET RNA.

GAM337013 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337013 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337013 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337013 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337013 RNA, herein designated GAM RNA, to target binding sites on GAM337013 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337013 target RNA into GAM337013 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337013 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337013 target genes. The mRNA of each one of this plurality of GAM337013 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337013 RNA, herein designated GAM RNA, and which when bound by GAM337013 RNA causes inhibition of translation of the GAM337013 target mRNA into a corresponding GAM337013 target protein.

The mechanism of the translational inhibition exerted by GAM337013 RNA, herein designated GAM RNA, on one or more GAM337013 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337013 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337013 RNA, herein designated GAM RNA, of GAM337013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337013 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337013 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337013 RNA correlate with, and may be deduced from, the identity of the GAM337013 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337015 6423 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGGAGG Messenger 337015 (GAM337015) oligonucleotides modulates expression of respective target
CGGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCAA GAM337015 is a novel bioinformatically detectable regulatory, non protein
GGTCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337015 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGGGCAAA encoded by the human genome.

ACTCTGTCTC GAM337015 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337015 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337015 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337015 precursor RNA is designated SEQ ID:6423, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6423 is located from position 65550880 to position 65550979 relative to chromosome 3 on the `-` strand.

GAM337015 precursor RNA folds onto itself, forming GAM337015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337015 precursor RNA, designated SEQ ID NO: 6423, and a schematic representation of a predicted secondary folding of GAM337015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337015 folded precursor RNA yielding a GAM337015 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337015 RNA, hereby incorporated herein. Expression of GAM337015 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337015 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337015 target RNA, herein designated GAM TARGET RNA.

GAM337015 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337015 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337015 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337015 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337015 RNA, herein designated GAM RNA, to target binding sites on GAM337015 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337015 target RNA into GAM337015 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337015 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337015 target genes. The mRNA of each one of this plurality of GAM337015 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337015 RNA, herein designated GAM RNA, and which when bound by GAM337015 RNA causes inhibition of translation of the GAM337015 target mRNA into a corresponding GAM337015 target protein.

The mechanism of the translational inhibition exerted by GAM337015 RNA, herein designated GAM RNA, on one or more GAM337015 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337015 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337015 RNA, herein designated GAM RNA, of GAM337015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337015 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337015 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337015 RNA correlate with, and may be deduced from, the identity of the GAM337015 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337016 5990 CAAGTTTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CAAGGGGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGTGTCCGA Messenger 337016 (GAM337016) oligonucleotides modulates expression of respective target
CTCCAAGGAG genes whose function and utility is known in the art.

CATCTCCGTT GAM337016 is a novel bioinformatically detectable regulatory, non protein
TCTGAGTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337016 was detected
AACTCTCATG is described with additional reference to Figs. 9-15.

ACACTGTGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTTGCCTCA encoded by the human genome.

GGCTTG GAM337016 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337016 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337016 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337016 precursor RNA is designated SEQ ID:5990, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5990 is located from position 65582433 to position 65582528 relative to chromosome 9 on the `+` strand.

GAM337016 precursor RNA folds onto itself, forming GAM337016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337016 precursor RNA, designated SEQ ID NO: 5990, and a schematic representation of a predicted secondary folding of GAM337016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337016 folded precursor RNA yielding a GAM337016 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337016 RNA, hereby incorporated herein.

GAM337016 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337016 target RNA, herein designated GAM TARGET RNA.

GAM337016 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337016 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337016 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337016 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337016 RNA, herein designated GAM RNA, to target binding sites on GAM337016 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337016 target RNA into GAM337016 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337016 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337016 target genes. The mRNA of each one of this plurality of GAM337016 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337016 RNA, herein designated GAM RNA, and which when bound by GAM337016 RNA causes inhibition of translation of the GAM337016 target mRNA into a corresponding GAM337016 target protein.

The mechanism of the translational inhibition exerted by GAM337016 RNA, herein designated GAM RNA, on one or more GAM337016 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337016 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337016 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337016 RNA, herein designated GAM RNA, of GAM337016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337016 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337016 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337016 RNA correlate with, and may be deduced from, the identity of the GAM337016 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337017 7201 TGCGGGCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATCACATATT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGAAAA Messenger 337017 (GAM337017) oligonucleotides modulates expression of respective target
CAATTCCAAG genes whose function and utility is known in the art.

CAAGGAGAGT GAM337017 is a novel bioinformatically detectable regulatory, non protein
TGCTGGGATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337017 was detected
ATTCTGCTCT is described with additional reference to Figs. 9-15.

GGTCGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337017 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337017 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337017 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337017 precursor RNA is designated SEQ ID:7201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7201 is located from position 65582733 to position 65582809 relative to chromosome 9 on the `+` strand.

GAM337017 precursor RNA folds onto itself, forming GAM337017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337017 precursor RNA, designated SEQ ID NO: 7201, and a schematic representation of a predicted secondary folding of GAM337017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337017 folded precursor RNA yielding a GAM337017 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337017 RNA, hereby incorporated herein.

GAM337017 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337017 target RNA, herein designated GAM TARGET RNA.

GAM337017 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337017 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337017 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337017 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337017 RNA, herein designated GAM RNA, to target binding sites on GAM337017 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337017 target RNA into GAM337017 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337017 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337017 target genes. The mRNA of each one of this plurality of GAM337017 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337017 RNA, herein designated GAM RNA, and which when bound by GAM337017 RNA causes inhibition of translation of the GAM337017 target mRNA into a corresponding GAM337017 target protein.

The mechanism of the translational inhibition exerted by GAM337017 RNA, herein

designated GAM RNA, on one or more GAM337017 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337017 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337017 RNA, herein designated GAM RNA, of GAM337017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337017 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337017 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337017 RNA correlate with, and may be deduced from, the identity of the GAM337017 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337018 5884 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337018 (GAM337018) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337018 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337018 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337018 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337018 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337018 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337018 precursor RNA is designated SEQ ID:5884, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5884 is located from position 65709159 to position 65709240

relative to chromosome 1 on the `-` strand.

GAM337018 precursor RNA folds onto itself, forming GAM337018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337018 precursor RNA, designated SEQ ID NO: 5884, and a schematic representation of a predicted secondary folding of GAM337018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337018 folded precursor RNA yielding a GAM337018 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337018 RNA, hereby incorporated herein.

GAM337018 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337018 target RNA, herein designated GAM TARGET RNA.

GAM337018 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337018 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337018 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337018 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337018 RNA, herein designated GAM RNA, to target binding sites on GAM337018 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337018 target RNA into GAM337018 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337018 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337018 target genes. The mRNA of each one of this plurality of GAM337018 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337018 RNA, herein designated GAM RNA, and which when bound by GAM337018 RNA causes inhibition of translation of the GAM337018 target mRNA into a corresponding GAM337018 target protein.

The mechanism of the translational inhibition exerted by GAM337018 RNA, herein designated GAM RNA, on one or more GAM337018 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337018 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337018 RNA, herein designated GAM RNA, of GAM337018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337018 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337018 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337018 RNA correlate with, and may be deduced from, the identity of the GAM337018 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337019 5885 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337019 (GAM337019) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337019 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337019 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337019 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337019 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337019 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337019 precursor RNA is designated SEQ ID:5885, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5885 is located from position 65710652 to position 65710733 relative to chromosome 5 on the `+` strand.

GAM337019 precursor RNA folds onto itself, forming GAM337019 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337019 precursor RNA, designated SEQ ID NO: 5885, and a schematic representation of a predicted secondary folding of GAM337019 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337019 folded precursor RNA yielding a GAM337019 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337019 RNA, hereby incorporated herein.

GAM337019 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337019 target RNA, herein designated GAM TARGET RNA.

GAM337019 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337019 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337019 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337019 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337019 RNA, herein designated GAM RNA, to target

binding sites on GAM337019 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337019 target RNA into GAM337019 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337019 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337019 target genes. The mRNA of each one of this plurality of GAM337019 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337019 RNA, herein designated GAM RNA, and which when bound by GAM337019 RNA causes inhibition of translation of the GAM337019 target mRNA into a corresponding GAM337019 target protein.

The mechanism of the translational inhibition exerted by GAM337019 RNA, herein designated GAM RNA, on one or more GAM337019 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337019 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337019 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337019 RNA, herein designated GAM RNA, of GAM337019 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337019 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337019 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337019 RNA correlate with, and may be deduced from, the identity of the GAM337019 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337022 7351 TTTTGGTAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACATTCATC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGTCGTTT Messenger 337022 (GAM337022) oligonucleotides modulates expression of respective target

CTCTCTCCCA genes whose function and utility is known in the art.

GCTTGACCTT GAM337022 is a novel bioinformatically detectable regulatory, non protein

AGGTTAATAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337022 was detected

TTCATTTGGG is described with additional reference to Figs. 9-15.

TCAAGAAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AATATGTAGG encoded by the human genome.

AGAGCTATGT GAM337022 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGCTTTAACA GAM337022 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AGA GAM337022 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337022 precursor RNA is designated SEQ ID:7351, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7351 is located from position 65754862 to position 65754974 relative to chromosome 12 on the `+` strand.

GAM337022 precursor RNA folds onto itself, forming GAM337022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337022 precursor RNA, designated SEQ ID NO: 7351, and a schematic representation of a predicted secondary folding of GAM337022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337022 folded precursor RNA yielding a GAM337022 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337022 RNA, hereby incorporated herein.

GAM337022 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337022 target RNA, herein designated GAM TARGET RNA.

GAM337022 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337022 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337022 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337022 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337022 RNA, herein designated GAM RNA, to target binding sites on GAM337022 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337022 target RNA into GAM337022 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337022 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337022 target genes. The mRNA of each one of this plurality of GAM337022 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337022 RNA, herein designated GAM RNA, and which when bound by GAM337022 RNA causes inhibition of translation of the GAM337022 target mRNA into a corresponding GAM337022 target protein.

The mechanism of the translational inhibition exerted by GAM337022 RNA, herein designated GAM RNA, on one or more GAM337022 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337022 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337022 RNA, herein designated GAM RNA, of GAM337022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337022 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337022 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337022 RNA correlate with, and may be deduced from, the identity of the GAM337022 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337023 6550 GCTGTCCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCCTGGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
TACTAGAGGG Messenger 337023 (GAM337023) oligonucleotides modulates expression of respective target
TAAAGGAATG genes whose function and utility is known in the art.

GAACCATGTC GAM337023 is a novel bioinformatically detectable regulatory, non protein
TGGGGTCCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337023 was detected
TTAGTAACTT is described with additional reference to Figs. 9-15.

GCAGGGTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAATTGACT encoded by the human genome.

GC GAM337023 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337023 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337023 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337023 precursor RNA is designated SEQ ID:6550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6550 is located from position 65815377 to position 65815468 relative to chromosome 7 on the `+` strand.

GAM337023 precursor RNA folds onto itself, forming GAM337023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337023 precursor RNA, designated SEQ ID NO: 6550, and a schematic representation of a predicted secondary folding of GAM337023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337023 folded precursor RNA yielding a GAM337023 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337023 RNA, hereby incorporated herein.

GAM337023 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337023 target RNA, herein designated GAM TARGET RNA.

GAM337023 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337023 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337023 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337023 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337023 RNA, herein designated GAM RNA, to target binding sites on GAM337023 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337023 target RNA into GAM337023 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337023 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337023 target genes. The mRNA of each one of this plurality of GAM337023 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337023 RNA, herein designated GAM RNA, and which when bound by GAM337023 RNA causes inhibition of translation of the GAM337023 target mRNA into a corresponding GAM337023 target protein.

The mechanism of the translational inhibition exerted by GAM337023 RNA, herein designated GAM RNA, on one or more GAM337023 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337023 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337023 RNA, herein designated GAM RNA, of GAM337023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337023 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337023 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337023

RNA correlate with, and may be deduced from, the identity of the GAM337023 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337024 7042 TCCTGAGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGAGATACT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAGGGTAAA Messenger 337024 (GAM337024) oligonucleotides modulates expression of respective target
GGAATGGAAC genes whose function and utility is known in the art.

CATGTCTGGG GAM337024 is a novel bioinformatically detectable regulatory, non protein
GTCCCTTTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337024 was detected
TAACTTGCAG is described with additional reference to Figs. 9-15.

GGTCTGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337024 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337024 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337024 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337024 precursor RNA is designated SEQ ID:7042, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7042 is located from position 65815381 to position 65815459 relative to chromosome 7 on the `+` strand.

GAM337024 precursor RNA folds onto itself, forming GAM337024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337024 precursor RNA, designated SEQ ID NO: 7042, and a schematic representation of a predicted secondary folding of GAM337024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337024 folded precursor RNA yielding a GAM337024 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337024 RNA, hereby incorporated herein.

GAM337024 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337024 target RNA, herein designated GAM TARGET RNA.

GAM337024 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337024 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337024 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337024 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337024 RNA, herein designated GAM RNA, to target binding sites on GAM337024 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337024 target RNA into GAM337024 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337024 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337024 target genes. The mRNA of each one of this plurality of GAM337024 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337024 RNA, herein designated GAM RNA, and which when bound by GAM337024 RNA causes inhibition of translation of the GAM337024 target mRNA into a corresponding GAM337024 target protein.

The mechanism of the translational inhibition exerted by GAM337024 RNA, herein designated GAM RNA, on one or more GAM337024 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337024 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337024 RNA, herein designated GAM RNA, of GAM337024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337024 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337024 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337024 RNA correlate with, and may be deduced from, the identity of the GAM337024 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337025 7224 TGGCAGGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGCTCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCTTTTCTG Messenger 337025 (GAM337025) oligonucleotides modulates expression of respective target
CAACCTGTTT genes whose function and utility is known in the art.

GCTCACTGGT GAM337025 is a novel bioinformatically detectable regulatory, non protein
TTATTTGTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337025 was detected
ATTGGGGCTA is described with additional reference to Figs. 9-15.

TGAGGGTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGCTGTCCC encoded by the human genome.

TGCCA GAM337025 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337025 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337025 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337025 precursor RNA is designated SEQ ID:7224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7224 is located from position 65938364 to position 65938458 relative to chromosome 11 on the `+` strand.

GAM337025 precursor RNA folds onto itself, forming GAM337025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337025 precursor RNA, designated SEQ ID NO: 7224, and a schematic representation of a predicted secondary folding of GAM337025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337025 folded precursor RNA yielding a GAM337025 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337025 RNA, hereby incorporated herein.

GAM337025 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337025 target RNA, herein designated GAM TARGET RNA.

GAM337025 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337025 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337025 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337025 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337025 RNA, herein designated GAM RNA, to target binding sites on GAM337025 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337025 target RNA into GAM337025 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337025 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337025 target genes. The mRNA of each one of this plurality of GAM337025 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337025 RNA, herein designated GAM RNA, and which when bound by GAM337025 RNA causes inhibition of translation of the GAM337025 target mRNA into a corresponding GAM337025 target protein.

The mechanism of the translational inhibition exerted by GAM337025 RNA, herein designated GAM RNA, on one or more GAM337025 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337025 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337025 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337025 RNA, herein designated GAM RNA, of GAM337025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337025 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337025 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337025 RNA correlate with, and may be deduced from, the identity of the GAM337025 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337027 7185 TGAGGTGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGATTACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGCCCAAGAG Messenger 337027 (GAM337027) oligonucleotides modulates expression of respective target

GAGGAGGCTG genes whose function and utility is known in the art.

CAGTGAGTCA GAM337027 is a novel bioinformatically detectable regulatory, non protein

ACATTGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337027 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGTG encoded by the human genome.

ACCCCATCTC GAM337027 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337027 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337027 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337027 precursor RNA is designated SEQ ID:7185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7185 is located from position 66122717 to position 66122817 relative to chromosome 7 on the `-` strand.

GAM337027 precursor RNA folds onto itself, forming GAM337027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337027 precursor RNA, designated SEQ ID NO: 7185, and a schematic representation of a predicted secondary folding of GAM337027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337027 folded precursor RNA yielding a GAM337027 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337027 RNA, hereby incorporated herein. Expression of GAM337027 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337027 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337027 target RNA, herein designated GAM TARGET RNA.

GAM337027 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337027 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337027 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337027 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337027 RNA, herein designated GAM RNA, to target binding sites on GAM337027 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337027 target RNA into GAM337027 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337027 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337027 target genes. The mRNA of each one of this plurality of GAM337027 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337027 RNA, herein designated GAM RNA, and which when bound by GAM337027 RNA causes inhibition of

translation of the GAM337027 target mRNA into a corresponding GAM337027 target protein.

The mechanism of the translational inhibition exerted by GAM337027 RNA, herein designated GAM RNA, on one or more GAM337027 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337027 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337027 RNA, herein designated GAM RNA, of GAM337027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337027 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337027 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337027 RNA correlate with, and may be deduced from, the identity of the GAM337027 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337028 6456 GAGGTGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATTACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCCAAGAGG Messenger 337028 (GAM337028) oligonucleotides modulates expression of respective target
AGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGTCAA GAM337028 is a novel bioinformatically detectable regulatory, non protein
CATTGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337028 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGTGA encoded by the human genome.

CCCCATCTC GAM337028 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337028 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337028 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337028 precursor RNA is designated SEQ ID:6456, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6456 is located from position 66122718 to position 66122816 relative to chromosome 7 on the `-` strand.

GAM337028 precursor RNA folds onto itself, forming GAM337028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337028 precursor RNA, designated SEQ ID NO: 6456, and a schematic representation of a predicted secondary folding of GAM337028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337028 folded precursor RNA yielding a GAM337028 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337028 RNA, hereby incorporated herein. Expression of GAM337028 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337028 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337028 target RNA, herein designated GAM TARGET RNA.

GAM337028 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337028 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337028 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337028 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337028 RNA, herein designated GAM RNA, to target binding sites on GAM337028 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337028 target RNA into GAM337028 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337028 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337028 target genes. The mRNA of each one of this plurality of GAM337028 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337028 RNA, herein designated GAM RNA, and which when bound by GAM337028 RNA causes inhibition of translation of the GAM337028 target mRNA into a corresponding GAM337028 target protein.

The mechanism of the translational inhibition exerted by GAM337028 RNA, herein designated GAM RNA, on one or more GAM337028 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337028 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337028 RNA, herein designated GAM RNA, of GAM337028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337028 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337028 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337028 RNA correlate with, and may be deduced from, the identity of the GAM337028 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337029 6983 TATGGGAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGCAGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGAAAAAAGT Messenger 337029 (GAM337029) oligonucleotides modulates expression of respective target
ACATTTGGTA genes whose function and utility is known in the art.

TACATGCATA GAM337029 is a novel bioinformatically detectable regulatory, non protein
GAGATGTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337029 was detected
TAGCAAATGG is described with additional reference to Figs. 9-15.

TCTGAATGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGCCTTAGA encoded by the human genome.

CCACAGTTTT GAM337029 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CATA GAM337029 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337029 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337029 precursor RNA is designated SEQ ID:6983, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6983 is located from position 66268768 to position 66268871 relative to chromosome 14 on the `-` strand.

GAM337029 precursor RNA folds onto itself, forming GAM337029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337029 precursor RNA, designated SEQ ID NO: 6983, and a schematic representation of a predicted secondary folding of GAM337029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337029 folded precursor RNA yielding a GAM337029 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337029 RNA, hereby incorporated herein.

GAM337029 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337029 target RNA, herein designated GAM TARGET RNA.

GAM337029 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337029 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337029 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337029 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337029 RNA, herein designated GAM RNA, to target binding sites on GAM337029 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337029 target RNA into GAM337029 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337029 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337029 target genes. The mRNA of each one of this plurality of GAM337029 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337029 RNA, herein designated GAM RNA, and which when bound by GAM337029 RNA causes inhibition of translation of the GAM337029 target mRNA into a corresponding GAM337029 target protein.

The mechanism of the translational inhibition exerted by GAM337029 RNA, herein designated GAM RNA, on one or more GAM337029 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337029 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337029 RNA, herein designated GAM RNA, of GAM337029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337029 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337029 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337029 RNA correlate with, and may be deduced from, the identity of the GAM337029 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337030 7231 TGGGAAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCAGTTTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAAAAAGTAC Messenger 337030 (GAM337030) oligonucleotides modulates expression of respective target

ATTTGGTATA genes whose function and utility is known in the art.

CATGCATAGA GAM337030 is a novel bioinformatically detectable regulatory, non protein

GATGTGCATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337030 was detected

GCAAATGGTC is described with additional reference to Figs. 9-15.

TGAATGAATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCCTTAGACC encoded by the human genome.

A GAM337030 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337030 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337030 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337030 precursor RNA is designated SEQ ID:7231, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7231 is located from position 66268779 to position 66268869 relative to chromosome 14 on the `-` strand.

GAM337030 precursor RNA folds onto itself, forming GAM337030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337030 precursor RNA, designated SEQ ID NO: 7231, and a schematic representation of a predicted secondary folding of GAM337030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337030 folded precursor RNA yielding a GAM337030 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337030 RNA, hereby incorporated herein.

GAM337030 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337030 target RNA, herein designated GAM TARGET RNA.

GAM337030 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337030 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337030 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337030 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337030 RNA, herein designated GAM RNA, to target binding sites on GAM337030 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337030 target RNA into GAM337030 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337030 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337030 target genes. The mRNA of each one of this plurality of GAM337030 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337030 RNA, herein designated GAM RNA, and which when bound by GAM337030 RNA causes inhibition of translation of the GAM337030 target mRNA into a corresponding GAM337030 target protein.

The mechanism of the translational inhibition exerted by GAM337030 RNA, herein designated GAM RNA, on one or more GAM337030 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337030 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337030 RNA, herein designated GAM RNA, of GAM337030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337030 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337030 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337030 RNA correlate with, and may be deduced from, the identity of the GAM337030 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337031 5765 AGGCACCTAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGACTTCACA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCTAATGGC Messenger 337031 (GAM337031) oligonucleotides modulates expression of respective target
AGTCCCTGGA genes whose function and utility is known in the art.

GCAGGAAGCA GAM337031 is a novel bioinformatically detectable regulatory, non protein
ACTTGTTATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337031 was detected
CTGCTCAAGA is described with additional reference to Figs. 9-15.

GAATCCACCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAGCTCTTG encoded by the human genome.

GCCT GAM337031 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337031 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337031 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337031 precursor RNA is designated SEQ ID:5765, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5765 is located from position 66387514 to position 66387607 relative to chromosome 16 on the `+` strand.

GAM337031 precursor RNA folds onto itself, forming GAM337031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337031 precursor RNA, designated SEQ ID NO: 5765, and a schematic representation of a predicted secondary folding of GAM337031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337031 folded precursor RNA yielding a GAM337031 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337031 RNA, hereby incorporated herein.

GAM337031 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337031 target RNA, herein designated GAM TARGET RNA.

GAM337031 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337031 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337031 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337031 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337031 RNA, herein designated GAM RNA, to target binding sites on GAM337031 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337031 target RNA into GAM337031 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337031 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337031 target genes. The mRNA of each one of this plurality of GAM337031 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337031 RNA, herein designated GAM RNA, and which when bound by GAM337031 RNA causes inhibition of translation of the GAM337031 target mRNA into a corresponding GAM337031 target protein.

The mechanism of the translational inhibition exerted by GAM337031 RNA, herein designated GAM RNA, on one or more GAM337031 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337031 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337031 RNA, herein designated GAM RNA, of GAM337031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337031 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337031 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337031 RNA correlate with, and may be deduced from, the identity of the GAM337031 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337032 7332 TTGGGAAACT Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGTAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AATCACTTGA Messenger 337032 (GAM337032) oligonucleotides modulates expression of respective target
GCCCCGGAGG genes whose function and utility is known in the art.

CAGGGGTTGC GAM337032 is a novel bioinformatically detectable regulatory, non protein
AGTGAGCTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337032 was detected
GATTGTGCCA is described with additional reference to Figs. 9-15.

CTGCACTCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCTGGGCAA encoded by the human genome.

CAGAGTGAAA GAM337032 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTCCATCATC GAM337032 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
ATCTCAA GAM337032 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337032 precursor RNA is designated SEQ ID:7332, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7332 is located from position 66457769 to position 66457885 relative to chromosome 12 on the `+` strand.

GAM337032 precursor RNA folds onto itself, forming GAM337032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337032 precursor RNA, designated SEQ ID NO: 7332, and a schematic representation of a predicted secondary folding of GAM337032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337032 folded precursor RNA yielding a GAM337032 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337032 RNA, hereby incorporated herein. Expression of GAM337032 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337032 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337032 target RNA, herein designated GAM TARGET RNA.

GAM337032 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337032 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337032 RNA, herein designated GAM RNA, to target binding sites on GAM337032 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337032 target RNA into GAM337032 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337032 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337032 target genes. The mRNA of each one of this plurality of GAM337032 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337032 RNA, herein designated GAM RNA, and which when bound by GAM337032 RNA causes inhibition of translation of the GAM337032 target mRNA into a corresponding GAM337032 target protein.

The mechanism of the translational inhibition exerted by GAM337032 RNA, herein designated GAM RNA, on one or more GAM337032 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337032 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337032 RNA, herein designated GAM RNA, of GAM337032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337032 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337032 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337032 RNA correlate with, and may be deduced from, the identity of the GAM337032 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337033 6620 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAGCCCCG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGGGG Messenger 337033 (GAM337033) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATTGT GAM337033 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337033 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAACTCC encoded by the human genome.

GAM337033 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337033 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337033 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337033 precursor RNA is designated SEQ ID:6620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6620 is located from position 66457785 to position 66457872 relative to chromosome 12 on the `+` strand.

GAM337033 precursor RNA folds onto itself, forming GAM337033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337033 precursor RNA, designated SEQ ID NO: 6620, and a schematic representation of a predicted secondary folding of GAM337033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337033 folded precursor RNA yielding a GAM337033 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337033 RNA, hereby incorporated herein. Expression of GAM337033 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337033 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337033 target RNA, herein designated GAM TARGET RNA.

GAM337033 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337033 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337033 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337033 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337033 RNA, herein designated GAM RNA, to target binding sites on GAM337033 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337033 target RNA into GAM337033 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337033 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337033 target genes. The mRNA of each one of this plurality of GAM337033 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337033 RNA,

herein designated GAM RNA, and which when bound by GAM337033 RNA causes inhibition of translation of the GAM337033 target mRNA into a corresponding GAM337033 target protein.

The mechanism of the translational inhibition exerted by GAM337033 RNA, herein designated GAM RNA, on one or more GAM337033 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337033 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337033 RNA, herein designated GAM RNA, of GAM337033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337033 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337033 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337033 RNA correlate with, and may be deduced from, the identity of the GAM337033 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337035 6249 CTTAAGTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTGCAGTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGTGTGTAT Messenger 337035 (GAM337035) oligonucleotides modulates expression of respective target

GTCTGTGTGT genes whose function and utility is known in the art.

GCATGCACGC GAM337035 is a novel bioinformatically detectable regulatory, non protein

ACATGTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337035 was detected

ATGCAGCAGG is described with additional reference to Figs. 9-15.

GAGAGTGGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTAAG encoded by the human genome.

GAM337035 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337035 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337035 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337035 precursor RNA is designated SEQ ID:6249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6249 is located from position 66813729 to position 66813813 relative to chromosome 12 on the `+` strand.

GAM337035 precursor RNA folds onto itself, forming GAM337035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337035 precursor RNA, designated SEQ ID NO: 6249, and a schematic representation of a predicted secondary folding of GAM337035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337035 folded precursor RNA yielding a GAM337035 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337035 RNA, hereby incorporated herein.

GAM337035 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337035 target RNA, herein designated GAM TARGET RNA.

GAM337035 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337035 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337035 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337035 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337035 RNA, herein designated GAM RNA, to target binding sites on GAM337035 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337035 target RNA

into GAM337035 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337035 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337035 target genes. The mRNA of each one of this plurality of GAM337035 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337035 RNA, herein designated GAM RNA, and which when bound by GAM337035 RNA causes inhibition of translation of the GAM337035 target mRNA into a corresponding GAM337035 target protein.

The mechanism of the translational inhibition exerted by GAM337035 RNA, herein designated GAM RNA, on one or more GAM337035 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337035 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337035 RNA, herein designated GAM RNA, of GAM337035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337035 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337035 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337035 RNA correlate with, and may be deduced from, the identity of the GAM337035 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337036 6824 GGGTGTGAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAACATCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCCCTTGTT Messenger 337036 (GAM337036) oligonucleotides modulates expression of respective target

TTCAACCTAG genes whose function and utility is known in the art.

TAGGCCAGTT GAM337036 is a novel bioinformatically detectable regulatory, non protein

TAGAAACAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337036 was detected

CCACAGGGAA is described with additional reference to Figs. 9-15.

GGTGTTGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCATTACTC encoded by the human genome.

GAM337036 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337036 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337036 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337036 precursor RNA is designated SEQ ID:6824, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6824 is located from position 66902019 to position 66902108 relative to chromosome 16 on the `+` strand.

GAM337036 precursor RNA folds onto itself, forming GAM337036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337036 precursor RNA, designated SEQ ID NO: 6824, and a schematic representation of a predicted secondary folding of GAM337036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337036 folded precursor RNA yielding a GAM337036 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337036 RNA, hereby incorporated herein.

GAM337036 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337036 target RNA, herein designated GAM TARGET RNA.

GAM337036 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337036 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337036 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337036 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337036 RNA, herein designated GAM RNA, to target binding sites on GAM337036 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337036 target RNA into GAM337036 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337036 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337036 target genes. The mRNA of each one of this plurality of GAM337036 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337036 RNA, herein designated GAM RNA, and which when bound by GAM337036 RNA causes inhibition of translation of the GAM337036 target mRNA into a corresponding GAM337036 target protein.

The mechanism of the translational inhibition exerted by GAM337036 RNA, herein designated GAM RNA, on one or more GAM337036 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337036 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337036 RNA, herein designated GAM RNA, of GAM337036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337036 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337036 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337036 RNA correlate with, and may be deduced from, the identity of the GAM337036 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337037 6785 GGGAGAGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTGAGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGAGGTGTC Messenger 337037 (GAM337037) oligonucleotides modulates expression of respective target

AGGAATGAAA genes whose function and utility is known in the art.

GAATGTCTTA GAM337037 is a novel bioinformatically detectable regulatory, non protein
AAATTCTAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337037 was detected
CAGTCTTTCT is described with additional reference to Figs. 9-15.

TCTTCTTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTATTAACA encoded by the human genome.

GCAATTAACT GAM337037 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTCTC GAM337037 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337037 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337037 precursor RNA is designated SEQ ID:6785, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6785 is located from position 66974964 to position 66975068 relative to chromosome 9 on the `+` strand.

GAM337037 precursor RNA folds onto itself, forming GAM337037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337037 precursor RNA, designated SEQ ID NO: 6785, and a schematic representation of a predicted secondary folding of GAM337037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337037 folded precursor RNA yielding a GAM337037 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337037 RNA, hereby incorporated herein.

GAM337037 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337037 target RNA, herein designated GAM TARGET RNA.

GAM337037 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337037 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337037 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337037 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337037 RNA, herein designated GAM RNA, to target binding sites on GAM337037 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337037 target RNA into GAM337037 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337037 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337037 target genes. The mRNA of each one of this plurality of GAM337037 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337037 RNA, herein designated GAM RNA, and which when bound by GAM337037 RNA causes inhibition of translation of the GAM337037 target mRNA into a corresponding GAM337037 target protein.

The mechanism of the translational inhibition exerted by GAM337037 RNA, herein designated GAM RNA, on one or more GAM337037 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337037 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337037 RNA, herein designated GAM RNA, of GAM337037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337037 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337037 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337037 RNA correlate with, and may be deduced from, the identity of the GAM337037 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337038 6707 GGAGAGGCAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTGAGGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAGGTGTCA Messenger 337038 (GAM337038) oligonucleotides modulates expression of respective target

GGAATGAAAG genes whose function and utility is known in the art.

AATGTCTTAA GAM337038 is a novel bioinformatically detectable regulatory, non protein

AATTCTAAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337038 was detected

AGTCTTTCTT is described with additional reference to Figs. 9-15.

CTTCTTCTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTATTAACAG encoded by the human genome.

CAATTAACTC GAM337038 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCT GAM337038 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337038 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337038 precursor RNA is designated SEQ ID:6707, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6707 is located from position 66974965 to position 66975067 relative to chromosome 9 on the `+` strand.

GAM337038 precursor RNA folds onto itself, forming GAM337038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337038 precursor RNA, designated SEQ ID NO: 6707, and a schematic representation of a predicted secondary folding of GAM337038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337038 folded precursor RNA yielding a GAM337038 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337038 RNA, hereby incorporated herein.

GAM337038 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337038 target RNA, herein designated GAM TARGET RNA.

GAM337038 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337038 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337038 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337038 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337038 RNA, herein designated GAM RNA, to target binding sites on GAM337038 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337038 target RNA into GAM337038 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337038 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337038 target genes. The mRNA of each one of this plurality of GAM337038 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337038 RNA, herein designated GAM RNA, and which when bound by GAM337038 RNA causes inhibition of translation of the GAM337038 target mRNA into a corresponding GAM337038 target protein.

The mechanism of the translational inhibition exerted by GAM337038 RNA, herein designated GAM RNA, on one or more GAM337038 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337038 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337038 RNA, herein designated GAM RNA, of GAM337038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337038 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337038 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337038 RNA correlate with, and may be deduced from, the identity of the GAM337038 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337039 6352 GAGAGGCATT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGAGGGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGTCAG Messenger 337039 (GAM337039) oligonucleotides modulates expression of respective target
GAATGAAAGA genes whose function and utility is known in the art.

ATGTCTTAAA GAM337039 is a novel bioinformatically detectable regulatory, non protein
ATTCTAAGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337039 was detected
GTCTTTCTTC is described with additional reference to Figs. 9-15.

TTCTTCTCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TATTAACAGC encoded by the human genome.

AATTAACTCT GAM337039 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM337039 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337039 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337039 precursor RNA is designated SEQ ID:6352, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6352 is located from position 66974966 to position 66975066 relative to chromosome 9 on the `+` strand.

GAM337039 precursor RNA folds onto itself, forming GAM337039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337039 precursor RNA, designated SEQ ID NO: 6352, and a schematic representation of a predicted secondary folding of GAM337039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337039 folded precursor RNA yielding a GAM337039 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337039 RNA, hereby incorporated herein.

GAM337039 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337039 target RNA, herein designated GAM TARGET RNA.

GAM337039 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337039 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337039 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337039 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337039 RNA, herein designated GAM RNA, to target binding sites on GAM337039 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337039 target RNA into GAM337039 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337039 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337039 target genes. The mRNA of each one of this plurality of GAM337039 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337039 RNA, herein designated GAM RNA, and which when bound by GAM337039 RNA causes inhibition of translation of the GAM337039 target mRNA into a corresponding GAM337039 target protein.

The mechanism of the translational inhibition exerted by GAM337039 RNA, herein designated GAM RNA, on one or more GAM337039 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337039 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337039 RNA, herein designated GAM RNA, of GAM337039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337039 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337039 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337039 RNA correlate with, and may be deduced from, the identity of the GAM337039 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337041 7312 TTGCTTGAAC CCAAGAGGCG GAGGTTGCAG TGAGCTAAGA TCATGCCACT GCACTCCAGC CTGGGTGACA GAGCAA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337041 (GAM337041) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337041 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337041 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337041 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337041 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337041 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337041 precursor RNA is designated SEQ ID:7312, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7312 is located from position 67244014 to position 67244089 relative to chromosome 17 on the `-` strand.

GAM337041 precursor RNA folds onto itself, forming GAM337041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337041 precursor RNA, designated SEQ ID NO: 7312, and a schematic representation of a predicted secondary folding of GAM337041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337041 folded precursor RNA yielding a GAM337041 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337041 RNA, hereby incorporated herein.

GAM337041 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337041 target RNA, herein designated GAM TARGET RNA.

GAM337041 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337041 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337041 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337041 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337041 RNA, herein designated GAM RNA, to target binding sites on GAM337041 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337041 target RNA into GAM337041 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337041 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337041 target genes. The mRNA of each one of this plurality of GAM337041 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337041 RNA, herein designated GAM RNA, and which when bound by GAM337041 RNA causes inhibition of translation of the GAM337041 target mRNA into a corresponding GAM337041 target protein.

The mechanism of the translational inhibition exerted by GAM337041 RNA, herein designated GAM RNA, on one or more GAM337041 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337041 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337041 RNA, herein designated GAM RNA, of GAM337041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337041 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337041 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337041 RNA correlate with, and may be deduced from, the identity of the GAM337041 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337042 6744 GGCCACCTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCCTATTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGCACTTC Messenger 337042 (GAM337042) oligonucleotides modulates expression of respective target
ATTCTTCTGA genes whose function and utility is known in the art.

TAATGGAGTA GAM337042 is a novel bioinformatically detectable regulatory, non protein
TGAGAGAGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337042 was detected
TGGGACATGA is described with additional reference to Figs. 9-15.

GGTGGACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337042 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337042 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337042 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337042 precursor RNA is designated SEQ ID:6744, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6744 is located from position 67268904 to position 67268981 relative to chromosome 16 on the `+` strand.

GAM337042 precursor RNA folds onto itself, forming GAM337042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337042 precursor RNA, designated SEQ ID NO: 6744, and a schematic representation of a predicted secondary folding of GAM337042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337042 folded precursor RNA yielding a GAM337042 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337042 RNA, hereby incorporated herein.

GAM337042 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337042 target RNA, herein designated GAM TARGET RNA.

GAM337042 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337042 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337042 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337042 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337042 RNA, herein designated GAM RNA, to target binding sites on GAM337042 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337042 target RNA into GAM337042 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337042 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337042 target genes. The mRNA of each one of this

plurality of GAM337042 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337042 RNA, herein designated GAM RNA, and which when bound by GAM337042 RNA causes inhibition of translation of the GAM337042 target mRNA into a corresponding GAM337042 target protein.

The mechanism of the translational inhibition exerted by GAM337042 RNA, herein designated GAM RNA, on one or more GAM337042 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337042 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337042 RNA, herein designated GAM RNA, of GAM337042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337042 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337042 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337042 RNA correlate with, and may be deduced from, the identity of the GAM337042 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337043 6878 GTCCCAAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGGAAAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGCAAGGG Messenger 337043 (GAM337043) oligonucleotides modulates expression of respective target

CATGGTCCAT genes whose function and utility is known in the art.

CTGCTGCCTT GAM337043 is a novel bioinformatically detectable regulatory, non protein

TTCTGGGCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337043 was detected

CCTTTTCTGC is described with additional reference to Figs. 9-15.

TGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337043 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337043 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337043 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337043 precursor RNA is designated SEQ ID:6878, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6878 is located from position 67274771 to position 67274844 relative to chromosome 11 on the `-` strand.

GAM337043 precursor RNA folds onto itself, forming GAM337043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337043 precursor RNA, designated SEQ ID NO: 6878, and a schematic representation of a predicted secondary folding of GAM337043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337043 folded precursor RNA yielding a GAM337043 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337043 RNA, hereby incorporated herein.

GAM337043 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337043 target RNA, herein designated GAM TARGET RNA.

GAM337043 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337043 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337043 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337043 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337043 RNA, herein designated GAM RNA, to target binding sites on GAM337043 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337043 target RNA into GAM337043 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337043 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337043 target genes. The mRNA of each one of this plurality of GAM337043 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337043 RNA, herein designated GAM RNA, and which when bound by GAM337043 RNA causes inhibition of translation of the GAM337043 target mRNA into a corresponding GAM337043 target protein.

The mechanism of the translational inhibition exerted by GAM337043 RNA, herein designated GAM RNA, on one or more GAM337043 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337043 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337043 RNA, herein designated GAM RNA, of GAM337043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337043 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337043 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337043 RNA correlate with, and may be deduced from, the identity of the GAM337043 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337045 5886 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337045 (GAM337045) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337045 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337045 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337045 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337045 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337045 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337045 precursor RNA is designated SEQ ID:5886, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5886 is located from position 67383500 to position 67383581 relative to chromosome 18 on the `-` strand.

GAM337045 precursor RNA folds onto itself, forming GAM337045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337045 precursor RNA, designated SEQ ID NO: 5886, and a schematic representation of a predicted secondary folding of GAM337045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337045 folded precursor RNA yielding a GAM337045 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337045 RNA, hereby incorporated herein.

GAM337045 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337045 target RNA, herein designated GAM TARGET RNA.

GAM337045 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337045 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337045 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337045 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337045 RNA, herein designated GAM RNA, to target binding sites on GAM337045 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337045 target RNA into GAM337045 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337045 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337045 target genes. The mRNA of each one of this plurality of GAM337045 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337045 RNA, herein designated GAM RNA, and which when bound by GAM337045 RNA causes inhibition of translation of the GAM337045 target mRNA into a corresponding GAM337045 target protein.

The mechanism of the translational inhibition exerted by GAM337045 RNA, herein designated GAM RNA, on one or more GAM337045 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337045 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337045 RNA, herein designated GAM RNA, of GAM337045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337045 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337045 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337045 RNA correlate with, and may be deduced from, the identity of the GAM337045 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337046 6274 CTTTGTGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTTTGAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTAATGAG Messenger 337046 (GAM337046) oligonucleotides modulates expression of respective target

CGCAGTTTAC genes whose function and utility is known in the art.

TGAGTCATTA GAM337046 is a novel bioinformatically detectable regulatory, non protein
CTAGTCTCGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337046 was detected
CCCATTCGTA is described with additional reference to Figs. 9-15.

GAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337046 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337046 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337046 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337046 precursor RNA is designated SEQ ID:6274, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6274 is located from position 67560293 to position 67560365 relative to chromosome 8 on the `-` strand.

GAM337046 precursor RNA folds onto itself, forming GAM337046 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337046 precursor RNA, designated SEQ ID NO: 6274, and a schematic representation of a predicted secondary folding of GAM337046 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337046 folded precursor RNA yielding a GAM337046 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337046 RNA, hereby incorporated herein.

GAM337046 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337046 target RNA, herein designated GAM TARGET RNA.

GAM337046 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337046 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337046 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337046 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337046 RNA, herein designated GAM RNA, to target binding sites on GAM337046 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337046 target RNA into GAM337046 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337046 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337046 target genes. The mRNA of each one of this plurality of GAM337046 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337046 RNA, herein designated GAM RNA, and which when bound by GAM337046 RNA causes inhibition of translation of the GAM337046 target mRNA into a corresponding GAM337046 target protein.

The mechanism of the translational inhibition exerted by GAM337046 RNA, herein designated GAM RNA, on one or more GAM337046 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337046 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337046 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337046 RNA, herein designated GAM RNA, of GAM337046 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337046 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337046 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337046 RNA correlate with, and may be deduced from, the identity of the GAM337046 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337047 6944 GTTTGGAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGTTGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTGAGGCAC Messenger 337047 (GAM337047) oligonucleotides modulates expression of respective target
GGTAAGGAGT genes whose function and utility is known in the art.

GGTTCCAATT GAM337047 is a novel bioinformatically detectable regulatory, non protein
TGGGGTGCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337047 was detected
ACGGGATCCA is described with additional reference to Figs. 9-15.

CAGATCTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTTCTTTCC encoded by the human genome.

TCTGCCTCCC GAM337047 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CATCTCCTGA GAM337047 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
T GAM337047 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337047 precursor RNA is designated SEQ ID:6944, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6944 is located from position 67697723 to position 67697833 relative to chromosome 12 on the `+` strand.

GAM337047 precursor RNA folds onto itself, forming GAM337047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337047 precursor RNA, designated SEQ ID NO: 6944, and a schematic representation of a predicted secondary folding of GAM337047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337047 folded precursor RNA yielding a GAM337047 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337047 RNA, hereby incorporated herein.

GAM337047 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337047 target RNA, herein designated GAM TARGET RNA.

GAM337047 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337047 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337047 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337047 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337047 RNA, herein designated GAM RNA, to target binding sites on GAM337047 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337047 target RNA into GAM337047 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337047 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337047 target genes. The mRNA of each one of this plurality of GAM337047 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337047 RNA, herein designated GAM RNA, and which when bound by GAM337047 RNA causes inhibition of translation of the GAM337047 target mRNA into a corresponding GAM337047 target protein.

The mechanism of the translational inhibition exerted by GAM337047 RNA, herein designated GAM RNA, on one or more GAM337047 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337047 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337047 RNA, herein designated GAM RNA, of GAM337047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337047 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337047 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337047 RNA correlate with, and may be deduced from, the identity of the GAM337047 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337051 6351 GAGAGAGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGAGAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCGGCTGGGG Messenger 337051 (GAM337051) oligonucleotides modulates expression of respective target
CGAGTGTGGA genes whose function and utility is known in the art.

CCGCAGCCCA GAM337051 is a novel bioinformatically detectable regulatory, non protein
GAGTTAGTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337051 was detected
TGGCTGCAGT is described with additional reference to Figs. 9-15.

GCAACTCTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAAAATGTT encoded by the human genome.

ATTCTCACGC GAM337051 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CCTTTCTT GAM337051 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337051 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337051 precursor RNA is designated SEQ ID:6351, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6351 is located from position 68096932 to position 68097039 relative to chromosome 9 on the `+` strand.

GAM337051 precursor RNA folds onto itself, forming GAM337051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337051 precursor RNA, designated SEQ ID NO: 6351, and a schematic representation of a predicted secondary folding of GAM337051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337051 folded precursor

RNA yielding a GAM337051 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337051 RNA, hereby incorporated herein.

GAM337051 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337051 target RNA, herein designated GAM TARGET RNA.

GAM337051 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337051 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337051 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337051 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337051 RNA, herein designated GAM RNA, to target binding sites on GAM337051 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337051 target RNA into GAM337051 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337051 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337051 target genes. The mRNA of each one of this plurality of GAM337051 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337051 RNA, herein designated GAM RNA, and which when bound by GAM337051 RNA causes inhibition of translation of the GAM337051 target mRNA into a corresponding GAM337051 target protein.

The mechanism of the translational inhibition exerted by GAM337051 RNA, herein designated GAM RNA, on one or more GAM337051 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337051 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337051 RNA, herein designated GAM RNA, of GAM337051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337051 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337051 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337051 RNA correlate with, and may be deduced from, the identity of the GAM337051 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337052 5725 AGAGAGGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGAGGAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CGGCTGGGGC Messenger 337052 (GAM337052) oligonucleotides modulates expression of respective target

GAGTGTGGAC genes whose function and utility is known in the art.

CGCAGCCCAG GAM337052 is a novel bioinformatically detectable regulatory, non protein

AGTTAGTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337052 was detected

GGCTGCAGTG is described with additional reference to Figs. 9-15.

CAACTCTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAAAATGTTA encoded by the human genome.

TTCTCACGCC GAM337052 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTTTCT GAM337052 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337052 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337052 precursor RNA is designated SEQ ID:5725, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5725 is located from position 68096933 to position 68097038 relative to chromosome 9 on the `+` strand.

GAM337052 precursor RNA folds onto itself, forming GAM337052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337052 precursor RNA, designated SEQ ID NO: 5725, and a schematic representation of a predicted secondary folding of GAM337052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337052 folded precursor RNA yielding a GAM337052 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337052 RNA, hereby incorporated herein.

GAM337052 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337052 target RNA, herein designated GAM TARGET RNA.

GAM337052 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337052 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337052 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337052 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337052 RNA, herein designated GAM RNA, to target binding sites on GAM337052 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337052 target RNA into GAM337052 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337052 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337052 target genes. The mRNA of each one of this plurality of GAM337052 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337052 RNA, herein designated GAM RNA, and which when bound by GAM337052 RNA causes inhibition of translation of the GAM337052 target mRNA into a corresponding GAM337052 target protein.

The mechanism of the translational inhibition exerted by GAM337052 RNA, herein designated GAM RNA, on one or more GAM337052 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337052 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337052 RNA, herein designated GAM RNA, of GAM337052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337052 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337052 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337052 RNA correlate with, and may be deduced from, the identity of the GAM337052 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337053 6743 GGCATTAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCAGTCACA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCAAGCAAG Messenger 337053 (GAM337053) oligonucleotides modulates expression of respective target

TGTGGACAGT genes whose function and utility is known in the art.

GAGTAATGTC GAM337053 is a novel bioinformatically detectable regulatory, non protein

TGAAGATTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337053 was detected

ATAGCTTGAT is described with additional reference to Figs. 9-15.

CACAGCTACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTTGTCCTGC encoded by the human genome.

TGTCTGAACT GAM337053 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CCATTGTC GAM337053 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337053 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337053 precursor RNA is designated SEQ ID:6743, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6743 is located from position 68550580 to position 68550687

relative to chromosome 12 on the `-` strand.

GAM337053 precursor RNA folds onto itself, forming GAM337053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337053 precursor RNA, designated SEQ ID NO: 6743, and a schematic representation of a predicted secondary folding of GAM337053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337053 folded precursor RNA yielding a GAM337053 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337053 RNA, hereby incorporated herein.

GAM337053 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337053 target RNA, herein designated GAM TARGET RNA.

GAM337053 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337053 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337053 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337053 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337053 RNA, herein designated GAM RNA, to target binding sites on GAM337053 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337053 target RNA into GAM337053 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337053 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337053 target genes. The mRNA of each one of this plurality of GAM337053 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337053 RNA, herein designated GAM RNA, and which when bound by GAM337053 RNA causes inhibition of translation of the GAM337053 target mRNA into a corresponding GAM337053 target protein.

The mechanism of the translational inhibition exerted by GAM337053 RNA, herein designated GAM RNA, on one or more GAM337053 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337053 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337053 RNA, herein designated GAM RNA, of GAM337053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337053 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337053 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337053 RNA correlate with, and may be deduced from, the identity of the GAM337053 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337055 7293 TTCAGGTACT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCATGTGATA detected oligonucleotides of the present invention, referred to here as Genomic Address
TATGGTTCCA Messenger 337055 (GAM337055) oligonucleotides modulates expression of respective target
CAATCCTCAG genes whose function and utility is known in the art.

CGTGTTAACT GAM337055 is a novel bioinformatically detectable regulatory, non protein
GAAGCCTTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337055 was detected
TGAGTTTAAC is described with additional reference to Figs. 9-15.

AAAGCTGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGAAGATCT encoded by the human genome.

GGGGAAAGTG GAM337055 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAGAAGTTGC GAM337055 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

AACAGAGTTT GAM337055 precursor RNA does not encode a protein. A nucleotide sequence identical or

TGGG highly similar to the nucleotide sequence of GAM337055 precursor RNA is designated SEQ ID:7293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7293 is located from position 68796420 to position 68796543 relative to chromosome 12 on the `-` strand.

GAM337055 precursor RNA folds onto itself, forming GAM337055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337055 precursor RNA, designated SEQ ID NO: 7293, and a schematic representation of a predicted secondary folding of GAM337055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337055 folded precursor RNA yielding a GAM337055 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337055 RNA, hereby incorporated herein.

GAM337055 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337055 target RNA, herein designated GAM TARGET RNA.

GAM337055 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337055 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337055 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337055 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337055 RNA, herein designated GAM RNA, to target binding sites on GAM337055 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337055 target RNA into GAM337055 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337055 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337055 target genes. The mRNA of each one of this plurality of GAM337055 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337055 RNA, herein designated GAM RNA, and which when bound by GAM337055 RNA causes inhibition of translation of the GAM337055 target mRNA into a corresponding GAM337055 target protein.

The mechanism of the translational inhibition exerted by GAM337055 RNA, herein designated GAM RNA, on one or more GAM337055 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337055 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337055 RNA, herein designated GAM RNA, of GAM337055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337055 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337055 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337055 RNA correlate with, and may be deduced from, the identity of the GAM337055 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337056 6027 CAGGTACTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGTGATATA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGTTCCACA Messenger 337056 (GAM337056) oligonucleotides modulates expression of respective target

ATCCTCAGCG genes whose function and utility is known in the art.

TGTTAACTGA GAM337056 is a novel bioinformatically detectable regulatory, non protein
AGCCTTGTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337056 was detected
AGTTTAACAA is described with additional reference to Figs. 9-15.

AGCTGCCATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAGATCTGG encoded by the human genome.

GGAAAGTGAA GAM337056 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAAGTTGCAA GAM337056 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CAGAGTTTTG GAM337056 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337056 precursor RNA is designated SEQ ID:6027, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6027 is located from position 68796422 to position 68796541 relative to chromosome 12 on the `-` strand.

GAM337056 precursor RNA folds onto itself, forming GAM337056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337056 precursor RNA, designated SEQ ID NO: 6027, and a schematic representation of a predicted secondary folding of GAM337056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337056 folded precursor RNA yielding a GAM337056 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337056 RNA, hereby incorporated herein.

GAM337056 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337056 target RNA, herein designated GAM TARGET RNA.

GAM337056 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337056 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337056 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337056 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337056 RNA, herein designated GAM RNA, to target binding sites on GAM337056 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337056 target RNA into GAM337056 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337056 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337056 target genes. The mRNA of each one of this plurality of GAM337056 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337056 RNA, herein designated GAM RNA, and which when bound by GAM337056 RNA causes inhibition of translation of the GAM337056 target mRNA into a corresponding GAM337056 target protein.

The mechanism of the translational inhibition exerted by GAM337056 RNA, herein designated GAM RNA, on one or more GAM337056 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337056 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337056 RNA, herein designated GAM RNA, of GAM337056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337056 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337056 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337056 RNA correlate with, and may be deduced from, the identity of the GAM337056 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337057 5992 CACAATCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCGTGTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGAAGCCTT Messenger 337057 (GAM337057) oligonucleotides modulates expression of respective target
GTTGAGTTTA genes whose function and utility is known in the art.

ACAAAGCTGC GAM337057 is a novel bioinformatically detectable regulatory, non protein
CATTGAAGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337057 was detected
CTGGGGAAAG is described with additional reference to Figs. 9-15.

TG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337057 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337057 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337057 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337057 precursor RNA is designated SEQ ID:5992, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5992 is located from position 68796444 to position 68796515 relative to chromosome 12 on the `-` strand.

GAM337057 precursor RNA folds onto itself, forming GAM337057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337057 precursor RNA, designated SEQ ID NO: 5992, and a schematic representation of a predicted secondary folding of GAM337057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337057 folded precursor RNA yielding a GAM337057 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337057 RNA, hereby incorporated herein.

GAM337057 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337057 target RNA, herein designated GAM TARGET RNA.

GAM337057 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337057 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337057 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337057 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337057 RNA, herein designated GAM RNA, to target binding sites on GAM337057 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337057 target RNA into GAM337057 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337057 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337057 target genes. The mRNA of each one of this plurality of GAM337057 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337057 RNA, herein designated GAM RNA, and which when bound by GAM337057 RNA causes inhibition of translation of the GAM337057 target mRNA into a corresponding GAM337057 target protein.

The mechanism of the translational inhibition exerted by GAM337057 RNA, herein designated GAM RNA, on one or more GAM337057 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337057 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337057 RNA, herein designated GAM RNA, of GAM337057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337057 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337057 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337057 RNA correlate with, and may be deduced from, the identity of the GAM337057 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337058 7037 TCCTCAGCGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTAACTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCTTGTTGA Messenger 337058 (GAM337058) oligonucleotides modulates expression of respective target

GTTTAACAAA genes whose function and utility is known in the art.

GCTGCCATTG GAM337058 is a novel bioinformatically detectable regulatory, non protein

AAGATCTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337058 was detected

GA is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337058 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337058 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337058 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337058 precursor RNA is designated SEQ ID:7037, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7037 is located from position 68796449 to position 68796510 relative to chromosome 12 on the `-` strand.

GAM337058 precursor RNA folds onto itself, forming GAM337058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337058 precursor RNA, designated SEQ ID NO: 7037, and a schematic representation of a predicted secondary folding of GAM337058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337058 folded precursor RNA yielding a GAM337058 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337058 RNA, hereby incorporated herein.

GAM337058 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337058 target RNA, herein designated GAM TARGET RNA.

GAM337058 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337058 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337058 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337058 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337058 RNA, herein designated GAM RNA, to target binding sites on GAM337058 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337058 target RNA into GAM337058 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337058 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337058 target genes. The mRNA of each one of this plurality of GAM337058 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337058 RNA, herein designated GAM RNA, and which when bound by GAM337058 RNA causes inhibition of translation of the GAM337058 target mRNA into a corresponding GAM337058 target protein.

The mechanism of the translational inhibition exerted by GAM337058 RNA, herein designated GAM RNA, on one or more GAM337058 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337058 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337058 RNA, herein designated GAM RNA, of GAM337058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337058 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337058 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337058 RNA correlate with, and may be deduced from, the identity of the GAM337058 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337059 6016 CAGCCTCAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
TGATCCACCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CCTCAGCTTC Messenger 337059 (GAM337059) oligonucleotides modulates expression of respective target
CCAAAGTGCT genes whose function and utility is known in the art.

GGGATTACAG GAM337059 is a novel bioinformatically detectable regulatory, non protein
GCATGATCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337059 was detected
CCACGCCTGG is described with additional reference to Figs. 9-15.

TCCCATTGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTTACATCT encoded by the human genome.

GATGGGCTGC GAM337059 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTTTGGGTTG GAM337059 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337059 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337059 precursor RNA is designated SEQ ID:6016, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6016 is located from position 68875043 to position 68875152 relative to chromosome 12 on the `+` strand.

GAM337059 precursor RNA folds onto itself, forming GAM337059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337059 precursor RNA, designated SEQ ID NO: 6016, and a schematic representation of a predicted secondary folding of GAM337059 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337059 folded precursor RNA yielding a GAM337059 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337059 RNA, hereby incorporated herein.

GAM337059 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337059 target RNA, herein designated GAM TARGET RNA.

GAM337059 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337059 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337059 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337059 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337059 RNA, herein designated GAM RNA, to target binding sites on GAM337059 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337059 target RNA into GAM337059 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337059 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337059 target genes. The mRNA of each one of this plurality of GAM337059 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337059 RNA, herein designated GAM RNA, and which when bound by GAM337059 RNA causes inhibition of translation of the GAM337059 target mRNA into a corresponding GAM337059 target protein.

The mechanism of the translational inhibition exerted by GAM337059 RNA, herein designated GAM RNA, on one or more GAM337059 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337059 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337059 RNA, herein designated GAM RNA, of GAM337059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337059 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337059 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337059 RNA correlate with, and may be deduced from, the identity of the GAM337059 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337060 7114 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAAGGC Messenger 337060 (GAM337060) oligonucleotides modulates expression of respective target

AGAGGTTGCA genes whose function and utility is known in the art.

GTCAGCAGAT GAM337060 is a novel bioinformatically detectable regulatory, non protein

ATTGCACCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337060 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGCAAGAC encoded by the human genome.

TCTGCCTCA GAM337060 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337060 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337060 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337060 precursor RNA is designated SEQ ID:7114, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7114 is located from position 69076604 to position 69076702 relative to chromosome 5 on the `-` strand.

GAM337060 precursor RNA folds onto itself, forming GAM337060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337060 precursor RNA, designated SEQ ID NO: 7114, and a schematic representation of a predicted secondary folding of GAM337060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337060 folded precursor RNA yielding a GAM337060 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337060 RNA, hereby incorporated herein. Expression of GAM337060 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337060 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337060 target RNA, herein designated GAM TARGET RNA.

GAM337060 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337060 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337060 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337060 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337060 RNA, herein designated GAM RNA, to target binding sites on GAM337060 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337060 target RNA into GAM337060 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337060 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337060 target genes. The mRNA of each one of this plurality of GAM337060 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337060 RNA,

herein designated GAM RNA, and which when bound by GAM337060 RNA causes inhibition of translation of the GAM337060 target mRNA into a corresponding GAM337060 target protein.

The mechanism of the translational inhibition exerted by GAM337060 RNA, herein designated GAM RNA, on one or more GAM337060 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337060 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337060 RNA, herein designated GAM RNA, of GAM337060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337060 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337060 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337060 RNA correlate with, and may be deduced from, the identity of the GAM337060 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337061 6131 CCTTTGAACA Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGGAACTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGAAAGAAA Messenger 337061 (GAM337061) oligonucleotides modulates expression of respective target

TGGGATCTGT genes whose function and utility is known in the art.

GCAGCTACTT GAM337061 is a novel bioinformatically detectable regulatory, non protein

CAGTTAGCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337061 was detected

GAATCCTACA is described with additional reference to Figs. 9-15.

GTTCTGGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTTCTTTAAT encoded by the human genome.

GCTAGTTTTC GAM337061 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CCTTTTCAGA GAM337061 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GG GAM337061 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337061 precursor RNA is designated SEQ ID:6131, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6131 is located from position 69104781 to position 69104892 relative to chromosome 9 on the `+` strand.

GAM337061 precursor RNA folds onto itself, forming GAM337061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337061 precursor RNA, designated SEQ ID NO: 6131, and a schematic representation of a predicted secondary folding of GAM337061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337061 folded precursor RNA yielding a GAM337061 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337061 RNA, hereby incorporated herein.

GAM337061 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337061 target RNA, herein designated GAM TARGET RNA.

GAM337061 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337061 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337061 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337061 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337061 RNA, herein designated GAM RNA, to target binding sites on GAM337061 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337061 target RNA

into GAM337061 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337061 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337061 target genes. The mRNA of each one of this plurality of GAM337061 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337061 RNA, herein designated GAM RNA, and which when bound by GAM337061 RNA causes inhibition of translation of the GAM337061 target mRNA into a corresponding GAM337061 target protein.

The mechanism of the translational inhibition exerted by GAM337061 RNA, herein designated GAM RNA, on one or more GAM337061 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337061 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337061 RNA, herein designated GAM RNA, of GAM337061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337061 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337061 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337061 RNA correlate with, and may be deduced from, the identity of the GAM337061 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337062 6636 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 337062 (GAM337062) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM337062 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337062 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337062 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337062 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337062 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337062 precursor RNA is designated SEQ ID:6636, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6636 is located from position 69278504 to position 69278591 relative to chromosome 5 on the `+` strand.

GAM337062 precursor RNA folds onto itself, forming GAM337062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337062 precursor RNA, designated SEQ ID NO: 6636, and a schematic representation of a predicted secondary folding of GAM337062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337062 folded precursor RNA yielding a GAM337062 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337062 RNA, hereby incorporated herein. Expression of GAM337062 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337062 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337062 target RNA, herein designated GAM TARGET RNA.

GAM337062 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337062 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337062 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337062 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337062 RNA, herein designated GAM RNA, to target binding sites on GAM337062 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337062 target RNA into GAM337062 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337062 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337062 target genes. The mRNA of each one of this plurality of GAM337062 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337062 RNA, herein designated GAM RNA, and which when bound by GAM337062 RNA causes inhibition of translation of the GAM337062 target mRNA into a corresponding GAM337062 target protein.

The mechanism of the translational inhibition exerted by GAM337062 RNA, herein designated GAM RNA, on one or more GAM337062 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337062 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337062 RNA, herein designated GAM RNA, of GAM337062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337062 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337062 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337062 RNA correlate with, and may be deduced from, the identity of the GAM337062 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337063 6186 CTCTTGACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTTCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGAGGGAC Messenger 337063 (GAM337063) oligonucleotides modulates expression of respective target

ATTTTACCTG genes whose function and utility is known in the art.

CCGGGGACAT GAM337063 is a novel bioinformatically detectable regulatory, non protein
TTCCAATGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337063 was detected

TGGGGACACT is described with additional reference to Figs. 9-15.

TTTGGTTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM337063 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337063 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337063 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337063 precursor RNA is designated SEQ ID:6186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6186 is located from position 69410140 to position 69410221 relative to chromosome 5 on the `+` strand.

GAM337063 precursor RNA folds onto itself, forming GAM337063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337063 precursor RNA, designated SEQ ID NO: 6186, and a schematic representation of a predicted secondary folding of GAM337063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337063 folded precursor RNA yielding a GAM337063 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM337063 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337063 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM337063 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337063 target RNA, herein designated GAM TARGET RNA.

GAM337063 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337063 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337063 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337063 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337063 RNA, herein designated GAM RNA, to target binding sites on GAM337063 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337063 target RNA into GAM337063 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337063 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337063 target genes. The mRNA of each one of this plurality of GAM337063 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337063 RNA, herein designated GAM RNA, and which when bound by GAM337063 RNA causes inhibition of translation of the GAM337063 target mRNA into a corresponding GAM337063 target protein.

The mechanism of the translational inhibition exerted by GAM337063 RNA, herein designated GAM RNA, on one or more GAM337063 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337063 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337063 RNA, herein designated GAM RNA, of GAM337063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337063 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337063 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337063 RNA correlate with, and may be deduced from, the identity of the GAM337063 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337064 6637 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 337064 (GAM337064) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM337064 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337064 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM337064 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337064 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337064 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337064 precursor RNA is designated SEQ ID:6637, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6637 is located from position 69429920 to position 69430007 relative to chromosome 5 on the `-` strand.

GAM337064 precursor RNA folds onto itself, forming GAM337064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337064 precursor RNA, designated SEQ ID NO: 6637, and a schematic representation of a predicted secondary folding of GAM337064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337064 folded precursor RNA yielding a GAM337064 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337064 RNA, hereby incorporated herein. Expression of GAM337064 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337064 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337064 target RNA, herein designated GAM TARGET RNA.

GAM337064 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337064 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337064 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337064 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337064 RNA, herein designated GAM RNA, to target binding sites on GAM337064 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337064 target RNA into GAM337064 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337064 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337064 target genes. The mRNA of each one of this plurality of GAM337064 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337064 RNA, herein designated GAM RNA, and which when bound by GAM337064 RNA causes inhibition of translation of the GAM337064 target mRNA into a corresponding GAM337064 target protein.

The mechanism of the translational inhibition exerted by GAM337064 RNA, herein designated GAM RNA, on one or more GAM337064 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337064 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337064 RNA, herein designated GAM RNA, of GAM337064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337064 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337064 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337064 RNA correlate with, and may be deduced from, the identity of the GAM337064 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337066 7291 TTCACTCCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTGGCTTTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTCTGGCAGA Messenger 337066 (GAM337066) oligonucleotides modulates expression of respective target
TTCCGGTGGA genes whose function and utility is known in the art.

TTATGCAAAG GAM337066 is a novel bioinformatically detectable regulatory, non protein
AGGGACTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337066 was detected
AGAGAATCTG is described with additional reference to Figs. 9-15.

AGCTGTTGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGACTTCTGA encoded by the human genome.

A GAM337066 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337066 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337066 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337066 precursor RNA is designated SEQ ID:7291, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7291 is located from position 69498130 to position 69498220 relative to chromosome 11 on the `-` strand.

GAM337066 precursor RNA folds onto itself, forming GAM337066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337066 precursor RNA, designated SEQ ID NO: 7291, and a schematic representation of a predicted secondary folding of GAM337066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337066 folded precursor RNA yielding a GAM337066 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337066 RNA, hereby incorporated herein.

GAM337066 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337066 target RNA, herein designated GAM TARGET RNA.

GAM337066 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337066 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337066 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337066 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337066 RNA, herein designated GAM RNA, to target binding sites on GAM337066 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337066 target RNA into GAM337066 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337066 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337066 target genes. The mRNA of each one of this plurality of GAM337066 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337066 RNA, herein designated GAM RNA, and which when bound by GAM337066 RNA causes inhibition of translation of the GAM337066 target mRNA into a corresponding GAM337066 target protein.

The mechanism of the translational inhibition exerted by GAM337066 RNA, herein designated GAM RNA, on one or more GAM337066 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337066 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337066 RNA, herein designated GAM RNA, of GAM337066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337066 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337066 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337066 RNA correlate with, and may be deduced from, the identity of the GAM337066 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337068 6279 GAAAAGGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GATCAGTATT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCTGATCCT Messenger 337068 (GAM337068) oligonucleotides modulates expression of respective target

AGTTCAGTGC genes whose function and utility is known in the art.

TAGTCAGGGA GAM337068 is a novel bioinformatically detectable regulatory, non protein

GACTGTCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337068 was detected

AAAGACCTTT is described with additional reference to Figs. 9-15.

TT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337068 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337068 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337068 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337068 precursor RNA is designated SEQ ID:6279, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6279 is located from position 69692764 to position 69692835 relative to chromosome 16 on the `+` strand.

GAM337068 precursor RNA folds onto itself, forming GAM337068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337068 precursor RNA, designated SEQ ID NO: 6279, and a schematic representation of a predicted secondary folding of GAM337068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337068 folded precursor RNA yielding a GAM337068 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337068 RNA, hereby incorporated herein.

GAM337068 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337068 target RNA, herein designated GAM TARGET RNA.

GAM337068 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337068 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337068 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337068 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337068 RNA, herein designated GAM RNA, to target binding sites on GAM337068 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337068 target RNA into GAM337068 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337068 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337068 target genes. The mRNA of each one of this plurality of GAM337068 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337068 RNA, herein designated GAM RNA, and which when bound by GAM337068 RNA causes inhibition of translation of the GAM337068 target mRNA into a corresponding GAM337068 target protein.

The mechanism of the translational inhibition exerted by GAM337068 RNA, herein designated GAM RNA, on one or more GAM337068 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337068 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337068 RNA, herein designated GAM RNA, of GAM337068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337068 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337068 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337068 RNA correlate with, and may be deduced from, the identity of the GAM337068 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337069 7115 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAAGGC Messenger 337069 (GAM337069) oligonucleotides modulates expression of respective target

AGAGGTTGCA genes whose function and utility is known in the art.

GTCAGCAGAT GAM337069 is a novel bioinformatically detectable regulatory, non protein

ATTGCACCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337069 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGCAAGAC encoded by the human genome.

TCTGCCTCA GAM337069 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337069 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337069 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337069 precursor RNA is designated SEQ

ID:7115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7115 is located from position 69818313 to position 69818411 relative to chromosome 5 on the `+` strand.

GAM337069 precursor RNA folds onto itself, forming GAM337069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337069 precursor RNA, designated SEQ ID NO: 7115, and a schematic representation of a predicted secondary folding of GAM337069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337069 folded precursor RNA yielding a GAM337069 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337069 RNA, hereby incorporated herein. Expression of GAM337069 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337069 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337069 target RNA, herein designated GAM TARGET RNA.

GAM337069 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337069 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337069 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337069 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337069 RNA, herein designated GAM RNA, to target binding sites on GAM337069 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337069 target RNA

into GAM337069 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337069 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337069 target genes. The mRNA of each one of this plurality of GAM337069 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337069 RNA, herein designated GAM RNA, and which when bound by GAM337069 RNA causes inhibition of translation of the GAM337069 target mRNA into a corresponding GAM337069 target protein.

The mechanism of the translational inhibition exerted by GAM337069 RNA, herein designated GAM RNA, on one or more GAM337069 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337069 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337069 RNA, herein designated GAM RNA, of GAM337069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337069 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337069 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337069 RNA correlate with, and may be deduced from, the identity of the GAM337069 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337070 6377 GAGGCAGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAAGGCA Messenger 337070 (GAM337070) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TCAGCAGATA GAM337070 is a novel bioinformatically detectable regulatory, non protein

TTGCACCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337070 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGCAAGACT encoded by the human genome.

CTGCCTC GAM337070 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337070 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337070 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337070 precursor RNA is designated SEQ ID:6377, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6377 is located from position 69818314 to position 69818410 relative to chromosome 5 on the `+` strand.

GAM337070 precursor RNA folds onto itself, forming GAM337070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337070 precursor RNA, designated SEQ ID NO: 6377, and a schematic representation of a predicted secondary folding of GAM337070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337070 folded precursor RNA yielding a GAM337070 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337070 RNA, hereby incorporated herein. Expression of GAM337070 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337070 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337070 target RNA, herein designated GAM TARGET RNA.

GAM337070 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337070 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337070 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337070 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337070 RNA, herein designated GAM RNA, to target binding sites on GAM337070 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337070 target RNA into GAM337070 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337070 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337070 target genes. The mRNA of each one of this plurality of GAM337070 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337070 RNA, herein designated GAM RNA, and which when bound by GAM337070 RNA causes inhibition of translation of the GAM337070 target mRNA into a corresponding GAM337070 target protein.

The mechanism of the translational inhibition exerted by GAM337070 RNA, herein designated GAM RNA, on one or more GAM337070 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337070 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337070 RNA, herein designated GAM RNA, of GAM337070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337070 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337070 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337070 RNA correlate with, and may be deduced from, the identity of the GAM337070 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337071 5780 AGGCTGAGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTGGTGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCTCGGCTC Messenger 337071 (GAM337071) oligonucleotides modulates expression of respective target
ACTGCAAGCT genes whose function and utility is known in the art.

CTGCCTCCCA GAM337071 is a novel bioinformatically detectable regulatory, non protein
GGTTCACGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337071 was detected
ATTGTCCTGC is described with additional reference to Figs. 9-15.

CTCAGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337071 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337071 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337071 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337071 precursor RNA is designated SEQ ID:5780, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5780 is located from position 69991881 to position 69991958 relative to chromosome 10 on the `+` strand.

GAM337071 precursor RNA folds onto itself, forming GAM337071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337071 precursor RNA, designated SEQ ID NO: 5780, and a schematic representation of a predicted secondary folding of GAM337071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337071 folded precursor RNA yielding a GAM337071 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337071 RNA, hereby incorporated herein.

GAM337071 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337071 target RNA, herein designated GAM TARGET RNA.

GAM337071 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337071 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337071 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337071 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337071 RNA, herein designated GAM RNA, to target binding sites on GAM337071 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337071 target RNA into GAM337071 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337071 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337071 target genes. The mRNA of each one of this plurality of GAM337071 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337071 RNA, herein designated GAM RNA, and which when bound by GAM337071 RNA causes inhibition of translation of the GAM337071 target mRNA into a corresponding GAM337071 target protein.

The mechanism of the translational inhibition exerted by GAM337071 RNA, herein designated GAM RNA, on one or more GAM337071 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337071 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337071 RNA, herein designated GAM RNA, of GAM337071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337071 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337071 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337071

RNA correlate with, and may be deduced from, the identity of the GAM337071 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337074 7099 TGAGACAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGGAG Messenger 337074 (GAM337074) oligonucleotides modulates expression of respective target
GTGGAGGTTA genes whose function and utility is known in the art.

CGGTGAGTGA GAM337074 is a novel bioinformatically detectable regulatory, non protein
GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337074 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCGAA encoded by the human genome.

ACTCCGTCTC GAM337074 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337074 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337074 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337074 precursor RNA is designated SEQ ID:7099, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7099 is located from position 70140212 to position 70140312 relative to chromosome 16 on the `+` strand.

GAM337074 precursor RNA folds onto itself, forming GAM337074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337074 precursor RNA, designated SEQ ID NO: 7099, and a schematic representation of a predicted secondary folding of GAM337074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337074 folded precursor RNA yielding a GAM337074 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337074 RNA, hereby incorporated herein. Expression of GAM337074 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337074 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337074 target RNA, herein designated GAM TARGET RNA.

GAM337074 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337074 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337074 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337074 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337074 RNA, herein designated GAM RNA, to target binding sites on GAM337074 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337074 target RNA into GAM337074 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337074 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337074 target genes. The mRNA of each one of this plurality of GAM337074 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337074 RNA, herein designated GAM RNA, and which when bound by GAM337074 RNA causes inhibition of translation of the GAM337074 target mRNA into a corresponding GAM337074 target protein.

The mechanism of the translational inhibition exerted by GAM337074 RNA, herein designated GAM RNA, on one or more GAM337074 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337074 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337074 RNA, herein designated GAM RNA, of GAM337074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337074 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337074 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337074 RNA correlate with, and may be deduced from, the identity of the GAM337074 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337075 6343 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGAGG Messenger 337075 (GAM337075) oligonucleotides modulates expression of respective target
TGGAGGTTAC genes whose function and utility is known in the art.

GGTGAGTGAG GAM337075 is a novel bioinformatically detectable regulatory, non protein
ATCGCGCCAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337075 was detected
TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGAGCGAAA encoded by the human genome.

CTCCGTCTC GAM337075 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337075 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337075 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337075 precursor RNA is designated SEQ ID:6343, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6343 is located from position 70140213 to position 70140311 relative to chromosome 16 on the `+` strand.

GAM337075 precursor RNA folds onto itself, forming GAM337075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337075 precursor RNA, designated SEQ ID NO: 6343, and a schematic representation of a predicted secondary folding of GAM337075 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337075 folded precursor RNA yielding a GAM337075 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337075 RNA, hereby incorporated herein. Expression of GAM337075 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337075 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337075 target RNA, herein designated GAM TARGET RNA.

GAM337075 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337075 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337075 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337075 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337075 RNA, herein designated GAM RNA, to target binding sites on GAM337075 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337075 target RNA into GAM337075 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337075 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337075 target genes. The mRNA of each one of this plurality of GAM337075 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337075 RNA, herein designated GAM RNA, and which when bound by GAM337075 RNA causes inhibition of translation of the GAM337075 target mRNA into a corresponding GAM337075 target protein.

The mechanism of the translational inhibition exerted by GAM337075 RNA, herein designated GAM RNA, on one or more GAM337075 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337075 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337075 RNA, herein designated GAM RNA, of GAM337075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337075 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337075 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337075 RNA correlate with, and may be deduced from, the identity of the GAM337075 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337076 6651 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 337076 (GAM337076) oligonucleotides modulates expression of respective target

TTACGGTGAG genes whose function and utility is known in the art.

TGAGATCGCG GAM337076 is a novel bioinformatically detectable regulatory, non protein

CCATTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337076 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAACTCC encoded by the human genome.

GAM337076 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337076 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337076 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337076 precursor RNA is designated SEQ ID:6651, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6651 is located from position 70140219 to position 70140306 relative to chromosome 16 on the `+` strand.

GAM337076 precursor RNA folds onto itself, forming GAM337076 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337076 precursor RNA, designated SEQ ID NO: 6651, and a schematic representation of a predicted secondary folding of GAM337076 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337076 folded precursor RNA yielding a GAM337076 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337076 RNA, hereby incorporated herein. Expression of GAM337076 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337076 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337076 target RNA, herein designated GAM TARGET RNA.

GAM337076 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337076 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337076 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337076 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337076 RNA, herein designated GAM RNA, to target binding sites on GAM337076 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337076 target RNA into GAM337076 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337076 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337076 target genes. The mRNA of each one of this

plurality of GAM337076 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337076 RNA, herein designated GAM RNA, and which when bound by GAM337076 RNA causes inhibition of translation of the GAM337076 target mRNA into a corresponding GAM337076 target protein.

The mechanism of the translational inhibition exerted by GAM337076 RNA, herein designated GAM RNA, on one or more GAM337076 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337076 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337076 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337076 RNA, herein designated GAM RNA, of GAM337076 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337076 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337076 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337076 RNA correlate with, and may be deduced from, the identity of the GAM337076 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337077 6187 CTCTTGACCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGTTCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AATGAGGGAC Messenger 337077 (GAM337077) oligonucleotides modulates expression of respective target

ATTTTACCTG genes whose function and utility is known in the art.

CCGGGGACAT GAM337077 is a novel bioinformatically detectable regulatory, non protein

TTCCAATGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337077 was detected

TGGGGACACT is described with additional reference to Figs. 9-15.

TTTGGTTATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM337077 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337077 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337077 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337077 precursor RNA is designated SEQ ID:6187, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6187 is located from position 70161182 to position 70161263 relative to chromosome 5 on the `+` strand.

GAM337077 precursor RNA folds onto itself, forming GAM337077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337077 precursor RNA, designated SEQ ID NO: 6187, and a schematic representation of a predicted secondary folding of GAM337077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337077 folded precursor RNA yielding a GAM337077 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides two possible nucleotide sequences of GAM337077 RNA: a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337077 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM337077 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337077 target RNA, herein designated GAM TARGET RNA.

GAM337077 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337077 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337077 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337077 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337077 RNA, herein designated GAM RNA, to target binding sites on GAM337077 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337077 target RNA into GAM337077 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337077 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337077 target genes. The mRNA of each one of this plurality of GAM337077 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337077 RNA, herein designated GAM RNA, and which when bound by GAM337077 RNA causes inhibition of translation of the GAM337077 target mRNA into a corresponding GAM337077 target protein.

The mechanism of the translational inhibition exerted by GAM337077 RNA, herein designated GAM RNA, on one or more GAM337077 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337077 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337077 RNA, herein designated GAM RNA, of GAM337077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337077 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337077 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337077 RNA correlate with, and may be deduced from, the identity of the GAM337077 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337078 6638 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 337078 (GAM337078) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM337078 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337078 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337078 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337078 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337078 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337078 precursor RNA is designated SEQ ID:6638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6638 is located from position 70180992 to position 70181079 relative to chromosome 5 on the `-` strand.

GAM337078 precursor RNA folds onto itself, forming GAM337078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337078 precursor RNA, designated SEQ ID NO: 6638, and a schematic representation of a predicted secondary folding of GAM337078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337078 folded precursor RNA yielding a GAM337078 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337078 RNA, hereby incorporated herein. Expression of GAM337078 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337078 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337078 target RNA, herein designated GAM TARGET RNA.

GAM337078 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337078 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337078 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337078 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337078 RNA, herein designated GAM RNA, to target binding sites on GAM337078 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337078 target RNA into GAM337078 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337078 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337078 target genes. The mRNA of each one of this plurality of GAM337078 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337078 RNA, herein designated GAM RNA, and which when bound by GAM337078 RNA causes inhibition of translation of the GAM337078 target mRNA into a corresponding GAM337078 target protein.

The mechanism of the translational inhibition exerted by GAM337078 RNA, herein designated GAM RNA, on one or more GAM337078 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337078 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337078 RNA, herein designated GAM RNA, of GAM337078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337078 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337078 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337078 RNA correlate with, and may be deduced from, the identity of the GAM337078 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337079 7107 TGAGGCAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCAGGAG Messenger 337079 (GAM337079) oligonucleotides modulates expression of respective target
GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCA GAM337079 is a novel bioinformatically detectable regulatory, non protein
AGATGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337079 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGA encoded by the human genome.

CTCTGTCTCA GAM337079 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337079 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337079 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337079 precursor RNA is designated SEQ ID:7107, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7107 is located from position 70204344 to position 70204443 relative to chromosome 15 on the `-` strand.

GAM337079 precursor RNA folds onto itself, forming GAM337079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337079 precursor RNA, designated SEQ ID NO: 7107, and a schematic representation of a predicted secondary folding of GAM337079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337079 folded precursor RNA yielding a GAM337079 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337079 RNA, hereby incorporated herein. Expression of GAM337079 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337079 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337079 target RNA, herein designated GAM TARGET RNA.

GAM337079 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337079 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337079 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337079 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337079 RNA, herein designated GAM RNA, to target binding sites on GAM337079 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337079 target RNA into GAM337079 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337079 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337079 target genes. The mRNA of each one of this plurality of GAM337079 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337079 RNA, herein designated GAM RNA, and which when bound by GAM337079 RNA causes inhibition of translation of the GAM337079 target mRNA into a corresponding GAM337079 target protein.

The mechanism of the translational inhibition exerted by GAM337079 RNA, herein designated GAM RNA, on one or more GAM337079 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337079 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337079 RNA, herein designated GAM RNA, of GAM337079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337079 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337079 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337079 RNA correlate with, and may be deduced from, the identity of the GAM337079 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337080 6714 GGAGGGGCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAGGAAATG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGAGTCTTA Messenger 337080 (GAM337080) oligonucleotides modulates expression of respective target
GTGATCTGGA genes whose function and utility is known in the art.

AACATTCCAG GAM337080 is a novel bioinformatically detectable regulatory, non protein
ACTAATTTAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337080 was detected
TATCTTCTCT is described with additional reference to Figs. 9-15.

TTTTTCCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
C encoded by the human genome.

GAM337080 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337080 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337080 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337080 precursor RNA is designated SEQ ID:6714, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6714 is located from position 70205172 to position 70205252 relative to chromosome 8 on the `+` strand.

GAM337080 precursor RNA folds onto itself, forming GAM337080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337080 precursor RNA, designated SEQ ID NO: 6714, and a schematic representation of a predicted secondary folding of GAM337080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337080 folded precursor

RNA yielding a GAM337080 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337080 RNA, hereby incorporated herein.

GAM337080 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337080 target RNA, herein designated GAM TARGET RNA.

GAM337080 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337080 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337080 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337080 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337080 RNA, herein designated GAM RNA, to target binding sites on GAM337080 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337080 target RNA into GAM337080 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337080 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337080 target genes. The mRNA of each one of this plurality of GAM337080 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337080 RNA, herein designated GAM RNA, and which when bound by GAM337080 RNA causes inhibition of translation of the GAM337080 target mRNA into a corresponding GAM337080 target protein.

The mechanism of the translational inhibition exerted by GAM337080 RNA, herein designated GAM RNA, on one or more GAM337080 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337080 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337080 RNA, herein designated GAM RNA, of GAM337080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337080 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337080 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337080 RNA correlate with, and may be deduced from, the identity of the GAM337080 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337081 7116 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAAGGC Messenger 337081 (GAM337081) oligonucleotides modulates expression of respective target

AGAGGTTGCA genes whose function and utility is known in the art.

GTCAGCAGAT GAM337081 is a novel bioinformatically detectable regulatory, non protein

ATTGCACCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337081 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAAGCAAGAC encoded by the human genome.

TCTGCCTCA GAM337081 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337081 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337081 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337081 precursor RNA is designated SEQ ID:7116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7116 is located from position 70361144 to position 70361242 relative to chromosome 5 on the `+` strand.

GAM337081 precursor RNA folds onto itself, forming GAM337081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337081 precursor RNA, designated SEQ ID NO: 7116, and a schematic representation of a predicted secondary folding of GAM337081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337081 folded precursor RNA yielding a GAM337081 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337081 RNA, hereby incorporated herein. Expression of GAM337081 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337081 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337081 target RNA, herein designated GAM TARGET RNA.

GAM337081 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337081 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337081 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337081 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337081 RNA, herein designated GAM RNA, to target binding sites on GAM337081 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337081 target RNA into GAM337081 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337081 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337081 target genes. The mRNA of each one of this plurality of GAM337081 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337081 RNA, herein designated GAM RNA, and which when bound by GAM337081 RNA causes inhibition of translation of the GAM337081 target mRNA into a corresponding GAM337081 target protein.

The mechanism of the translational inhibition exerted by GAM337081 RNA, herein designated GAM RNA, on one or more GAM337081 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337081 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337081 RNA, herein designated GAM RNA, of GAM337081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337081 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337081 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337081 RNA correlate with, and may be deduced from, the identity of the GAM337081 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337082 6378 GAGGCAGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAAGGCA Messenger 337082 (GAM337082) oligonucleotides modulates expression of respective target

GAGGTTGCAG genes whose function and utility is known in the art.

TCAGCAGATA GAM337082 is a novel bioinformatically detectable regulatory, non protein

TTGCACCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337082 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGCAAGACT encoded by the human genome.

CTGCCTC GAM337082 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337082 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337082 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337082 precursor RNA is designated SEQ

ID:6378, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6378 is located from position 70361145 to position 70361241 relative to chromosome 5 on the `+` strand.

GAM337082 precursor RNA folds onto itself, forming GAM337082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337082 precursor RNA, designated SEQ ID NO: 6378, and a schematic representation of a predicted secondary folding of GAM337082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337082 folded precursor RNA yielding a GAM337082 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337082 RNA, hereby incorporated herein. Expression of GAM337082 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337082 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337082 target RNA, herein designated GAM TARGET RNA.

GAM337082 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337082 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337082 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337082 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337082 RNA, herein designated GAM RNA, to target binding sites on GAM337082 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337082 target RNA

into GAM337082 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337082 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337082 target genes. The mRNA of each one of this plurality of GAM337082 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337082 RNA, herein designated GAM RNA, and which when bound by GAM337082 RNA causes inhibition of translation of the GAM337082 target mRNA into a corresponding GAM337082 target protein.

The mechanism of the translational inhibition exerted by GAM337082 RNA, herein designated GAM RNA, on one or more GAM337082 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337082 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337082 RNA, herein designated GAM RNA, of GAM337082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337082 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337082 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337082 RNA correlate with, and may be deduced from, the identity of the GAM337082 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337083 6792 GGGAGGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTTGAGCCTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGCTGGAG Messenger 337083 (GAM337083) oligonucleotides modulates expression of respective target
CCTGCAGTGA genes whose function and utility is known in the art.

ACTATCATTG GAM337083 is a novel bioinformatically detectable regulatory, non protein
TGCCACTGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337083 was detected
CTCCAGCCTA is described with additional reference to Figs. 9-15.

GGCAACAAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAAATCCTG encoded by the human genome.

TC GAM337083 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337083 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337083 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337083 precursor RNA is designated SEQ ID:6792, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6792 is located from position 70411479 to position 70411570 relative to chromosome 10 on the `+` strand.

GAM337083 precursor RNA folds onto itself, forming GAM337083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337083 precursor RNA, designated SEQ ID NO: 6792, and a schematic representation of a predicted secondary folding of GAM337083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337083 folded precursor RNA yielding a GAM337083 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337083 RNA, hereby incorporated herein.

GAM337083 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337083 target RNA, herein designated GAM TARGET RNA.

GAM337083 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337083 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337083 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337083 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337083 RNA, herein designated GAM RNA, to target binding sites on GAM337083 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337083 target RNA into GAM337083 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337083 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337083 target genes. The mRNA of each one of this plurality of GAM337083 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337083 RNA, herein designated GAM RNA, and which when bound by GAM337083 RNA causes inhibition of translation of the GAM337083 target mRNA into a corresponding GAM337083 target protein.

The mechanism of the translational inhibition exerted by GAM337083 RNA, herein designated GAM RNA, on one or more GAM337083 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337083 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337083 RNA, herein designated GAM RNA, of GAM337083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337083 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337083 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337083 RNA correlate with, and may be deduced from, the identity of the GAM337083 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337084 5762 AGGATTGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGCCTGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTGGAGCCT Messenger 337084 (GAM337084) oligonucleotides modulates expression of respective target

GCAGTGAACT genes whose function and utility is known in the art.

ATCATTGTGC GAM337084 is a novel bioinformatically detectable regulatory, non protein
CACTGTACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337084 was detected
CAGCCTAGGC is described with additional reference to Figs. 9-15.

AACAAAATGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATCCT encoded by the human genome.

GAM337084 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337084 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337084 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337084 precursor RNA is designated SEQ ID:5762, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5762 is located from position 70411482 to position 70411567 relative to chromosome 10 on the `+` strand.

GAM337084 precursor RNA folds onto itself, forming GAM337084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337084 precursor RNA, designated SEQ ID NO: 5762, and a schematic representation of a predicted secondary folding of GAM337084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337084 folded precursor RNA yielding a GAM337084 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337084 RNA, hereby incorporated herein.

GAM337084 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337084 target RNA, herein designated GAM TARGET RNA.

GAM337084 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337084 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337084 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337084 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337084 RNA, herein designated GAM RNA, to target binding sites on GAM337084 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337084 target RNA into GAM337084 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337084 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337084 target genes. The mRNA of each one of this plurality of GAM337084 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337084 RNA, herein designated GAM RNA, and which when bound by GAM337084 RNA causes inhibition of translation of the GAM337084 target mRNA into a corresponding GAM337084 target protein.

The mechanism of the translational inhibition exerted by GAM337084 RNA, herein designated GAM RNA, on one or more GAM337084 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337084 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337084 RNA, herein designated GAM RNA, of GAM337084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337084 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337084 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337084 RNA correlate with, and may be deduced from, the identity of the GAM337084 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337087 6492 GCAGGAGGAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCTTGAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGAGTTCA Messenger 337087 (GAM337087) oligonucleotides modulates expression of respective target
AGGCTACAAT genes whose function and utility is known in the art.

GAGCTATGAT GAM337087 is a novel bioinformatically detectable regulatory, non protein
CACACTACTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337087 was detected
CACTCCAGCC is described with additional reference to Figs. 9-15.

TGGGCAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCAAGACCC encoded by the human genome.

TGT GAM337087 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337087 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337087 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337087 precursor RNA is designated SEQ ID:6492, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6492 is located from position 70589904 to position 70589996 relative to chromosome 7 on the `+` strand.

GAM337087 precursor RNA folds onto itself, forming GAM337087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337087 precursor RNA, designated SEQ ID NO: 6492, and a schematic representation of a predicted secondary folding of GAM337087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337087 folded precursor RNA yielding a GAM337087 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337087 RNA, hereby incorporated herein.

GAM337087 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337087 target RNA, herein designated GAM TARGET RNA.

GAM337087 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337087 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337087 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337087 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337087 RNA, herein designated GAM RNA, to target binding sites on GAM337087 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337087 target RNA into GAM337087 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337087 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337087 target genes. The mRNA of each one of this plurality of GAM337087 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337087 RNA, herein designated GAM RNA, and which when bound by GAM337087 RNA causes inhibition of translation of the GAM337087 target mRNA into a corresponding GAM337087 target protein.

The mechanism of the translational inhibition exerted by GAM337087 RNA, herein designated GAM RNA, on one or more GAM337087 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337087 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337087 RNA, herein designated GAM RNA, of GAM337087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337087 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337087 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337087 RNA correlate with, and may be deduced from, the identity of the GAM337087 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337088 5805 AGTCCTCTTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCTGTTGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTCCCCAT Messenger 337088 (GAM337088) oligonucleotides modulates expression of respective target
GTGATGCTAT genes whose function and utility is known in the art.

TGCTTCTCTT GAM337088 is a novel bioinformatically detectable regulatory, non protein
TGGAGGCTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337088 was detected
GCAGTAAATG is described with additional reference to Figs. 9-15.

GGGTTAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGGGCT encoded by the human genome.

GAM337088 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337088 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337088 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337088 precursor RNA is designated SEQ ID:5805, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5805 is located from position 70649160 to position 70649247 relative to chromosome 12 on the `-` strand.

GAM337088 precursor RNA folds onto itself, forming GAM337088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337088 precursor RNA, designated SEQ ID NO: 5805, and a schematic representation of a predicted secondary folding of GAM337088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337088 folded precursor RNA yielding a GAM337088 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337088 RNA, hereby incorporated herein.

GAM337088 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337088 target RNA, herein designated GAM TARGET RNA.

GAM337088 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337088 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337088 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337088 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337088 RNA, herein designated GAM RNA, to target binding sites on GAM337088 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337088 target RNA into GAM337088 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337088 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337088 target genes. The mRNA of each one of this plurality of GAM337088 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337088 RNA, herein designated GAM RNA, and which when bound by GAM337088 RNA causes inhibition of translation of the GAM337088 target mRNA into a corresponding GAM337088 target protein.

The mechanism of the translational inhibition exerted by GAM337088 RNA, herein designated GAM RNA, on one or more GAM337088 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337088 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337088 RNA, herein designated GAM RNA, of GAM337088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337088 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337088 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337088 RNA correlate with, and may be deduced from, the identity of the GAM337088 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337089 7209 TGCTGTTGAC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTTCCCCAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGATGCTAT Messenger 337089 (GAM337089) oligonucleotides modulates expression of respective target
TGCTTCTCTT genes whose function and utility is known in the art.

TGGAGGCTAA GAM337089 is a novel bioinformatically detectable regulatory, non protein
GCAGTAAATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337089 was detected
GGGTTAACAG is described with additional reference to Figs. 9-15.

CA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337089 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337089 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337089 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337089 precursor RNA is designated SEQ ID:7209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7209 is located from position 70649166 to position 70649237 relative to chromosome 12 on the `-` strand.

GAM337089 precursor RNA folds onto itself, forming GAM337089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337089 precursor RNA, designated SEQ ID NO: 7209, and a schematic representation of a predicted secondary folding of GAM337089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337089 folded precursor RNA yielding a GAM337089 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337089 RNA, hereby incorporated herein.

GAM337089 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337089 target RNA, herein designated GAM TARGET RNA.

GAM337089 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337089 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337089 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337089 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337089 RNA, herein designated GAM RNA, to target binding sites on GAM337089 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337089 target RNA into GAM337089 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337089 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337089 target genes. The mRNA of each one of this plurality of GAM337089 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337089 RNA, herein designated GAM RNA, and which when bound by GAM337089 RNA causes inhibition of translation of the GAM337089 target mRNA into a corresponding GAM337089 target protein.

The mechanism of the translational inhibition exerted by GAM337089 RNA, herein designated GAM RNA, on one or more GAM337089 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337089 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337089 RNA, herein designated GAM RNA, of GAM337089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337089 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337089 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337089 RNA correlate with, and may be deduced from, the identity of the GAM337089 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337091 7158 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 337091 (GAM337091) oligonucleotides modulates expression of respective target

GCGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM337091 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337091 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGTGAG encoded by the human genome.

ACTCCGTCTC GAM337091 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337091 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337091 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337091 precursor RNA is designated SEQ ID:7158, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7158 is located from position 70793499 to position 70793599 relative to chromosome 9 on the `+` strand.

GAM337091 precursor RNA folds onto itself, forming GAM337091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337091 precursor RNA, designated SEQ ID NO: 7158, and a schematic representation of a predicted secondary folding of GAM337091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337091 folded precursor RNA yielding a GAM337091 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337091 RNA, hereby incorporated herein. Expression of GAM337091 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337091 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337091 target RNA, herein designated GAM TARGET RNA.

GAM337091 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337091 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337091 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337091 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337091 RNA, herein designated GAM RNA, to target binding sites on GAM337091 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337091 target RNA into GAM337091 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337091 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337091 target genes. The mRNA of each one of this plurality of GAM337091 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337091 RNA,

herein designated GAM RNA, and which when bound by GAM337091 RNA causes inhibition of translation of the GAM337091 target mRNA into a corresponding GAM337091 target protein.

The mechanism of the translational inhibition exerted by GAM337091 RNA, herein designated GAM RNA, on one or more GAM337091 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337091 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337091 RNA, herein designated GAM RNA, of GAM337091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337091 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337091 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337091 RNA correlate with, and may be deduced from, the identity of the GAM337091 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337092 5887 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337092 (GAM337092) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337092 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337092 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337092 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337092 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337092 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337092 precursor RNA is designated SEQ ID:5887, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5887 is located from position 70852306 to position 70852387 relative to chromosome 14 on the `+` strand.

GAM337092 precursor RNA folds onto itself, forming GAM337092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337092 precursor RNA, designated SEQ ID NO: 5887, and a schematic representation of a predicted secondary folding of GAM337092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337092 folded precursor RNA yielding a GAM337092 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337092 RNA, hereby incorporated herein.

GAM337092 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337092 target RNA, herein designated GAM TARGET RNA.

GAM337092 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337092 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337092 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337092 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337092 RNA, herein designated GAM RNA, to target binding sites on GAM337092 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337092 target RNA

into GAM337092 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337092 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337092 target genes. The mRNA of each one of this plurality of GAM337092 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337092 RNA, herein designated GAM RNA, and which when bound by GAM337092 RNA causes inhibition of translation of the GAM337092 target mRNA into a corresponding GAM337092 target protein.

The mechanism of the translational inhibition exerted by GAM337092 RNA, herein designated GAM RNA, on one or more GAM337092 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337092 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337092 RNA, herein designated GAM RNA, of GAM337092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337092 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337092 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337092 RNA correlate with, and may be deduced from, the identity of the GAM337092 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337093 6814 GGGGCTTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCTGGCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTCCTGGGA Messenger 337093 (GAM337093) oligonucleotides modulates expression of respective target

TTTCAAACTA genes whose function and utility is known in the art.

CCTCACCAAC GAM337093 is a novel bioinformatically detectable regulatory, non protein

AGGACGCTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337093 was detected

ACCAGGAGCC is described with additional reference to Figs. 9-15.

TGCCACCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGGCCCC encoded by the human genome.

GAM337093 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337093 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337093 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337093 precursor RNA is designated SEQ ID:6814, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6814 is located from position 71022428 to position 71022515 relative to chromosome 14 on the `+` strand.

GAM337093 precursor RNA folds onto itself, forming GAM337093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337093 precursor RNA, designated SEQ ID NO: 6814, and a schematic representation of a predicted secondary folding of GAM337093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337093 folded precursor RNA yielding a GAM337093 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337093 RNA, hereby incorporated herein.

GAM337093 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337093 target RNA, herein designated GAM TARGET RNA.

GAM337093 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337093 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337093 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337093 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337093 RNA, herein designated GAM RNA, to target binding sites on GAM337093 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337093 target RNA into GAM337093 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337093 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337093 target genes. The mRNA of each one of this plurality of GAM337093 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337093 RNA, herein designated GAM RNA, and which when bound by GAM337093 RNA causes inhibition of translation of the GAM337093 target mRNA into a corresponding GAM337093 target protein.

The mechanism of the translational inhibition exerted by GAM337093 RNA, herein designated GAM RNA, on one or more GAM337093 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337093 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337093 RNA, herein designated GAM RNA, of GAM337093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337093 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337093 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337093 RNA correlate with, and may be deduced from, the identity of the GAM337093 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337094 5888 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337094 (GAM337094) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337094 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337094 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337094 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337094 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337094 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337094 precursor RNA is designated SEQ ID:5888, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5888 is located from position 71135679 to position 71135760 relative to chromosome 15 on the `+` strand.

GAM337094 precursor RNA folds onto itself, forming GAM337094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337094 precursor RNA, designated SEQ ID NO: 5888, and a schematic representation of a predicted secondary folding of GAM337094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337094 folded precursor RNA yielding a GAM337094 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337094 RNA, hereby incorporated herein.

GAM337094 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337094 target RNA, herein designated GAM TARGET RNA.

GAM337094 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337094 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337094 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337094 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337094 RNA, herein designated GAM RNA, to target binding sites on GAM337094 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337094 target RNA into GAM337094 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337094 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337094 target genes. The mRNA of each one of this plurality of GAM337094 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337094 RNA, herein designated GAM RNA, and which when bound by GAM337094 RNA causes inhibition of translation of the GAM337094 target mRNA into a corresponding GAM337094 target protein.

The mechanism of the translational inhibition exerted by GAM337094 RNA, herein designated GAM RNA, on one or more GAM337094 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337094 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337094 RNA, herein designated GAM RNA, of GAM337094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337094 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337094 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337094 RNA correlate with, and may be deduced from, the identity of the GAM337094 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337095 6566 GCTTGGCATC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTTCATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCAAAACAT Messenger 337095 (GAM337095) oligonucleotides modulates expression of respective target
GGCTTTGATA genes whose function and utility is known in the art.

ATTGCATCAG GAM337095 is a novel bioinformatically detectable regulatory, non protein
ATCTGCAAGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337095 was detected
CTGTGTAGGC is described with additional reference to Figs. 9-15.

AGAATTCTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGCCAAGT encoded by the human genome.

GAM337095 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337095 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337095 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337095 precursor RNA is designated SEQ ID:6566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6566 is located from position 71404046 to position 71404134 relative to chromosome 17 on the `+` strand.

GAM337095 precursor RNA folds onto itself, forming GAM337095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337095 precursor RNA, designated SEQ ID NO: 6566, and a schematic representation of a predicted secondary folding of GAM337095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337095 folded precursor RNA yielding a GAM337095 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337095 RNA, hereby incorporated herein.

GAM337095 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337095 target RNA, herein designated GAM TARGET RNA.

GAM337095 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337095 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337095 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337095 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337095 RNA, herein designated GAM RNA, to target binding sites on GAM337095 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337095 target RNA into GAM337095 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337095 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337095 target genes. The mRNA of each one of this plurality of GAM337095 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337095 RNA, herein designated GAM RNA, and which when bound by GAM337095 RNA causes inhibition of translation of the GAM337095 target mRNA into a corresponding GAM337095 target protein.

The mechanism of the translational inhibition exerted by GAM337095 RNA, herein designated GAM RNA, on one or more GAM337095 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337095 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337095 RNA, herein designated GAM RNA, of GAM337095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337095 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337095 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337095 RNA correlate with, and may be deduced from, the identity of the GAM337095 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337096 6384 GAGGCAGGAG AATCACTTGA ACCCGGGAGG CTGAGGGTAC AGTGAGCCGA GATCATGCCA CTGCACTCTA GCCTCGGTGA CCGAAGGAGA CTCTGTCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337096 (GAM337096) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337096 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337096 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337096 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337096 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337096 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337096 precursor RNA is designated SEQ ID:6384, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6384 is located from position 71522779 to position 71522877 relative to chromosome 7 on the `+` strand.

GAM337096 precursor RNA folds onto itself, forming GAM337096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337096 precursor RNA, designated SEQ ID NO: 6384, and a schematic representation of a predicted secondary folding of GAM337096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337096 folded precursor RNA yielding a GAM337096 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337096 RNA, hereby incorporated herein.

GAM337096 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337096 target RNA, herein designated GAM TARGET RNA.

GAM337096 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337096 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337096 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337096 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337096 RNA, herein designated GAM RNA, to target binding sites on GAM337096 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337096 target RNA into GAM337096 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337096 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337096 target genes. The mRNA of each one of this plurality of GAM337096 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337096 RNA, herein designated GAM RNA, and which when bound by GAM337096 RNA causes inhibition of translation of the GAM337096 target mRNA into a corresponding GAM337096 target protein.

The mechanism of the translational inhibition exerted by GAM337096 RNA, herein designated GAM RNA, on one or more GAM337096 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337096 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337096 RNA, herein designated GAM RNA, of

GAM337096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337096 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337096 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337096 RNA correlate with, and may be deduced from, the identity of the GAM337096 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337097 6528 GCTAGTGTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

ACACACAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTGGAAAGC Messenger 337097 (GAM337097) oligonucleotides modulates expression of respective target

ATGTACATTT genes whose function and utility is known in the art.

GGAGGATATA GAM337097 is a novel bioinformatically detectable regulatory, non protein

GTGTCTTCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337097 was detected

AATAATTATA is described with additional reference to Figs. 9-15.

CACTTTCTAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGAGTAGGG encoded by the human genome.

TGGCTTACAG GAM337097 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGGC GAM337097 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337097 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337097 precursor RNA is designated SEQ ID:6528, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6528 is located from position 71688944 to position 71689047 relative to chromosome 17 on the `+` strand.

GAM337097 precursor RNA folds onto itself, forming GAM337097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337097 precursor RNA, designated SEQ ID NO: 6528, and a schematic representation of a predicted secondary folding of GAM337097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337097 folded precursor RNA yielding a GAM337097 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337097 RNA, hereby incorporated herein.

GAM337097 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337097 target RNA, herein designated GAM TARGET RNA.

GAM337097 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337097 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337097 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337097 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337097 RNA, herein designated GAM RNA, to target binding sites on GAM337097 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337097 target RNA into GAM337097 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337097 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337097 target genes. The mRNA of each one of this plurality of GAM337097 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337097 RNA, herein designated GAM RNA, and which when bound by GAM337097 RNA causes inhibition of translation of the GAM337097 target mRNA into a corresponding GAM337097 target protein.

The mechanism of the translational inhibition exerted by GAM337097 RNA, herein designated GAM RNA, on one or more GAM337097 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337097 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337097 RNA, herein designated GAM RNA, of GAM337097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337097 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337097 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337097 RNA correlate with, and may be deduced from, the identity of the GAM337097 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337098 7082 TCTTTTCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTAGGCTAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CCTTCGAGAC Messenger 337098 (GAM337098) oligonucleotides modulates expression of respective target

TGCATTACCC genes whose function and utility is known in the art.

TCCCCAACTT GAM337098 is a novel bioinformatically detectable regulatory, non protein

AAAATCTTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337098 was detected

GATAACCCAG is described with additional reference to Figs. 9-15.

GCAGCTGGGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TATCCCCAAT encoded by the human genome.

TTAAAGTCTT GAM337098 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTTGTTGTAG GAM337098 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

CTGTATGGCA GAM337098 precursor RNA does not encode a protein. A nucleotide sequence identical or

TTTATCTAGA highly similar to the nucleotide sequence of GAM337098 precursor RNA is designated SEQ

ID:7082, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:7082 is located from position 71710852 to position 71710981

relative to chromosome X on the `-` strand.

GAM337098 precursor RNA folds onto itself, forming GAM337098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337098 precursor RNA, designated SEQ ID NO: 7082, and a schematic representation of a predicted secondary folding of GAM337098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337098 folded precursor RNA yielding a GAM337098 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337098 RNA, hereby incorporated herein.

GAM337098 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337098 target RNA, herein designated GAM TARGET RNA.

GAM337098 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337098 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337098 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337098 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337098 RNA, herein designated GAM RNA, to target binding sites on GAM337098 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337098 target RNA into GAM337098 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337098 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337098 target genes. The mRNA of each one of this plurality of GAM337098 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337098 RNA, herein designated GAM RNA, and which when bound by GAM337098 RNA causes inhibition of translation of the GAM337098 target mRNA into a corresponding GAM337098 target protein.

The mechanism of the translational inhibition exerted by GAM337098 RNA, herein designated GAM RNA, on one or more GAM337098 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337098 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337098 RNA, herein designated GAM RNA, of GAM337098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337098 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337098 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337098 RNA correlate with, and may be deduced from, the identity of the GAM337098 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337099 5889 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337099 (GAM337099) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337099 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337099 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337099 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337099 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337099 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337099 precursor RNA is designated SEQ ID:5889, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5889 is located from position 71711305 to position 71711386 relative to chromosome 13 on the `+` strand.

GAM337099 precursor RNA folds onto itself, forming GAM337099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337099 precursor RNA, designated SEQ ID NO: 5889, and a schematic representation of a predicted secondary folding of GAM337099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337099 folded precursor RNA yielding a GAM337099 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337099 RNA, hereby incorporated herein.

GAM337099 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337099 target RNA, herein designated GAM TARGET RNA.

GAM337099 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337099 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337099 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337099 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337099 RNA, herein designated GAM RNA, to target

binding sites on GAM337099 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337099 target RNA into GAM337099 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337099 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337099 target genes. The mRNA of each one of this plurality of GAM337099 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337099 RNA, herein designated GAM RNA, and which when bound by GAM337099 RNA causes inhibition of translation of the GAM337099 target mRNA into a corresponding GAM337099 target protein.

The mechanism of the translational inhibition exerted by GAM337099 RNA, herein designated GAM RNA, on one or more GAM337099 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337099 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337099 RNA, herein designated GAM RNA, of GAM337099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337099 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337099 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337099 RNA correlate with, and may be deduced from, the identity of the GAM337099 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337100 6567 GCTTGGTATG Fig. 8 further provides a conceptual description of another novel bioinformatically

CTCAGAAGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTAAAGTGT Messenger 337100 (GAM337100) oligonucleotides modulates expression of respective target

GTATGGGCAG genes whose function and utility is known in the art.

GTGTGGGGGC GAM337100 is a novel bioinformatically detectable regulatory, non protein

AATTTCTTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337100 was detected

TCCTAGCACT is described with additional reference to Figs. 9-15.

TCCATATATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACTTTCTTT encoded by the human genome.

TCTGGCTGCT GAM337100 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAGT GAM337100 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337100 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337100 precursor RNA is designated SEQ ID:6567, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6567 is located from position 71825337 to position 71825440 relative to chromosome 16 on the `+` strand.

GAM337100 precursor RNA folds onto itself, forming GAM337100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337100 precursor RNA, designated SEQ ID NO: 6567, and a schematic representation of a predicted secondary folding of GAM337100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337100 folded precursor RNA yielding a GAM337100 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337100 RNA, hereby incorporated herein.

GAM337100 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337100 target RNA, herein designated GAM TARGET RNA.

GAM337100 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337100 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337100 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337100 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337100 RNA, herein designated GAM RNA, to target binding sites on GAM337100 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337100 target RNA into GAM337100 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337100 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337100 target genes. The mRNA of each one of this plurality of GAM337100 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337100 RNA, herein designated GAM RNA, and which when bound by GAM337100 RNA causes inhibition of translation of the GAM337100 target mRNA into a corresponding GAM337100 target protein.

The mechanism of the translational inhibition exerted by GAM337100 RNA, herein designated GAM RNA, on one or more GAM337100 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337100 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337100 RNA, herein designated GAM RNA, of GAM337100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337100 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337100 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337100 RNA correlate with, and may be deduced from, the identity of the GAM337100 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337101 6860 GTAGAGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCATCATGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTTGAGAAT Messenger 337101 (GAM337101) oligonucleotides modulates expression of respective target
AGCTTTAGAG genes whose function and utility is known in the art.

TTACTCTTGG GAM337101 is a novel bioinformatically detectable regulatory, non protein
GATAGTGTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337101 was detected
CATGGCCCTG is described with additional reference to Figs. 9-15.

TGAGGGAACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAC encoded by the human genome.

GAM337101 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337101 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337101 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337101 precursor RNA is designated SEQ ID:6860, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6860 is located from position 71906731 to position 71906814 relative to chromosome 12 on the `+` strand.

GAM337101 precursor RNA folds onto itself, forming GAM337101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337101 precursor RNA, designated SEQ ID NO: 6860, and a schematic representation of a predicted secondary folding of GAM337101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337101 folded precursor RNA yielding a GAM337101 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337101 RNA, hereby incorporated herein.

GAM337101 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337101 target RNA, herein designated GAM TARGET RNA.

GAM337101 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337101 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337101 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337101 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337101 RNA, herein designated GAM RNA, to target binding sites on GAM337101 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337101 target RNA into GAM337101 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337101 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337101 target genes. The mRNA of each one of this plurality of GAM337101 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337101 RNA, herein designated GAM RNA, and which when bound by GAM337101 RNA causes inhibition of translation of the GAM337101 target mRNA into a corresponding GAM337101 target protein.

The mechanism of the translational inhibition exerted by GAM337101 RNA, herein designated GAM RNA, on one or more GAM337101 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337101 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337101 RNA, herein designated GAM RNA, of GAM337101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337101 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337101 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337101

RNA correlate with, and may be deduced from, the identity of the GAM337101 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337105 6802 GGGCCAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCAAGATGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCATTTGCAA Messenger 337105 (GAM337105) oligonucleotides modulates expression of respective target
GTTGTCTTCT genes whose function and utility is known in the art.

AGGGTGTTGC GAM337105 is a novel bioinformatically detectable regulatory, non protein
CTGAACCTAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337105 was detected
GCTGCAGTAG is described with additional reference to Figs. 9-15.

AAGTGGGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGAGGTAGG encoded by the human genome.

CGATATTGAA GAM337105 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ATCCC GAM337105 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337105 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337105 precursor RNA is designated SEQ ID:6802, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6802 is located from position 71960660 to position 71960764 relative to chromosome 11 on the `-` strand.

GAM337105 precursor RNA folds onto itself, forming GAM337105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337105 precursor RNA, designated SEQ ID NO: 6802, and a schematic representation of a predicted secondary folding of GAM337105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337105 folded precursor RNA yielding a GAM337105 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337105 RNA, hereby incorporated herein.

GAM337105 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337105 target RNA, herein designated GAM TARGET RNA.

GAM337105 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337105 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337105 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337105 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337105 RNA, herein designated GAM RNA, to target binding sites on GAM337105 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337105 target RNA into GAM337105 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337105 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337105 target genes. The mRNA of each one of this plurality of GAM337105 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337105 RNA, herein designated GAM RNA, and which when bound by GAM337105 RNA causes inhibition of translation of the GAM337105 target mRNA into a corresponding GAM337105 target protein.

The mechanism of the translational inhibition exerted by GAM337105 RNA, herein designated GAM RNA, on one or more GAM337105 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337105 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337105 RNA, herein designated GAM RNA, of GAM337105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337105 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337105 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337105 RNA correlate with, and may be deduced from, the identity of the GAM337105 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337106 6021 CAGCTTGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACACACAGC detected oligonucleotides of the present invention, referred to here as Genomic Address
ATTGGTCATG Messenger 337106 (GAM337106) oligonucleotides modulates expression of respective target
AGGTCAGCTG genes whose function and utility is known in the art.

CTCTCTGACC GAM337106 is a novel bioinformatically detectable regulatory, non protein
CACTTGCTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337106 was detected
GAGTTGTTTG is described with additional reference to Figs. 9-15.

CTGCCTGTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337106 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337106 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337106 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337106 precursor RNA is designated SEQ ID:6021, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6021 is located from position 72006752 to position 72006831 relative to chromosome 14 on the `+` strand.

GAM337106 precursor RNA folds onto itself, forming GAM337106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337106 precursor RNA, designated SEQ ID NO: 6021, and a schematic representation of a predicted secondary folding of GAM337106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337106 folded precursor RNA yielding a GAM337106 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337106 RNA, hereby incorporated herein.

GAM337106 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337106 target RNA, herein designated GAM TARGET RNA.

GAM337106 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337106 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337106 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337106 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337106 RNA, herein designated GAM RNA, to target binding sites on GAM337106 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337106 target RNA into GAM337106 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337106 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337106 target genes. The mRNA of each one of this plurality of GAM337106 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337106 RNA, herein designated GAM RNA, and which when bound by GAM337106 RNA causes inhibition of translation of the GAM337106 target mRNA into a corresponding GAM337106 target protein.

The mechanism of the translational inhibition exerted by GAM337106 RNA, herein designated GAM RNA, on one or more GAM337106 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337106 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337106 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337106 RNA, herein designated GAM RNA, of GAM337106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337106 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337106 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337106 RNA correlate with, and may be deduced from, the identity of the GAM337106 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337108 6022 CAGCTTGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACACACAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGGTCATG Messenger 337108 (GAM337108) oligonucleotides modulates expression of respective target

AGGTCAGCTG genes whose function and utility is known in the art.

CTCTCTGACC GAM337108 is a novel bioinformatically detectable regulatory, non protein

CACTTGCTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337108 was detected

GAGTTGTTTG is described with additional reference to Figs. 9-15.

CTGCCTGTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337108 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337108 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337108 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337108 precursor RNA is designated SEQ ID:6022, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6022 is located from position 72038936 to position 72039015 relative to chromosome 14 on the `+` strand.

GAM337108 precursor RNA folds onto itself, forming GAM337108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337108 precursor RNA, designated SEQ ID NO: 6022, and a schematic representation of a predicted secondary folding of GAM337108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337108 folded precursor RNA yielding a GAM337108 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337108 RNA, hereby incorporated herein.

GAM337108 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337108 target RNA, herein designated GAM TARGET RNA.

GAM337108 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337108 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337108 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337108 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337108 RNA, herein designated GAM RNA, to target binding sites on GAM337108 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337108 target RNA into GAM337108 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337108 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337108 target genes. The mRNA of each one of this plurality of GAM337108 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337108 RNA, herein designated GAM RNA, and which when bound by GAM337108 RNA causes inhibition of translation of the GAM337108 target mRNA into a corresponding GAM337108 target protein.

The mechanism of the translational inhibition exerted by GAM337108 RNA, herein

designated GAM RNA, on one or more GAM337108 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337108 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337108 RNA, herein designated GAM RNA, of GAM337108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337108 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337108 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337108 RNA correlate with, and may be deduced from, the identity of the GAM337108 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337109 6806 GGGCTGGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGATGGCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTTTGTAGT Messenger 337109 (GAM337109) oligonucleotides modulates expression of respective target

CTCAGTACTT genes whose function and utility is known in the art.

TGGGAGGCCA GAM337109 is a novel bioinformatically detectable regulatory, non protein

AAGATGGGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337109 was detected

GATTGCTTGA is described with additional reference to Figs. 9-15.

GCCCGTGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTGAGACCAG encoded by the human genome.

CCT GAM337109 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337109 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337109 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337109 precursor RNA is designated SEQ ID:6806, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6806 is located from position 72098256 to position 72098348

relative to chromosome 7 on the `-` strand.

GAM337109 precursor RNA folds onto itself, forming GAM337109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337109 precursor RNA, designated SEQ ID NO: 6806, and a schematic representation of a predicted secondary folding of GAM337109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337109 folded precursor RNA yielding a GAM337109 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337109 RNA, hereby incorporated herein.

GAM337109 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337109 target RNA, herein designated GAM TARGET RNA.

GAM337109 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337109 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337109 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337109 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337109 RNA, herein designated GAM RNA, to target binding sites on GAM337109 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337109 target RNA into GAM337109 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337109 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337109 target genes. The mRNA of each one of this plurality of GAM337109 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337109 RNA, herein designated GAM RNA, and which when bound by GAM337109 RNA causes inhibition of translation of the GAM337109 target mRNA into a corresponding GAM337109 target protein.

The mechanism of the translational inhibition exerted by GAM337109 RNA, herein designated GAM RNA, on one or more GAM337109 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337109 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337109 RNA, herein designated GAM RNA, of GAM337109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337109 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337109 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337109 RNA correlate with, and may be deduced from, the identity of the GAM337109 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337110 5890 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337110 (GAM337110) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337110 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337110 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337110 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337110 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337110 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337110 precursor RNA is designated SEQ ID:5890, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5890 is located from position 72187619 to position 72187700 relative to chromosome 13 on the `-` strand.

GAM337110 precursor RNA folds onto itself, forming GAM337110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337110 precursor RNA, designated SEQ ID NO: 5890, and a schematic representation of a predicted secondary folding of GAM337110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337110 folded precursor RNA yielding a GAM337110 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337110 RNA, hereby incorporated herein.

GAM337110 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337110 target RNA, herein designated GAM TARGET RNA.

GAM337110 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337110 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337110 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337110 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337110 RNA, herein designated GAM RNA, to target

binding sites on GAM337110 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337110 target RNA into GAM337110 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337110 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337110 target genes. The mRNA of each one of this plurality of GAM337110 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337110 RNA, herein designated GAM RNA, and which when bound by GAM337110 RNA causes inhibition of translation of the GAM337110 target mRNA into a corresponding GAM337110 target protein.

The mechanism of the translational inhibition exerted by GAM337110 RNA, herein designated GAM RNA, on one or more GAM337110 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337110 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337110 RNA, herein designated GAM RNA, of GAM337110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337110 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337110 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337110 RNA correlate with, and may be deduced from, the identity of the GAM337110 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337111 6356 GAGATGGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCACTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCCAGGAAT Messenger 337111 (GAM337111) oligonucleotides modulates expression of respective target

TTGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCAAT GAM337111 is a novel bioinformatically detectable regulatory, non protein

GACTGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337111 was detected

CTGTACTTCA is described with additional reference to Figs. 9-15.

GCCTGGGTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGGGGAC encoded by the human genome.

TTCATTTC GAM337111 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337111 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337111 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337111 precursor RNA is designated SEQ ID:6356, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6356 is located from position 72274763 to position 72274860 relative to chromosome 7 on the `+` strand.

GAM337111 precursor RNA folds onto itself, forming GAM337111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337111 precursor RNA, designated SEQ ID NO: 6356, and a schematic representation of a predicted secondary folding of GAM337111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337111 folded precursor RNA yielding a GAM337111 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337111 RNA, hereby incorporated herein.

GAM337111 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337111 target RNA, herein designated GAM TARGET RNA.

GAM337111 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337111 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337111 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337111 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337111 RNA, herein designated GAM RNA, to target binding sites on GAM337111 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337111 target RNA into GAM337111 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337111 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337111 target genes. The mRNA of each one of this plurality of GAM337111 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337111 RNA, herein designated GAM RNA, and which when bound by GAM337111 RNA causes inhibition of translation of the GAM337111 target mRNA into a corresponding GAM337111 target protein.

The mechanism of the translational inhibition exerted by GAM337111 RNA, herein designated GAM RNA, on one or more GAM337111 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337111 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337111 RNA, herein designated GAM RNA, of GAM337111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337111 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337111 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337111 RNA correlate with, and may be deduced from, the identity of the GAM337111 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337112 6603 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAAGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAATTTGAGG Messenger 337112 (GAM337112) oligonucleotides modulates expression of respective target
CTGCAGTGAG genes whose function and utility is known in the art.

CAATGACTGT GAM337112 is a novel bioinformatically detectable regulatory, non protein
GCCACTGTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337112 was detected
TTCAGCCTGG is described with additional reference to Figs. 9-15.

GTAACAGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGACTTC encoded by the human genome.

GAM337112 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337112 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337112 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337112 precursor RNA is designated SEQ ID:6603, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6603 is located from position 72274769 to position 72274855 relative to chromosome 7 on the `+` strand.

GAM337112 precursor RNA folds onto itself, forming GAM337112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337112 precursor RNA, designated SEQ ID NO: 6603, and a schematic representation of a predicted secondary folding of GAM337112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337112 folded precursor RNA yielding a GAM337112 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337112 RNA, hereby incorporated herein.

GAM337112 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337112 target RNA, herein designated GAM TARGET RNA.

GAM337112 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337112 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337112 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337112 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337112 RNA, herein designated GAM RNA, to target binding sites on GAM337112 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337112 target RNA into GAM337112 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337112 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337112 target genes. The mRNA of each one of this plurality of GAM337112 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337112 RNA, herein designated GAM RNA, and which when bound by GAM337112 RNA causes inhibition of translation of the GAM337112 target mRNA into a corresponding GAM337112 target protein.

The mechanism of the translational inhibition exerted by GAM337112 RNA, herein designated GAM RNA, on one or more GAM337112 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337112 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337112 RNA, herein designated GAM RNA, of GAM337112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337112 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337112 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337112

RNA correlate with, and may be deduced from, the identity of the GAM337112 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337113 6303 GAATCACTTA AGCCCAGGAA TTTGAGGCTG CAGTGAGCAA TGACTGTGCC ACTGTACTTC AGCCTGGGTA ACAGAGGGGA CTTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337113 (GAM337113) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337113 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337113 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337113 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337113 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337113 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337113 precursor RNA is designated SEQ ID:6303, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6303 is located from position 72274772 to position 72274855 relative to chromosome 7 on the `+` strand.

GAM337113 precursor RNA folds onto itself, forming GAM337113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337113 precursor RNA, designated SEQ ID NO: 6303, and a schematic representation of a predicted secondary folding of GAM337113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337113 folded precursor RNA yielding a GAM337113 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337113 RNA, hereby incorporated herein.

GAM337113 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337113 target RNA, herein designated GAM TARGET RNA.

GAM337113 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337113 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337113 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337113 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337113 RNA, herein designated GAM RNA, to target binding sites on GAM337113 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337113 target RNA into GAM337113 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337113 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337113 target genes. The mRNA of each one of this plurality of GAM337113 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337113 RNA, herein designated GAM RNA, and which when bound by GAM337113 RNA causes inhibition of translation of the GAM337113 target mRNA into a corresponding GAM337113 target protein.

The mechanism of the translational inhibition exerted by GAM337113 RNA, herein designated GAM RNA, on one or more GAM337113 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337113 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337113 RNA, herein designated GAM RNA, of GAM337113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337113 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337113 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337113 RNA correlate with, and may be deduced from, the identity of the GAM337113 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337115 5781 AGGCTGGGAA Fig. 8 further provides a conceptual description of another novel bioinformatically
CATTCAGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCTCAAGCC Messenger 337115 (GAM337115) oligonucleotides modulates expression of respective target
CAGGGTTGGC genes whose function and utility is known in the art.

AACCCCCACT GAM337115 is a novel bioinformatically detectable regulatory, non protein
CCCTCCAACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337115 was detected
CAAGCAGCTC is described with additional reference to Figs. 9-15.

AAGTCTTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGACCT encoded by the human genome.

GAM337115 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337115 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337115 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337115 precursor RNA is designated SEQ ID:5781, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5781 is located from position 72530482 to position 72530568 relative to chromosome 17 on the `+` strand.

GAM337115 precursor RNA folds onto itself, forming GAM337115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337115 precursor RNA, designated SEQ ID NO: 5781, and a schematic representation of a predicted secondary folding of GAM337115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337115 folded precursor RNA yielding a GAM337115 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337115 RNA, hereby incorporated herein.

GAM337115 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337115 target RNA, herein designated GAM TARGET RNA.

GAM337115 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337115 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337115 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337115 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337115 RNA, herein designated GAM RNA, to target binding sites on GAM337115 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337115 target RNA into GAM337115 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337115 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337115 target genes. The mRNA of each one of this plurality of GAM337115 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337115 RNA, herein designated GAM RNA, and which when bound by GAM337115 RNA causes inhibition of translation of the GAM337115 target mRNA into a corresponding GAM337115 target protein.

The mechanism of the translational inhibition exerted by GAM337115 RNA, herein designated GAM RNA, on one or more GAM337115 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337115 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337115 RNA, herein designated GAM RNA, of GAM337115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337115 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337115 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337115 RNA correlate with, and may be deduced from, the identity of the GAM337115 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337118 6239 CTGTCCTGTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GATACATGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGATGATCAT Messenger 337118 (GAM337118) oligonucleotides modulates expression of respective target

AAGTGAGCTT genes whose function and utility is known in the art.

TTATAAGCGC GAM337118 is a novel bioinformatically detectable regulatory, non protein

AGAGTATTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337118 was detected

CTATATCACC is described with additional reference to Figs. 9-15.

GTGAAAGTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATCGCATACA encoded by the human genome.

GGACAG GAM337118 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337118 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337118 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337118 precursor RNA is designated SEQ ID:6239, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6239 is located from position 72678382 to position 72678477 relative to chromosome 18 on the `-` strand.

GAM337118 precursor RNA folds onto itself, forming GAM337118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337118 precursor RNA, designated SEQ ID NO: 6239, and a schematic representation of a predicted secondary folding of GAM337118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337118 folded precursor RNA yielding a GAM337118 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337118 RNA, hereby incorporated herein.

GAM337118 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337118 target RNA, herein designated GAM TARGET RNA.

GAM337118 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337118 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337118 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337118 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337118 RNA, herein designated GAM RNA, to target binding sites on GAM337118 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337118 target RNA into GAM337118 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337118 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337118 target genes. The mRNA of each one of this plurality of GAM337118 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337118 RNA, herein designated GAM RNA, and which when bound by GAM337118 RNA causes inhibition of translation of the GAM337118 target mRNA into a corresponding GAM337118 target protein.

The mechanism of the translational inhibition exerted by GAM337118 RNA, herein

designated GAM RNA, on one or more GAM337118 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337118 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337118 RNA, herein designated GAM RNA, of GAM337118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337118 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337118 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337118 RNA correlate with, and may be deduced from, the identity of the GAM337118 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337119 6839 GGTCTCCCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCCCAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGGAGTGCAG Messenger 337119 (GAM337119) oligonucleotides modulates expression of respective target

TGATGCAATC genes whose function and utility is known in the art.

ATAGTTCACT GAM337119 is a novel bioinformatically detectable regulatory, non protein

GCAACCTTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337119 was detected

GGGTTCAAGT is described with additional reference to Figs. 9-15.

GATTTTCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTCAGCCTC encoded by the human genome.

CCAAGTAGTT GAM337119 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAGACT GAM337119 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337119 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337119 precursor RNA is designated SEQ ID:6839, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6839 is located from position 73042551 to position 73042656 relative to chromosome 7 on the `-` strand.

GAM337119 precursor RNA folds onto itself, forming GAM337119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337119 precursor RNA, designated SEQ ID NO: 6839, and a schematic representation of a predicted secondary folding of GAM337119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337119 folded precursor RNA yielding a GAM337119 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337119 RNA, hereby incorporated herein.

GAM337119 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337119 target RNA, herein designated GAM TARGET RNA.

GAM337119 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337119 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337119 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337119 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337119 RNA, herein designated GAM RNA, to target binding sites on GAM337119 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337119 target RNA into GAM337119 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337119 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337119 target genes. The mRNA of each one of this plurality of GAM337119 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337119 RNA, herein designated GAM RNA, and which when bound by GAM337119 RNA causes inhibition of translation of the GAM337119 target mRNA into a corresponding GAM337119 target protein.

The mechanism of the translational inhibition exerted by GAM337119 RNA, herein designated GAM RNA, on one or more GAM337119 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337119 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337119 RNA, herein designated GAM RNA, of GAM337119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337119 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337119 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337119 RNA correlate with, and may be deduced from, the identity of the GAM337119 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337126 6360 GAGCCATTAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTCGGGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGCCTCTC Messenger 337126 (GAM337126) oligonucleotides modulates expression of respective target

TTAACGGACC genes whose function and utility is known in the art.

TTCCAGGCAC GAM337126 is a novel bioinformatically detectable regulatory, non protein

TGCTGAGAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337126 was detected

ACCAGGTTAA is described with additional reference to Figs. 9-15.

TGGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337126 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337126 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337126 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337126 precursor RNA is designated SEQ ID:6360, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6360 is located from position 73205614 to position 73205689 relative to chromosome 11 on the `+` strand.

GAM337126 precursor RNA folds onto itself, forming GAM337126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337126 precursor RNA, designated SEQ ID NO: 6360, and a schematic representation of a predicted secondary folding of GAM337126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337126 folded precursor RNA yielding a GAM337126 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337126 RNA, hereby incorporated herein.

GAM337126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337126 target RNA, herein designated GAM TARGET RNA.

GAM337126 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337126 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337126 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337126 RNA, herein designated GAM RNA, to target binding sites on GAM337126 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337126 target RNA into GAM337126 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337126 target genes. The mRNA of each one of this plurality of GAM337126 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337126 RNA, herein designated GAM RNA, and which when bound by GAM337126 RNA causes inhibition of translation of the GAM337126 target mRNA into a corresponding GAM337126 target protein.

The mechanism of the translational inhibition exerted by GAM337126 RNA, herein designated GAM RNA, on one or more GAM337126 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337126 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337126 RNA, herein designated GAM RNA, of GAM337126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337126 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337126 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337126 RNA correlate with, and may be deduced from, the identity of the GAM337126 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337127 7146 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGCAG Messenger 337127 (GAM337127) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM337127 is a novel bioinformatically detectable regulatory, non protein

AGATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337127 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGCACAA encoded by the human genome.

AACTGTCTCA GAM337127 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337127 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337127 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337127 precursor RNA is designated SEQ ID:7146, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7146 is located from position 73215042 to position 73215141 relative to chromosome 7 on the `+` strand.

GAM337127 precursor RNA folds onto itself, forming GAM337127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337127 precursor RNA, designated SEQ ID NO: 7146, and a schematic representation of a predicted secondary folding of GAM337127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337127 folded precursor RNA yielding a GAM337127 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337127 RNA, hereby incorporated herein. Expression of GAM337127 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337127 target RNA, herein designated GAM TARGET RNA.

GAM337127 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337127 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337127 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337127 RNA, herein designated GAM RNA, to target binding sites on GAM337127 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337127 target RNA into GAM337127 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337127 target genes. The mRNA of each one of this plurality of GAM337127 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337127 RNA, herein designated GAM RNA, and which when bound by GAM337127 RNA causes inhibition of translation of the GAM337127 target mRNA into a corresponding GAM337127 target protein.

The mechanism of the translational inhibition exerted by GAM337127 RNA, herein designated GAM RNA, on one or more GAM337127 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337127 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337127 RNA, herein designated GAM RNA, of GAM337127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337127 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337127 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337127 RNA correlate with, and may be deduced from, the identity of the GAM337127 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337128 6399 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCTGGCAGG Messenger 337128 (GAM337128) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337128 is a novel bioinformatically detectable regulatory, non protein
GATCGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337128 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGCACAAA encoded by the human genome.

ACTGTCTC GAM337128 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337128 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337128 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337128 precursor RNA is designated SEQ ID:6399, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6399 is located from position 73215043 to position 73215140 relative to chromosome 7 on the `+` strand.

GAM337128 precursor RNA folds onto itself, forming GAM337128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337128 precursor RNA, designated SEQ ID NO: 6399, and a schematic representation of a predicted secondary folding of GAM337128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337128 folded precursor RNA yielding a GAM337128 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337128 RNA, hereby incorporated herein. Expression of GAM337128 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337128 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337128 target RNA, herein designated GAM TARGET RNA.

GAM337128 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337128 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337128 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337128 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337128 RNA, herein designated GAM RNA, to target binding sites on GAM337128 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337128 target RNA into GAM337128 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337128 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337128 target genes. The mRNA of each one of this plurality of GAM337128 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337128 RNA, herein designated GAM RNA, and which when bound by GAM337128 RNA causes inhibition of translation of the GAM337128 target mRNA into a corresponding GAM337128 target protein.

The mechanism of the translational inhibition exerted by GAM337128 RNA, herein designated GAM RNA, on one or more GAM337128 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337128 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337128 RNA, herein designated GAM RNA, of GAM337128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337128 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337128 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337128 RNA correlate with, and may be deduced from, the identity of the GAM337128 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337129 6412 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATGGCGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGAGG Messenger 337129 (GAM337129) oligonucleotides modulates expression of respective target
CGGAGCTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337129 is a novel bioinformatically detectable regulatory, non protein
GATCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337129 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCCGTCTC GAM337129 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337129 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337129 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337129 precursor RNA is designated SEQ ID:6412, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6412 is located from position 73257733 to position 73257831 relative to chromosome 3 on the `-` strand.

GAM337129 precursor RNA folds onto itself, forming GAM337129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337129 precursor RNA, designated SEQ ID NO: 6412, and a schematic representation of a predicted secondary folding of GAM337129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337129 folded precursor RNA yielding a GAM337129 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337129 RNA, hereby incorporated herein. Expression of GAM337129 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337129 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337129 target RNA, herein designated GAM TARGET RNA.

GAM337129 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337129 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337129 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337129 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337129 RNA, herein designated GAM RNA, to target binding sites on GAM337129 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337129 target RNA into GAM337129 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337129 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337129 target genes. The mRNA of each one of this plurality of GAM337129 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337129 RNA, herein designated GAM RNA, and which when bound by GAM337129 RNA causes inhibition of translation of the GAM337129 target mRNA into a corresponding GAM337129 target protein.

The mechanism of the translational inhibition exerted by GAM337129 RNA, herein designated GAM RNA, on one or more GAM337129 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337129 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337129 RNA, herein designated GAM RNA, of GAM337129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337129 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337129 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337129 RNA correlate with, and may be deduced from, the identity of the GAM337129 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337130 6609 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 337130 (GAM337130) oligonucleotides modulates expression of respective target
TTGTAGTGAG genes whose function and utility is known in the art.

CTGAGATTGC GAM337130 is a novel bioinformatically detectable regulatory, non protein
ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337130 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCGATAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAAACTCC encoded by the human genome.

GAM337130 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337130 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337130 precursor RNA is designated SEQ ID:6609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6609 is located from position 73327088 to position 73327176 relative to chromosome 15 on the `+` strand.

GAM337130 precursor RNA folds onto itself, forming GAM337130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337130 precursor RNA, designated SEQ ID NO: 6609, and a schematic representation of a predicted secondary folding of GAM337130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337130 folded precursor RNA yielding a GAM337130 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337130 RNA, hereby incorporated herein.

GAM337130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337130 target RNA, herein designated GAM TARGET RNA.

GAM337130 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337130 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337130 RNA, herein designated GAM RNA, to target binding sites on GAM337130 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337130 target RNA into GAM337130 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337130 target genes. The mRNA of each one of this plurality of GAM337130 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337130 RNA, herein designated GAM RNA, and which when bound by GAM337130 RNA causes inhibition of translation of the GAM337130 target mRNA into a corresponding GAM337130 target protein.

The mechanism of the translational inhibition exerted by GAM337130 RNA, herein designated GAM RNA, on one or more GAM337130 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337130 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337130 RNA, herein designated GAM RNA, of GAM337130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337130 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337130 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337130 RNA correlate with, and may be deduced from, the identity of the GAM337130 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337131 7172 TGAGGCGCCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAAAACATA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGCTGGGCTT Messenger 337131 (GAM337131) oligonucleotides modulates expression of respective target

GTGTGAGATG genes whose function and utility is known in the art.

GGAGAAAGAC GAM337131 is a novel bioinformatically detectable regulatory, non protein

CAGAAGTATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337131 was detected

GTCTAAACTT is described with additional reference to Figs. 9-15.

CTCCCTGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACACATCCAG encoded by the human genome.

CTTCATGGCA GAM337131 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTGTGCTACA GAM337131 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337131 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337131 precursor RNA is designated SEQ ID:7172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7172 is located from position 73549131 to position 73549240 relative to chromosome 17 on the `+` strand.

GAM337131 precursor RNA folds onto itself, forming GAM337131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337131 precursor RNA, designated SEQ ID NO: 7172, and a schematic representation of a predicted secondary folding of GAM337131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337131 folded precursor RNA yielding a GAM337131 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337131 RNA, hereby incorporated herein.

GAM337131 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337131 target RNA, herein designated GAM TARGET RNA.

GAM337131 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337131 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337131 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337131 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337131 RNA, herein designated GAM RNA, to target binding sites on GAM337131 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337131 target RNA into GAM337131 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM337131 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337131 target genes. The mRNA of each one of this plurality of GAM337131 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337131 RNA, herein designated GAM RNA, and which when bound by GAM337131 RNA causes inhibition of translation of the GAM337131 target mRNA into a corresponding GAM337131 target protein.

The mechanism of the translational inhibition exerted by GAM337131 RNA, herein designated GAM RNA, on one or more GAM337131 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337131 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337131 RNA, herein designated GAM RNA, of GAM337131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337131 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337131 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337131 RNA correlate with, and may be deduced from, the identity of the GAM337131 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337133 6018 CAGCGCGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCGCCACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAATAAATG Messenger 337133 (GAM337133) oligonucleotides modulates expression of respective target

TTGCTTGGAG genes whose function and utility is known in the art.

TGGACCGAGG GAM337133 is a novel bioinformatically detectable regulatory, non protein

CTCTGCAGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337133 was detected

ATGCAGGGAG is described with additional reference to Figs. 9-15.

GGCCGGGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGCCCCAGGG encoded by the human genome.

TTATTTCTAA GAM337133 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTTGAGGACA GAM337133 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GGAGGTTGTG GAM337133 precursor RNA does not encode a protein. A nucleotide sequence identical or

AGTTCTGCTG highly similar to the nucleotide sequence of GAM337133 precursor RNA is designated SEQ

ID:6018, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6018 is located from position 73601903 to position 73602032 relative to chromosome 7 on the `+` strand.

GAM337133 precursor RNA folds onto itself, forming GAM337133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337133 precursor RNA, designated SEQ ID NO: 6018, and a schematic representation of a predicted secondary folding of GAM337133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337133 folded precursor RNA yielding a GAM337133 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337133 RNA, hereby incorporated herein.

GAM337133 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337133 target RNA, herein designated GAM TARGET RNA.

GAM337133 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337133 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337133 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337133 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337133 RNA, herein designated GAM RNA, to target binding sites on GAM337133 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337133 target RNA into GAM337133 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337133 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337133 target genes. The mRNA of each one of this plurality of GAM337133 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337133 RNA, herein designated GAM RNA, and which when bound by GAM337133 RNA causes inhibition of translation of the GAM337133 target mRNA into a corresponding GAM337133 target protein.

The mechanism of the translational inhibition exerted by GAM337133 RNA, herein designated GAM RNA, on one or more GAM337133 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337133 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337133 RNA, herein designated GAM RNA, of GAM337133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337133 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337133 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337133 RNA correlate with, and may be deduced from, the identity of the GAM337133 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337135 6524 GCTAGGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACCACTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCCAACCTG Messenger 337135 (GAM337135) oligonucleotides modulates expression of respective target

GACAACAGAG genes whose function and utility is known in the art.

CAAGACCCTG GAM337135 is a novel bioinformatically detectable regulatory, non protein
TCTCTAGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337135 was detected
AGGTGCAGTG is described with additional reference to Figs. 9-15.

GCTCACACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTAATCCCAG encoded by the human genome.

C GAM337135 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337135 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337135 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337135 precursor RNA is designated SEQ ID:6524, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6524 is located from position 73747698 to position 73747788 relative to chromosome 7 on the `+` strand.

GAM337135 precursor RNA folds onto itself, forming GAM337135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337135 precursor RNA, designated SEQ ID NO: 6524, and a schematic representation of a predicted secondary folding of GAM337135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337135 folded precursor RNA yielding a GAM337135 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337135 RNA, hereby incorporated herein.

GAM337135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337135 target RNA, herein designated GAM TARGET RNA.

GAM337135 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337135 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337135 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337135 RNA, herein designated GAM RNA, to target binding sites on GAM337135 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337135 target RNA into GAM337135 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337135 target genes. The mRNA of each one of this plurality of GAM337135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337135 RNA, herein designated GAM RNA, and which when bound by GAM337135 RNA causes inhibition of translation of the GAM337135 target mRNA into a corresponding GAM337135 target protein.

The mechanism of the translational inhibition exerted by GAM337135 RNA, herein designated GAM RNA, on one or more GAM337135 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337135 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337135 RNA, herein designated GAM RNA, of GAM337135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337135 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337135 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337135 RNA correlate with, and may be deduced from, the identity of the GAM337135 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337136 6990 TCACATTCTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CATAACTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TATGAGGGAA Messenger 337136 (GAM337136) oligonucleotides modulates expression of respective target

GCATGGGACC genes whose function and utility is known in the art.

ATGATCCCTG GAM337136 is a novel bioinformatically detectable regulatory, non protein

GAGGGACTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337136 was detected

AGGGATTGCC is described with additional reference to Figs. 9-15.

CACGCTAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATCTCACTGT encoded by the human genome.

ACAGCTGGAG GAM337136 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAACTGA GAM337136 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337136 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337136 precursor RNA is designated SEQ ID:6990, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6990 is located from position 73803663 to position 73803769 relative to chromosome 7 on the `+` strand.

GAM337136 precursor RNA folds onto itself, forming GAM337136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337136 precursor RNA, designated SEQ ID NO: 6990, and a schematic representation of a predicted secondary folding of GAM337136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337136 folded precursor RNA yielding a GAM337136 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337136 RNA, hereby incorporated herein.

GAM337136 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337136 target RNA, herein designated GAM TARGET RNA.

GAM337136 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337136 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337136 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337136 RNA, herein designated GAM RNA, to target binding sites on GAM337136 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337136 target RNA into GAM337136 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337136 target genes. The mRNA of each one of this plurality of GAM337136 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337136 RNA, herein designated GAM RNA, and which when bound by GAM337136 RNA causes inhibition of translation of the GAM337136 target mRNA into a corresponding GAM337136 target protein.

The mechanism of the translational inhibition exerted by GAM337136 RNA, herein designated GAM RNA, on one or more GAM337136 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337136 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337136 RNA, herein designated GAM RNA, of GAM337136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337136 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337136 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337136 RNA correlate with, and may be deduced from, the identity of the GAM337136 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337138 6348 GAGACCTCTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTATAAAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGAGGCAGG Messenger 337138 (GAM337138) oligonucleotides modulates expression of respective target
AGTTGGCAAG genes whose function and utility is known in the art.

AGGTCAAGAC GAM337138 is a novel bioinformatically detectable regulatory, non protein
TGCAATGAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337138 was detected
CATGATCCTG is described with additional reference to Figs. 9-15.

CCACTATACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTGCCTGGG encoded by the human genome.

TGATGGGAGA GAM337138 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CCCTGTCTC GAM337138 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337138 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337138 precursor RNA is designated SEQ ID:6348, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6348 is located from position 73912141 to position 73912249 relative to chromosome 9 on the `-` strand.

GAM337138 precursor RNA folds onto itself, forming GAM337138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337138 precursor RNA, designated SEQ ID NO: 6348, and a schematic representation of a predicted secondary folding of GAM337138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337138 folded precursor

RNA yielding a GAM337138 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337138 RNA, hereby incorporated herein.

GAM337138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337138 target RNA, herein designated GAM TARGET RNA.

GAM337138 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337138 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337138 RNA, herein designated GAM RNA, to target binding sites on GAM337138 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337138 target RNA into GAM337138 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337138 target genes. The mRNA of each one of this plurality of GAM337138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337138 RNA, herein designated GAM RNA, and which when bound by GAM337138 RNA causes inhibition of translation of the GAM337138 target mRNA into a corresponding GAM337138 target protein.

The mechanism of the translational inhibition exerted by GAM337138 RNA, herein designated GAM RNA, on one or more GAM337138 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337138 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337138 RNA, herein designated GAM RNA, of GAM337138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337138 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337138 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337138 RNA correlate with, and may be deduced from, the identity of the GAM337138 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337140 6019 CAGCGCGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCCGCCACCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAATAAATG Messenger 337140 (GAM337140) oligonucleotides modulates expression of respective target

TTGCTTGGAG genes whose function and utility is known in the art.

TGGACCGAGG GAM337140 is a novel bioinformatically detectable regulatory, non protein

CTCTGCAGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337140 was detected

ATGCAGGGAG is described with additional reference to Figs. 9-15.

GGCCGGGCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGCCCCAGGG encoded by the human genome.

TTATTTCTAA GAM337140 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTTGAGGACA GAM337140 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GGAGGTTGTG GAM337140 precursor RNA does not encode a protein. A nucleotide sequence identical or

AGTTCTGCTG highly similar to the nucleotide sequence of GAM337140 precursor RNA is designated SEQ

ID:6019, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6019 is located from position 73970646 to position 73970775 relative to chromosome 7 on the `-` strand.

GAM337140 precursor RNA folds onto itself, forming GAM337140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337140 precursor RNA, designated SEQ ID NO: 6019, and a schematic representation of a predicted secondary folding of GAM337140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337140 folded precursor RNA yielding a GAM337140 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337140 RNA, hereby incorporated herein.

GAM337140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337140 target RNA, herein designated GAM TARGET RNA.

GAM337140 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337140 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337140 RNA, herein designated GAM RNA, to target binding sites on GAM337140 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337140 target RNA into GAM337140 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337140 target genes. The mRNA of each one of this plurality of GAM337140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337140 RNA, herein designated GAM RNA, and which when bound by GAM337140 RNA causes inhibition of translation of the GAM337140 target mRNA into a corresponding GAM337140 target protein.

The mechanism of the translational inhibition exerted by GAM337140 RNA, herein designated GAM RNA, on one or more GAM337140 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337140 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337140 RNA, herein designated GAM RNA, of GAM337140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337140 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337140 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337140 RNA correlate with, and may be deduced from, the identity of the GAM337140 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337143 6525 GCTAGGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CACCACTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCCAACCTG Messenger 337143 (GAM337143) oligonucleotides modulates expression of respective target

GACAACAGAG genes whose function and utility is known in the art.

CAAGACCCTG GAM337143 is a novel bioinformatically detectable regulatory, non protein

TCTCTAGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337143 was detected

AGGTGCAGTG is described with additional reference to Figs. 9-15.

GCTCACACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTAATCCCAG encoded by the human genome.

C GAM337143 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337143 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337143 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337143 precursor RNA is designated SEQ ID:6525, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:6525 is located from position 74080872 to position 74080962 relative to chromosome 7 on the `-` strand.

GAM337143 precursor RNA folds onto itself, forming GAM337143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337143 precursor RNA, designated SEQ ID NO: 6525, and a schematic representation of a predicted secondary folding of GAM337143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337143 folded precursor RNA yielding a GAM337143 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337143 RNA, hereby incorporated herein.

GAM337143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337143 target RNA, herein designated GAM TARGET RNA.

GAM337143 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337143 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337143 RNA, herein designated GAM RNA, to target binding sites on GAM337143 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337143 target RNA into GAM337143 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337143 target genes. The mRNA of each one of this plurality of GAM337143 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337143 RNA, herein designated GAM RNA, and which when bound by GAM337143 RNA causes inhibition of translation of the GAM337143 target mRNA into a corresponding GAM337143 target protein.

The mechanism of the translational inhibition exerted by GAM337143 RNA, herein designated GAM RNA, on one or more GAM337143 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337143 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337143 RNA, herein designated GAM RNA, of GAM337143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337143 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337143 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337143 RNA correlate with, and may be deduced from, the identity of the GAM337143 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337144 6069 CCCACAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTCTGTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGCCATGG Messenger 337144 (GAM337144) oligonucleotides modulates expression of respective target

TTGGCAGGCT genes whose function and utility is known in the art.

GTTCACGGTG GAM337144 is a novel bioinformatically detectable regulatory, non protein

CTGTTCAACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337144 was detected

GGTCCTGCTG is described with additional reference to Figs. 9-15.

TGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337144 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337144 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337144 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337144 precursor RNA is designated SEQ ID:6069, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6069 is located from position 74099672 to position 74099745 relative to chromosome 18 on the `+` strand.

GAM337144 precursor RNA folds onto itself, forming GAM337144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337144 precursor RNA, designated SEQ ID NO: 6069, and a schematic representation of a predicted secondary folding of GAM337144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337144 folded precursor RNA yielding a GAM337144 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337144 RNA, hereby incorporated herein.

GAM337144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337144 target RNA, herein designated GAM TARGET RNA.

GAM337144 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337144 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337144 RNA, herein designated GAM RNA, to target binding sites on GAM337144 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337144 target RNA into GAM337144 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337144 target genes. The mRNA of each one of this plurality of GAM337144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337144 RNA, herein designated GAM RNA, and which when bound by GAM337144 RNA causes inhibition of translation of the GAM337144 target mRNA into a corresponding GAM337144 target protein.

The mechanism of the translational inhibition exerted by GAM337144 RNA, herein designated GAM RNA, on one or more GAM337144 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337144 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337144 RNA, herein designated GAM RNA, of GAM337144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337144 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337144 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337144 RNA correlate with, and may be deduced from, the identity of the GAM337144 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337145 7272 TGTGCCTGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCAATCTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTTTTATTGC Messenger 337145 (GAM337145) oligonucleotides modulates expression of respective target

TGGCCACCTG genes whose function and utility is known in the art.

TAGCCAGGCA GAM337145 is a novel bioinformatically detectable regulatory, non protein

CTGTGCAGGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337145 was detected

TGATGGGATC is described with additional reference to Figs. 9-15.

CAGCAGTGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CA encoded by the human genome.

GAM337145 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337145 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337145 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337145 precursor RNA is designated SEQ ID:7272, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7272 is located from position 74141948 to position 74142029 relative to chromosome 16 on the `+` strand.

GAM337145 precursor RNA folds onto itself, forming GAM337145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337145 precursor RNA, designated SEQ ID NO: 7272, and a schematic representation of a predicted secondary folding of GAM337145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337145 folded precursor RNA yielding a GAM337145 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337145 RNA, hereby incorporated herein.

GAM337145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337145 target RNA, herein designated GAM TARGET RNA.

GAM337145 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337145 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337145 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337145 RNA, herein designated GAM RNA, to target binding sites on GAM337145 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337145 target RNA into GAM337145 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337145 target genes. The mRNA of each one of this plurality of GAM337145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337145 RNA, herein designated GAM RNA, and which when bound by GAM337145 RNA causes inhibition of translation of the GAM337145 target mRNA into a corresponding GAM337145 target protein.

The mechanism of the translational inhibition exerted by GAM337145 RNA, herein designated GAM RNA, on one or more GAM337145 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337145 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337145 RNA, herein designated GAM RNA, of GAM337145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337145 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337145 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337145 RNA correlate with, and may be deduced from, the identity of the GAM337145 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337146 7096 TGAGACAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCGGGCG Messenger 337146 (GAM337146) oligonucleotides modulates expression of respective target
GCGGAAGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM337146 is a novel bioinformatically detectable regulatory, non protein
AGATTGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337146 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGTGAGAC encoded by the human genome.

TCTGTCTCA GAM337146 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337146 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337146 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337146 precursor RNA is designated SEQ ID:7096, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7096 is located from position 74273377 to position 74273475 relative to chromosome 2 on the `+` strand.

GAM337146 precursor RNA folds onto itself, forming GAM337146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337146 precursor RNA, designated SEQ ID NO: 7096, and a schematic representation of a predicted secondary folding of GAM337146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337146 folded precursor RNA yielding a GAM337146 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337146 RNA, hereby incorporated herein. Expression of GAM337146 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337146 target RNA, herein designated GAM TARGET RNA.

GAM337146 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337146 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337146 RNA, herein designated GAM RNA, to target binding sites on GAM337146 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337146 target RNA into GAM337146 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337146 target genes. The mRNA of each one of this plurality of GAM337146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337146 RNA, herein designated GAM RNA, and which when bound by GAM337146 RNA causes inhibition of translation of the GAM337146 target mRNA into a corresponding GAM337146 target protein.

The mechanism of the translational inhibition exerted by GAM337146 RNA, herein designated GAM RNA, on one or more GAM337146 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337146 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337146 RNA, herein designated GAM RNA, of GAM337146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337146 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337146 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337146 RNA correlate with, and may be deduced from, the identity of the GAM337146 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337147 6336 GAGACAGAAG AATCGCTTGA ACTCGGGCGG CGGAAGTTGC AGTGAGCTGA GATTGCACCA CTGCACTCCA GCCTGGGCAA CAGTGAGACT CTGTCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337147 (GAM337147) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337147 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337147 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337147 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337147 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337147 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337147 precursor RNA is designated SEQ ID:6336, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6336 is located from position 74273378 to position 74273474 relative to chromosome 2 on the `+` strand.

GAM337147 precursor RNA folds onto itself, forming GAM337147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337147 precursor RNA, designated SEQ ID NO: 6336, and a schematic representation of a predicted secondary folding of GAM337147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337147 folded precursor RNA yielding a GAM337147 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337147 RNA, hereby incorporated herein. Expression of GAM337147 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337147 target RNA, herein designated GAM TARGET RNA.

GAM337147 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337147 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337147 RNA, herein designated GAM RNA, to target binding sites on GAM337147 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337147 target RNA into GAM337147 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337147 target genes. The mRNA of each one of this plurality of GAM337147 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337147 RNA, herein designated GAM RNA, and which when bound by GAM337147 RNA causes inhibition of translation of the GAM337147 target mRNA into a corresponding GAM337147 target protein.

The mechanism of the translational inhibition exerted by GAM337147 RNA, herein designated GAM RNA, on one or more GAM337147 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337147 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337147 RNA, herein designated GAM RNA, of GAM337147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337147 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337147 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337147 RNA correlate with, and may be deduced from, the identity of the GAM337147 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337148 7059 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGCGGCG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGTTGCAG Messenger 337148 (GAM337148) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

TTGCACCACT GAM337148 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337148 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337148 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337148 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337148 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337148 precursor RNA is designated SEQ ID:7059, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7059 is located from position 74273390 to position 74273463 relative to chromosome 2 on the `+` strand.

GAM337148 precursor RNA folds onto itself, forming GAM337148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337148 precursor RNA, designated SEQ ID NO: 7059, and a schematic representation of a predicted secondary folding of GAM337148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337148 folded precursor RNA yielding a GAM337148 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337148 RNA, hereby incorporated herein. Expression of GAM337148 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337148 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337148 target RNA, herein designated GAM TARGET RNA.

GAM337148 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337148 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337148 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337148 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337148 RNA, herein designated GAM RNA, to target binding sites on GAM337148 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337148 target RNA into GAM337148 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337148 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337148 target genes. The mRNA of each one of this plurality of GAM337148 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337148 RNA, herein designated GAM RNA, and which when bound by GAM337148 RNA causes inhibition of translation of the GAM337148 target mRNA into a corresponding GAM337148 target protein.

The mechanism of the translational inhibition exerted by GAM337148 RNA, herein

designated GAM RNA, on one or more GAM337148 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337148 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337148 RNA, herein designated GAM RNA, of GAM337148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337148 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337148 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337148 RNA correlate with, and may be deduced from, the identity of the GAM337148 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337149 5655 AAATTTTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAATTTTAC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCCCTAGAG Messenger 337149 (GAM337149) oligonucleotides modulates expression of respective target

GACTGGTTCT genes whose function and utility is known in the art.

AGCCACTTTC GAM337149 is a novel bioinformatically detectable regulatory, non protein

CCAGGGCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337149 was detected

GGATCTCTGC is described with additional reference to Figs. 9-15.

AAAGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337149 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337149 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337149 precursor RNA is designated SEQ ID:5655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5655 is located from position 74455579 to position 74455655

relative to chromosome 8 on the `+` strand.

GAM337149 precursor RNA folds onto itself, forming GAM337149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337149 precursor RNA, designated SEQ ID NO: 5655, and a schematic representation of a predicted secondary folding of GAM337149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337149 folded precursor RNA yielding a GAM337149 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337149 RNA, hereby incorporated herein.

GAM337149 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337149 target RNA, herein designated GAM TARGET RNA.

GAM337149 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337149 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337149 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337149 RNA, herein designated GAM RNA, to target binding sites on GAM337149 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337149 target RNA into GAM337149 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337149 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337149 target genes. The mRNA of each one of this plurality of GAM337149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337149 RNA, herein designated GAM RNA, and which when bound by GAM337149 RNA causes inhibition of translation of the GAM337149 target mRNA into a corresponding GAM337149 target protein.

The mechanism of the translational inhibition exerted by GAM337149 RNA, herein designated GAM RNA, on one or more GAM337149 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337149 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337149 RNA, herein designated GAM RNA, of GAM337149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337149 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337149 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337149 RNA correlate with, and may be deduced from, the identity of the GAM337149 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337150 6526 GCTAGGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACCACTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTCCAACCTG Messenger 337150 (GAM337150) oligonucleotides modulates expression of respective target
GACAACAGAG genes whose function and utility is known in the art.

CAAGACCCTG GAM337150 is a novel bioinformatically detectable regulatory, non protein
TCTCTAGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337150 was detected
AGGTGCAGTG is described with additional reference to Figs. 9-15.

GCTCACACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTAATCCCAG encoded by the human genome.

C GAM337150 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337150 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337150 precursor RNA is designated SEQ ID:6526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6526 is located from position 74495125 to position 74495215 relative to chromosome 7 on the `-` strand.

GAM337150 precursor RNA folds onto itself, forming GAM337150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337150 precursor RNA, designated SEQ ID NO: 6526, and a schematic representation of a predicted secondary folding of GAM337150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337150 folded precursor RNA yielding a GAM337150 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337150 RNA, hereby incorporated herein.

GAM337150 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337150 target RNA, herein designated GAM TARGET RNA.

GAM337150 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337150 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337150 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337150 RNA, herein designated GAM RNA, to target

binding sites on GAM337150 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337150 target RNA into GAM337150 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337150 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337150 target genes. The mRNA of each one of this plurality of GAM337150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337150 RNA, herein designated GAM RNA, and which when bound by GAM337150 RNA causes inhibition of translation of the GAM337150 target mRNA into a corresponding GAM337150 target protein.

The mechanism of the translational inhibition exerted by GAM337150 RNA, herein designated GAM RNA, on one or more GAM337150 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337150 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337150 RNA, herein designated GAM RNA, of GAM337150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337150 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337150 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337150 RNA correlate with, and may be deduced from, the identity of the GAM337150 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337151 6390 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCATTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAAG Messenger 337151 (GAM337151) oligonucleotides modulates expression of respective target

TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337151 is a novel bioinformatically detectable regulatory, non protein

GATCGTGTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337151 was detected

CTGCACTCTA is described with additional reference to Figs. 9-15.

GCCTAGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAAAGCGAGA encoded by the human genome.

CTCAGTCTC GAM337151 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337151 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337151 precursor RNA is designated SEQ ID:6390, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6390 is located from position 74600951 to position 74601049 relative to chromosome 7 on the `+` strand.

GAM337151 precursor RNA folds onto itself, forming GAM337151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337151 precursor RNA, designated SEQ ID NO: 6390, and a schematic representation of a predicted secondary folding of GAM337151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337151 folded precursor RNA yielding a GAM337151 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337151 RNA, hereby incorporated herein.

GAM337151 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337151 target RNA, herein designated GAM TARGET RNA.

GAM337151 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337151 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337151 RNA, herein designated GAM RNA, to target binding sites on GAM337151 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337151 target RNA into GAM337151 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337151 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337151 target genes. The mRNA of each one of this plurality of GAM337151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337151 RNA, herein designated GAM RNA, and which when bound by GAM337151 RNA causes inhibition of translation of the GAM337151 target mRNA into a corresponding GAM337151 target protein.

The mechanism of the translational inhibition exerted by GAM337151 RNA, herein designated GAM RNA, on one or more GAM337151 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337151 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337151 RNA, herein designated GAM RNA, of GAM337151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337151 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337151 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337151 RNA correlate with, and may be deduced from, the identity of the GAM337151 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337152 6484 GCACAGTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAAACAGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCACCACAC Messenger 337152 (GAM337152) oligonucleotides modulates expression of respective target
CTTCTTGGCT genes whose function and utility is known in the art.

GTGCAAGGAA GAM337152 is a novel bioinformatically detectable regulatory, non protein
GTCAGATGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337152 was detected
GTTGGAGTCT is described with additional reference to Figs. 9-15.

GTGCTACTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GC encoded by the human genome.

GAM337152 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337152 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337152 precursor RNA is designated SEQ ID:6484, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6484 is located from position 74682720 to position 74682801 relative to chromosome 8 on the `-` strand.

GAM337152 precursor RNA folds onto itself, forming GAM337152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337152 precursor RNA, designated SEQ ID NO: 6484, and a schematic representation of a predicted secondary folding of GAM337152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337152 folded precursor RNA yielding a GAM337152 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337152 RNA, hereby incorporated herein.

GAM337152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337152 target RNA, herein designated GAM TARGET RNA.

GAM337152 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337152 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337152 RNA, herein designated GAM RNA, to target binding sites on GAM337152 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337152 target RNA into GAM337152 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337152 target genes. The mRNA of each one of this plurality of GAM337152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337152 RNA, herein designated GAM RNA, and which when bound by GAM337152 RNA causes inhibition of translation of the GAM337152 target mRNA into a corresponding GAM337152 target protein.

The mechanism of the translational inhibition exerted by GAM337152 RNA, herein designated GAM RNA, on one or more GAM337152 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337152 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337152 RNA, herein designated GAM RNA, of GAM337152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337152 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337152 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337152

RNA correlate with, and may be deduced from, the identity of the GAM337152 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337153 6439 GAGGCTGAGG AAAGAAGATT GCTTGAGCCC AGGAATTAGA GGCTGCAATG AGCTATGATC ATGCCACTGC ACTCCATCCT GGGGAGCAGA GCTAGACTCT GTCTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337153 (GAM337153) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337153 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337153 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337153 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337153 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337153 precursor RNA is designated SEQ ID:6439, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6439 is located from position 74726081 to position 74726185 relative to chromosome 7 on the `-` strand.

GAM337153 precursor RNA folds onto itself, forming GAM337153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337153 precursor RNA, designated SEQ ID NO: 6439, and a schematic representation of a predicted secondary folding of GAM337153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337153 folded precursor RNA yielding a GAM337153 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337153 RNA, hereby incorporated herein.

GAM337153 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337153 target RNA, herein designated GAM TARGET RNA.

GAM337153 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337153 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337153 RNA, herein designated GAM RNA, to target binding sites on GAM337153 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337153 target RNA into GAM337153 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337153 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337153 target genes. The mRNA of each one of this plurality of GAM337153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337153 RNA, herein designated GAM RNA, and which when bound by GAM337153 RNA causes inhibition of translation of the GAM337153 target mRNA into a corresponding GAM337153 target protein.

The mechanism of the translational inhibition exerted by GAM337153 RNA, herein designated GAM RNA, on one or more GAM337153 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337153 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337153 RNA, herein designated GAM RNA, of GAM337153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337153 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337153 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337153 RNA correlate with, and may be deduced from, the identity of the GAM337153 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337154 7133 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCGGGAG Messenger 337154 (GAM337154) oligonucleotides modulates expression of respective target
GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM337154 is a novel bioinformatically detectable regulatory, non protein
AGATTGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337154 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCGAG encoded by the human genome.

ACTCCATCTC GAM337154 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337154 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337154 precursor RNA is designated SEQ ID:7133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7133 is located from position 74733011 to position 74733111 relative to chromosome 10 on the `+` strand.

GAM337154 precursor RNA folds onto itself, forming GAM337154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337154 precursor RNA, designated SEQ ID NO: 7133, and a schematic representation of a predicted secondary folding of GAM337154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337154 folded precursor RNA yielding a GAM337154 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337154 RNA, hereby incorporated herein. Expression of GAM337154 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337154 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337154 target RNA, herein designated GAM TARGET RNA.

GAM337154 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337154 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337154 RNA, herein designated GAM RNA, to target binding sites on GAM337154 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337154 target RNA into GAM337154 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337154 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337154 target genes. The mRNA of each one of this plurality of GAM337154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337154 RNA, herein designated GAM RNA, and which when bound by GAM337154 RNA causes inhibition of translation of the GAM337154 target mRNA into a corresponding GAM337154 target protein.

The mechanism of the translational inhibition exerted by GAM337154 RNA, herein designated GAM RNA, on one or more GAM337154 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337154 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337154 RNA, herein designated GAM RNA, of GAM337154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337154 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337154 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337154 RNA correlate with, and may be deduced from, the identity of the GAM337154 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337155 6385 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGAGG Messenger 337155 (GAM337155) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM337155 is a novel bioinformatically detectable regulatory, non protein
GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337155 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCCATCTC GAM337155 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337155 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337155 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337155 precursor RNA is designated SEQ ID:6385, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6385 is located from position 74733012 to position 74733110 relative to chromosome 10 on the `+` strand.

GAM337155 precursor RNA folds onto itself, forming GAM337155 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337155 precursor RNA, designated SEQ ID NO: 6385, and a schematic representation of a predicted secondary folding of GAM337155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337155 folded precursor RNA yielding a GAM337155 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337155 RNA, hereby incorporated herein. Expression of GAM337155 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337155 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337155 target RNA, herein designated GAM TARGET RNA.

GAM337155 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337155 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337155 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337155 RNA, herein designated GAM RNA, to target binding sites on GAM337155 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337155 target RNA into GAM337155 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337155 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337155 target genes. The mRNA of each one of this

plurality of GAM337155 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337155 RNA, herein designated GAM RNA, and which when bound by GAM337155 RNA causes inhibition of translation of the GAM337155 target mRNA into a corresponding GAM337155 target protein.

The mechanism of the translational inhibition exerted by GAM337155 RNA, herein designated GAM RNA, on one or more GAM337155 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337155 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337155 RNA, herein designated GAM RNA, of GAM337155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337155 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337155 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337155 RNA correlate with, and may be deduced from, the identity of the GAM337155 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337156 6614 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 337156 (GAM337156) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATTGC GAM337156 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337156 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM337156 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337156 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337156 precursor RNA is designated SEQ ID:6614, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6614 is located from position 74733018 to position 74733105 relative to chromosome 10 on the `+` strand.

GAM337156 precursor RNA folds onto itself, forming GAM337156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337156 precursor RNA, designated SEQ ID NO: 6614, and a schematic representation of a predicted secondary folding of GAM337156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337156 folded precursor RNA yielding a GAM337156 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337156 RNA, hereby incorporated herein. Expression of GAM337156 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337156 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337156 target RNA, herein designated GAM TARGET RNA.

GAM337156 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337156 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337156 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337156 RNA, herein designated GAM RNA, to target binding sites on GAM337156 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337156 target RNA into GAM337156 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337156 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337156 target genes. The mRNA of each one of this plurality of GAM337156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337156 RNA, herein designated GAM RNA, and which when bound by GAM337156 RNA causes inhibition of translation of the GAM337156 target mRNA into a corresponding GAM337156 target protein.

The mechanism of the translational inhibition exerted by GAM337156 RNA, herein designated GAM RNA, on one or more GAM337156 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337156 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337156 RNA, herein designated GAM RNA, of GAM337156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337156 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337156 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337156 RNA correlate with, and may be deduced from, the identity of the GAM337156 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337157 6701 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAGG Messenger 337157 (GAM337157) oligonucleotides modulates expression of respective target

TTGTGGTGAG genes whose function and utility is known in the art.

CTGAGATCGT GAM337157 is a novel bioinformatically detectable regulatory, non protein

CCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337157 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAAACTCC encoded by the human genome.

GAM337157 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337157 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337157 precursor RNA is designated SEQ ID:6701, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6701 is located from position 74841732 to position 74841819 relative to chromosome 17 on the `-` strand.

GAM337157 precursor RNA folds onto itself, forming GAM337157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337157 precursor RNA, designated SEQ ID NO: 6701, and a schematic representation of a predicted secondary folding of GAM337157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337157 folded precursor RNA yielding a GAM337157 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337157 RNA, hereby incorporated herein.

GAM337157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337157 target RNA, herein designated GAM TARGET RNA.

GAM337157 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337157 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337157 RNA, herein designated GAM RNA, to target binding sites on GAM337157 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337157 target RNA into GAM337157 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337157 target genes. The mRNA of each one of this plurality of GAM337157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337157 RNA, herein designated GAM RNA, and which when bound by GAM337157 RNA causes inhibition of translation of the GAM337157 target mRNA into a corresponding GAM337157 target protein.

The mechanism of the translational inhibition exerted by GAM337157 RNA, herein designated GAM RNA, on one or more GAM337157 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337157 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337157 RNA, herein designated GAM RNA, of GAM337157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337157 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337157 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337157 RNA correlate with, and may be deduced from, the identity of the GAM337157 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337158 6721 GGATGGTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGAAGAGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTGCATGGA Messenger 337158 (GAM337158) oligonucleotides modulates expression of respective target
TCGCTCAGAA genes whose function and utility is known in the art.

CTGACCCAGA GAM337158 is a novel bioinformatically detectable regulatory, non protein
GGCAATGAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337158 was detected
ATTTGTGTGC is described with additional reference to Figs. 9-15.

CATGTGGATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCTCCAAAA encoded by the human genome.

TGTCC GAM337158 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337158 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337158 precursor RNA is designated SEQ ID:6721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6721 is located from position 74959089 to position 74959183 relative to chromosome 15 on the `-` strand.

GAM337158 precursor RNA folds onto itself, forming GAM337158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337158 precursor RNA, designated SEQ ID NO: 6721, and a schematic representation of a predicted secondary folding of GAM337158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337158 folded precursor RNA yielding a GAM337158 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337158 RNA, hereby incorporated herein.

GAM337158 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337158 target RNA, herein designated GAM TARGET RNA.

GAM337158 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337158 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337158 RNA, herein designated GAM RNA, to target binding sites on GAM337158 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337158 target RNA into GAM337158 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337158 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337158 target genes. The mRNA of each one of this plurality of GAM337158 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337158 RNA, herein designated GAM RNA, and which when bound by GAM337158 RNA causes inhibition of translation of the GAM337158 target mRNA into a corresponding GAM337158 target protein.

The mechanism of the translational inhibition exerted by GAM337158 RNA, herein designated GAM RNA, on one or more GAM337158 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337158 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337158 RNA, herein designated GAM RNA, of GAM337158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337158 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337158 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337158 RNA correlate with, and may be deduced from, the identity of the GAM337158 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337159 5891 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337159 (GAM337159) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337159 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337159 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337159 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337159 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337159 precursor RNA is designated SEQ ID:5891, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5891 is located from position 75061068 to position 75061149 relative to chromosome 18 on the `-` strand.

GAM337159 precursor RNA folds onto itself, forming GAM337159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337159 precursor RNA, designated SEQ ID NO: 5891, and a schematic representation of a predicted secondary folding of GAM337159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337159 folded precursor RNA yielding a GAM337159 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337159 RNA, hereby incorporated herein.

GAM337159 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337159 target RNA, herein designated GAM TARGET RNA.

GAM337159 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337159 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337159 RNA, herein designated GAM RNA, to target binding sites on GAM337159 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337159 target RNA into GAM337159 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337159 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337159 target genes. The mRNA of each one of this plurality of GAM337159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337159 RNA, herein designated GAM RNA, and which when bound by GAM337159 RNA causes inhibition of translation of the GAM337159 target mRNA into a corresponding GAM337159 target protein.

The mechanism of the translational inhibition exerted by GAM337159 RNA, herein designated GAM RNA, on one or more GAM337159 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337159 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337159 RNA, herein designated GAM RNA, of GAM337159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337159 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337159 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337159 RNA correlate with, and may be deduced from, the identity of the GAM337159 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337160 6338 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATCCGGGAGG Messenger 337160 (GAM337160) oligonucleotides modulates expression of respective target
CAAAGGTTGC genes whose function and utility is known in the art.

AGTGTGTCAA GAM337160 is a novel bioinformatically detectable regulatory, non protein
GATCACACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337160 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGA encoded by the human genome.

CTTCATCTC GAM337160 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337160 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337160 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337160 precursor RNA is designated SEQ ID:6338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6338 is located from position 75203402 to position 75203500 relative to chromosome X on the `-` strand.

GAM337160 precursor RNA folds onto itself, forming GAM337160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337160 precursor RNA, designated SEQ ID NO: 6338, and a schematic representation of a predicted secondary folding of GAM337160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337160 folded precursor RNA yielding a GAM337160 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337160 RNA, hereby incorporated herein. Expression of GAM337160 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337160 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337160 target RNA, herein designated GAM TARGET RNA.

GAM337160 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337160 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337160 RNA, herein designated GAM RNA, to target binding sites on GAM337160 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337160 target RNA into GAM337160 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337160 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337160 target genes. The mRNA of each one of this plurality of GAM337160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337160 RNA, herein designated GAM RNA, and which when bound by GAM337160 RNA causes inhibition of translation of the GAM337160 target mRNA into a corresponding GAM337160 target protein.

The mechanism of the translational inhibition exerted by GAM337160 RNA, herein designated GAM RNA, on one or more GAM337160 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337160 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337160 RNA, herein designated GAM RNA, of GAM337160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337160 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337160 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337160 RNA correlate with, and may be deduced from, the identity of the GAM337160 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337161 6937 GTTATGAAGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTAGGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTAGCTCCA Messenger 337161 (GAM337161) oligonucleotides modulates expression of respective target

CAGGGTCAGA genes whose function and utility is known in the art.

CCTGCAGGTG GAM337161 is a novel bioinformatically detectable regulatory, non protein

CAAACAGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337161 was detected

CTAGGCGAAC is described with additional reference to Figs. 9-15.

CCCCTGGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAACGTTGAC encoded by the human genome.

GAM337161 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337161 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337161 precursor RNA is designated SEQ ID:6937, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6937 is located from position 75209026 to position 75209115 relative to chromosome 14 on the `-` strand.

GAM337161 precursor RNA folds onto itself, forming GAM337161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337161 precursor RNA, designated SEQ ID NO: 6937, and a schematic representation of a predicted secondary folding of GAM337161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337161 folded precursor RNA yielding a GAM337161 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337161 RNA, hereby incorporated herein.

GAM337161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337161 target RNA, herein designated GAM TARGET RNA.

GAM337161 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337161 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337161 RNA, herein designated GAM RNA, to target binding sites on GAM337161 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337161 target RNA into GAM337161 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337161 target genes. The mRNA of each one of this plurality of GAM337161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337161 RNA, herein designated GAM RNA, and which when bound by GAM337161 RNA causes inhibition of translation of the GAM337161 target mRNA into a corresponding GAM337161 target protein.

The mechanism of the translational inhibition exerted by GAM337161 RNA, herein designated GAM RNA, on one or more GAM337161 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337161 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337161 RNA, herein designated GAM RNA, of GAM337161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337161 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337161 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337161 RNA correlate with, and may be deduced from, the identity of the GAM337161 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337162 6669 GGAGAATGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGC Messenger 337162 (GAM337162) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CAGAGATCAC GAM337162 is a novel bioinformatically detectable regulatory, non protein

GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337162 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337162 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337162 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337162 precursor RNA is designated SEQ

ID:6669, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6669 is located from position 75245669 to position 75245756 relative to chromosome 3 on the `-` strand.

GAM337162 precursor RNA folds onto itself, forming GAM337162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337162 precursor RNA, designated SEQ ID NO: 6669, and a schematic representation of a predicted secondary folding of GAM337162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337162 folded precursor RNA yielding a GAM337162 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337162 RNA, hereby incorporated herein. Expression of GAM337162 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337162 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337162 target RNA, herein designated GAM TARGET RNA.

GAM337162 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337162 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337162 RNA, herein designated GAM RNA, to target binding sites on GAM337162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337162 target RNA

into GAM337162 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337162 target genes. The mRNA of each one of this plurality of GAM337162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337162 RNA, herein designated GAM RNA, and which when bound by GAM337162 RNA causes inhibition of translation of the GAM337162 target mRNA into a corresponding GAM337162 target protein.

The mechanism of the translational inhibition exerted by GAM337162 RNA, herein designated GAM RNA, on one or more GAM337162 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337162 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337162 RNA, herein designated GAM RNA, of GAM337162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337162 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337162 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337162 RNA correlate with, and may be deduced from, the identity of the GAM337162 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337166 6440 GAGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGAAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGCCC Messenger 337166 (GAM337166) oligonucleotides modulates expression of respective target
AGGAATTAGA genes whose function and utility is known in the art.

GGCTGCAATG GAM337166 is a novel bioinformatically detectable regulatory, non protein
AGCTATGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337166 was detected
ATGCCACTGC is described with additional reference to Figs. 9-15.

ACTCCATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGGAGCAGA encoded by the human genome.

GCTAGACTCT GAM337166 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTCTC GAM337166 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337166 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337166 precursor RNA is designated SEQ ID:6440, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6440 is located from position 75764518 to position 75764622 relative to chromosome 7 on the `+` strand.

GAM337166 precursor RNA folds onto itself, forming GAM337166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337166 precursor RNA, designated SEQ ID NO: 6440, and a schematic representation of a predicted secondary folding of GAM337166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337166 folded precursor RNA yielding a GAM337166 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337166 RNA, hereby incorporated herein.

GAM337166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337166 target RNA, herein designated GAM TARGET RNA.

GAM337166 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337166 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337166 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337166 RNA, herein designated GAM RNA, to target binding sites on GAM337166 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337166 target RNA into GAM337166 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337166 target genes. The mRNA of each one of this plurality of GAM337166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337166 RNA, herein designated GAM RNA, and which when bound by GAM337166 RNA causes inhibition of translation of the GAM337166 target mRNA into a corresponding GAM337166 target protein.

The mechanism of the translational inhibition exerted by GAM337166 RNA, herein designated GAM RNA, on one or more GAM337166 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337166 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337166 RNA, herein designated GAM RNA, of GAM337166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337166 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337166 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337166 RNA correlate with, and may be deduced from, the identity of the GAM337166 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337167 6582 GGAATAAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGCAACGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCAGCTTC Messenger 337167 (GAM337167) oligonucleotides modulates expression of respective target

CAAATTTCTG genes whose function and utility is known in the art.

AAGAAACTAA GAM337167 is a novel bioinformatically detectable regulatory, non protein
TCTCAGATTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337167 was detected
GCAGTTAAAG is described with additional reference to Figs. 9-15.

TCAAAATGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCAAATATT encoded by the human genome.

TATTCC GAM337167 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337167 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337167 precursor RNA is designated SEQ ID:6582, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6582 is located from position 75774294 to position 75774389 relative to chromosome 10 on the `-` strand.

GAM337167 precursor RNA folds onto itself, forming GAM337167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337167 precursor RNA, designated SEQ ID NO: 6582, and a schematic representation of a predicted secondary folding of GAM337167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337167 folded precursor RNA yielding a GAM337167 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337167 RNA, hereby incorporated herein.

GAM337167 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337167 target RNA, herein designated GAM TARGET RNA.

GAM337167 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337167 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337167 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337167 RNA, herein designated GAM RNA, to target binding sites on GAM337167 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337167 target RNA into GAM337167 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337167 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337167 target genes. The mRNA of each one of this plurality of GAM337167 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337167 RNA, herein designated GAM RNA, and which when bound by GAM337167 RNA causes inhibition of translation of the GAM337167 target mRNA into a corresponding GAM337167 target protein.

The mechanism of the translational inhibition exerted by GAM337167 RNA, herein designated GAM RNA, on one or more GAM337167 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337167 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337167 RNA, herein designated GAM RNA, of GAM337167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337167 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337167 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337167 RNA correlate with, and may be deduced from, the identity of the GAM337167 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337168 6890 GTCTGGCATT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCCTAGTGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGAACCCGG Messenger 337168 (GAM337168) oligonucleotides modulates expression of respective target
TACCTCAGAT genes whose function and utility is known in the art.

GGAAATGCAG GAM337168 is a novel bioinformatically detectable regulatory, non protein
AAATCACCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337168 was detected
TCTTCTGTGT is described with additional reference to Figs. 9-15.

CGCTCATGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGAGCTGTA encoded by the human genome.

GAC GAM337168 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337168 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337168 precursor RNA is designated SEQ ID:6890, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6890 is located from position 75794832 to position 75794924 relative to chromosome 7 on the `+` strand.

GAM337168 precursor RNA folds onto itself, forming GAM337168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337168 precursor RNA, designated SEQ ID NO: 6890, and a schematic representation of a predicted secondary folding of GAM337168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337168 folded precursor RNA yielding a GAM337168 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337168 RNA, hereby incorporated herein.

GAM337168 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337168 target RNA, herein designated GAM TARGET RNA.

GAM337168 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337168 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337168 RNA, herein designated GAM RNA, to target binding sites on GAM337168 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337168 target RNA into GAM337168 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337168 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337168 target genes. The mRNA of each one of this plurality of GAM337168 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337168 RNA, herein designated GAM RNA, and which when bound by GAM337168 RNA causes inhibition of translation of the GAM337168 target mRNA into a corresponding GAM337168 target protein.

The mechanism of the translational inhibition exerted by GAM337168 RNA, herein designated GAM RNA, on one or more GAM337168 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337168 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337168 RNA, herein designated GAM RNA, of GAM337168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337168 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337168 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337168 RNA correlate with, and may be deduced from, the identity of the GAM337168 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337169 6306 GAATGATTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGGGGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAGAGAAGT Messenger 337169 (GAM337169) oligonucleotides modulates expression of respective target
AGGAATATCA genes whose function and utility is known in the art.

GGAGTGGTGG GAM337169 is a novel bioinformatically detectable regulatory, non protein
TCTGATTACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337169 was detected
CTGAGATGTG is described with additional reference to Figs. 9-15.

TCTTGATTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTTTGTTTT encoded by the human genome.

CTTTGAAATT GAM337169 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM337169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337169 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337169 precursor RNA is designated SEQ ID:6306, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6306 is located from position 75944727 to position 75944827 relative to chromosome 11 on the `+` strand.

GAM337169 precursor RNA folds onto itself, forming GAM337169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337169 precursor RNA, designated SEQ ID NO: 6306, and a schematic representation of a predicted secondary folding of GAM337169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337169 folded precursor

RNA yielding a GAM337169 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337169 RNA, hereby incorporated herein.

GAM337169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337169 target RNA, herein designated GAM TARGET RNA.

GAM337169 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337169 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337169 RNA, herein designated GAM RNA, to target binding sites on GAM337169 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337169 target RNA into GAM337169 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337169 target genes. The mRNA of each one of this plurality of GAM337169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337169 RNA, herein designated GAM RNA, and which when bound by GAM337169 RNA causes inhibition of translation of the GAM337169 target mRNA into a corresponding GAM337169 target protein.

The mechanism of the translational inhibition exerted by GAM337169 RNA, herein designated GAM RNA, on one or more GAM337169 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337169 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337169 RNA, herein designated GAM RNA, of GAM337169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337169 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337169 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337169 RNA correlate with, and may be deduced from, the identity of the GAM337169 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337170 6247 CTGTTGTTAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AACCTGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCACTGCTC Messenger 337170 (GAM337170) oligonucleotides modulates expression of respective target

AGCCTGCCAT genes whose function and utility is known in the art.

CAGCCATCCA GAM337170 is a novel bioinformatically detectable regulatory, non protein

GCTGCAGAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337170 was detected

AGTGGAGAGT is described with additional reference to Figs. 9-15.

AGGTCTCACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AG encoded by the human genome.

GAM337170 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337170 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337170 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337170 precursor RNA is designated SEQ ID:6247, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6247 is located from position 76136262 to position 76136343 relative to chromosome 12 on the `+` strand.

GAM337170 precursor RNA folds onto itself, forming GAM337170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337170 precursor RNA, designated SEQ ID NO: 6247, and a schematic representation of a predicted secondary folding of GAM337170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337170 folded precursor RNA yielding a GAM337170 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337170 RNA, hereby incorporated herein.

GAM337170 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337170 target RNA, herein designated GAM TARGET RNA.

GAM337170 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337170 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337170 RNA, herein designated GAM RNA, to target binding sites on GAM337170 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337170 target RNA into GAM337170 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337170 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337170 target genes. The mRNA of each one of this plurality of GAM337170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337170 RNA, herein designated GAM RNA, and which when bound by GAM337170 RNA causes inhibition of translation of the GAM337170 target mRNA into a corresponding GAM337170 target protein.

The mechanism of the translational inhibition exerted by GAM337170 RNA, herein designated GAM RNA, on one or more GAM337170 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337170 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337170 RNA, herein designated GAM RNA, of GAM337170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337170 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337170 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337170 RNA correlate with, and may be deduced from, the identity of the GAM337170 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337171 6441 GAGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGAAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGCCC Messenger 337171 (GAM337171) oligonucleotides modulates expression of respective target
AGGAATTAGA genes whose function and utility is known in the art.

GGCTGCAATG GAM337171 is a novel bioinformatically detectable regulatory, non protein
AGCTATGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337171 was detected
ATGCCACTGC is described with additional reference to Figs. 9-15.

ACTCCATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGGAGCAGA encoded by the human genome.

GCTAGACTCT GAM337171 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTCTC GAM337171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337171 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337171 precursor RNA is designated SEQ ID:6441, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6441 is located from position 76283582 to position 76283686 relative to chromosome 7 on the `+` strand.

GAM337171 precursor RNA folds onto itself, forming GAM337171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337171 precursor RNA, designated SEQ ID NO: 6441, and a schematic representation of a predicted secondary folding of GAM337171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337171 folded precursor RNA yielding a GAM337171 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337171 RNA, hereby incorporated herein.

GAM337171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337171 target RNA, herein designated GAM TARGET RNA.

GAM337171 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337171 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337171 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337171 RNA, herein designated GAM RNA, to target binding sites on GAM337171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337171 target RNA into GAM337171 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337171 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337171 target genes. The mRNA of each one of this

plurality of GAM337171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337171 RNA, herein designated GAM RNA, and which when bound by GAM337171 RNA causes inhibition of translation of the GAM337171 target mRNA into a corresponding GAM337171 target protein.

The mechanism of the translational inhibition exerted by GAM337171 RNA, herein designated GAM RNA, on one or more GAM337171 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337171 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337171 RNA, herein designated GAM RNA, of GAM337171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337171 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337171 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337171 RNA correlate with, and may be deduced from, the identity of the GAM337171 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337172 7256 TGGTTGAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGAATTCG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGACAAGTCT Messenger 337172 (GAM337172) oligonucleotides modulates expression of respective target

GGGCAACAAA genes whose function and utility is known in the art.

GTGAGATCCC GAM337172 is a novel bioinformatically detectable regulatory, non protein

ATCTCTACAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337172 was detected

AAAATTAGCC is described with additional reference to Figs. 9-15.

AGACTGGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTCCCTTAG encoded by the human genome.

CCTCAGCTA GAM337172 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337172 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337172 precursor RNA is designated SEQ ID:7256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7256 is located from position 76484385 to position 76484483 relative to chromosome 12 on the `+` strand.

GAM337172 precursor RNA folds onto itself, forming GAM337172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337172 precursor RNA, designated SEQ ID NO: 7256, and a schematic representation of a predicted secondary folding of GAM337172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337172 folded precursor RNA yielding a GAM337172 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337172 RNA, hereby incorporated herein.

GAM337172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337172 target RNA, herein designated GAM TARGET RNA.

GAM337172 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337172 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337172 RNA, herein designated GAM RNA, to target binding sites on GAM337172 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337172 target RNA into GAM337172 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337172 target genes. The mRNA of each one of this plurality of GAM337172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337172 RNA, herein designated GAM RNA, and which when bound by GAM337172 RNA causes inhibition of translation of the GAM337172 target mRNA into a corresponding GAM337172 target protein.

The mechanism of the translational inhibition exerted by GAM337172 RNA, herein designated GAM RNA, on one or more GAM337172 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337172 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337172 RNA, herein designated GAM RNA, of GAM337172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337172 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337172 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337172 RNA correlate with, and may be deduced from, the identity of the GAM337172 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337173 5991 CAATGGGGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CATTTGCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTGAGAA Messenger 337173 (GAM337173) oligonucleotides modulates expression of respective target

TGCTGTAATT genes whose function and utility is known in the art.

GGAGGCCTGA GAM337173 is a novel bioinformatically detectable regulatory, non protein

GAGGTGGGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337173 was detected

CCAATTCTTA is described with additional reference to Figs. 9-15.

CATTTTCCAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCCACAAACT encoded by the human genome.

GTCTCCTTTT GAM337173 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

G GAM337173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337173 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337173 precursor RNA is designated SEQ ID:5991, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5991 is located from position 76490700 to position 76490800 relative to chromosome 15 on the `-` strand.

GAM337173 precursor RNA folds onto itself, forming GAM337173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337173 precursor RNA, designated SEQ ID NO: 5991, and a schematic representation of a predicted secondary folding of GAM337173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337173 folded precursor RNA yielding a GAM337173 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337173 RNA, hereby incorporated herein.

GAM337173 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337173 target RNA, herein designated GAM TARGET RNA.

GAM337173 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337173 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337173 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337173 RNA, herein designated GAM RNA, to target binding sites on GAM337173 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337173 target RNA into GAM337173 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337173 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337173 target genes. The mRNA of each one of this plurality of GAM337173 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337173 RNA, herein designated GAM RNA, and which when bound by GAM337173 RNA causes inhibition of translation of the GAM337173 target mRNA into a corresponding GAM337173 target protein.

The mechanism of the translational inhibition exerted by GAM337173 RNA, herein designated GAM RNA, on one or more GAM337173 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337173 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337173 RNA, herein designated GAM RNA, of GAM337173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337173 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337173 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337173 RNA correlate with, and may be deduced from, the identity of the GAM337173 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337174 5815 AGTGGCAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGCAAATCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACTTGGCC Messenger 337174 (GAM337174) oligonucleotides modulates expression of respective target

TCCCAAACTA genes whose function and utility is known in the art.

AGGTACAAAG GAM337174 is a novel bioinformatically detectable regulatory, non protein
TTGTGAGTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337174 was detected

CACGTCTGCC is described with additional reference to Figs. 9-15.

ACT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337174 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337174 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337174 precursor RNA is designated SEQ ID:5815, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5815 is located from position 76516598 to position 76516670 relative to chromosome 7 on the `+` strand.

GAM337174 precursor RNA folds onto itself, forming GAM337174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337174 precursor RNA, designated SEQ ID NO: 5815, and a schematic representation of a predicted secondary folding of GAM337174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337174 folded precursor RNA yielding a GAM337174 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337174 RNA, hereby incorporated herein.

GAM337174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337174 target RNA, herein designated GAM TARGET RNA.

GAM337174 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337174 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337174 RNA, herein designated GAM RNA, to target binding sites on GAM337174 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337174 target RNA into GAM337174 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337174 target genes. The mRNA of each one of this plurality of GAM337174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337174 RNA, herein designated GAM RNA, and which when bound by GAM337174 RNA causes inhibition of translation of the GAM337174 target mRNA into a corresponding GAM337174 target protein.

The mechanism of the translational inhibition exerted by GAM337174 RNA, herein designated GAM RNA, on one or more GAM337174 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337174 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337174 RNA, herein designated GAM RNA, of GAM337174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337174 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337174 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337174 RNA correlate with, and may be deduced from, the identity of the GAM337174 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337177 6805 GGGCTGACTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGACTCTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGTTAAGCA Messenger 337177 (GAM337177) oligonucleotides modulates expression of respective target
ACTTGCTCTC genes whose function and utility is known in the art.

CAGGAGTCCT GAM337177 is a novel bioinformatically detectable regulatory, non protein
GTGAAGAAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337177 was detected
TGCTTCATCC is described with additional reference to Figs. 9-15.

TTTTGAAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGCCC encoded by the human genome.

GAM337177 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337177 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337177 precursor RNA is designated SEQ ID:6805, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6805 is located from position 76741418 to position 76741502 relative to chromosome 17 on the `-` strand.

GAM337177 precursor RNA folds onto itself, forming GAM337177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337177 precursor RNA, designated SEQ ID NO: 6805, and a schematic representation of a predicted secondary folding of GAM337177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337177 folded precursor RNA yielding a GAM337177 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337177 RNA, hereby incorporated herein.

GAM337177 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337177 target RNA, herein designated GAM TARGET RNA.

GAM337177 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337177 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337177 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337177 RNA, herein designated GAM RNA, to target binding sites on GAM337177 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337177 target RNA into GAM337177 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337177 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337177 target genes. The mRNA of each one of this plurality of GAM337177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337177 RNA, herein designated GAM RNA, and which when bound by GAM337177 RNA causes inhibition of translation of the GAM337177 target mRNA into a corresponding GAM337177 target protein.

The mechanism of the translational inhibition exerted by GAM337177 RNA, herein designated GAM RNA, on one or more GAM337177 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337177 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337177 RNA, herein designated GAM RNA, of GAM337177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337177 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337177 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337177 RNA correlate with, and may be deduced from, the identity of the GAM337177 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337179 7218 TGGAGCTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCTGTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAGAGAGTG Messenger 337179 (GAM337179) oligonucleotides modulates expression of respective target
GGAGAGTGTC genes whose function and utility is known in the art.

TGTGGGCTGA GAM337179 is a novel bioinformatically detectable regulatory, non protein
GCACTGGTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337179 was detected
TTTCTGACTC is described with additional reference to Figs. 9-15.

ACAGCTCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGCCCA encoded by the human genome.

GAM337179 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337179 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337179 precursor RNA is designated SEQ ID:7218, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7218 is located from position 77038644 to position 77038729 relative to chromosome 11 on the `+` strand.

GAM337179 precursor RNA folds onto itself, forming GAM337179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337179 precursor RNA, designated SEQ ID NO: 7218, and a schematic representation of a predicted secondary folding of GAM337179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337179 folded precursor

RNA yielding a GAM337179 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337179 RNA, hereby incorporated herein.

GAM337179 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337179 target RNA, herein designated GAM TARGET RNA.

GAM337179 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337179 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337179 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337179 RNA, herein designated GAM RNA, to target binding sites on GAM337179 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337179 target RNA into GAM337179 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337179 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337179 target genes. The mRNA of each one of this plurality of GAM337179 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337179 RNA, herein designated GAM RNA, and which when bound by GAM337179 RNA causes inhibition of translation of the GAM337179 target mRNA into a corresponding GAM337179 target protein.

The mechanism of the translational inhibition exerted by GAM337179 RNA, herein designated GAM RNA, on one or more GAM337179 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337179 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337179 RNA, herein designated GAM RNA, of GAM337179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337179 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337179 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337179 RNA correlate with, and may be deduced from, the identity of the GAM337179 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337180 6046 CCAATCCCCA ACCCCTGCAG TGCTTTGATT ATGAGAAAGT TCTGCATGAC TTAGCATAAC TGCTCTTTTC TAAAAGCCTC TGCAATTAGA TCCAAAGGGT TGGGGTTTGG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337180 (GAM337180) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337180 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337180 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337180 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337180 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337180 precursor RNA is designated SEQ ID:6046, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6046 is located from position 77109458 to position 77109567 relative to chromosome 16 on the `+` strand.

GAM337180 precursor RNA folds onto itself, forming GAM337180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337180 precursor RNA, designated SEQ ID NO: 6046, and a schematic representation of a predicted secondary folding of GAM337180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337180 folded precursor RNA yielding a GAM337180 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337180 RNA, hereby incorporated herein.

GAM337180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337180 target RNA, herein designated GAM TARGET RNA.

GAM337180 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337180 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337180 RNA, herein designated GAM RNA, to target binding sites on GAM337180 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337180 target RNA into GAM337180 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337180 target genes. The mRNA of each one of this plurality of GAM337180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337180 RNA, herein designated GAM RNA, and which when bound by GAM337180 RNA causes inhibition of translation of the GAM337180 target mRNA into a corresponding GAM337180 target protein.

The mechanism of the translational inhibition exerted by GAM337180 RNA, herein designated GAM RNA, on one or more GAM337180 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337180 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337180 RNA, herein designated GAM RNA, of GAM337180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337180 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337180 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337180 RNA correlate with, and may be deduced from, the identity of the GAM337180 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337181 6066 CCCAACCCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCAGTGCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GATTATGAGA Messenger 337181 (GAM337181) oligonucleotides modulates expression of respective target

AAGTTCTGCA genes whose function and utility is known in the art.

TGACTTAGCA GAM337181 is a novel bioinformatically detectable regulatory, non protein

TAACTGCTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337181 was detected

TTTCTAAAAG is described with additional reference to Figs. 9-15.

CCTCTGCAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAGATCCAAA encoded by the human genome.

GGGTTGGG GAM337181 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337181 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337181 precursor RNA is designated SEQ ID:6066, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6066 is located from position 77109464 to position 77109561

relative to chromosome 16 on the `+` strand.

GAM337181 precursor RNA folds onto itself, forming GAM337181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337181 precursor RNA, designated SEQ ID NO: 6066, and a schematic representation of a predicted secondary folding of GAM337181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337181 folded precursor RNA yielding a GAM337181 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337181 RNA, hereby incorporated herein.

GAM337181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337181 target RNA, herein designated GAM TARGET RNA.

GAM337181 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337181 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337181 RNA, herein designated GAM RNA, to target binding sites on GAM337181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337181 target RNA into GAM337181 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337181 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337181 target genes. The mRNA of each one of this plurality of GAM337181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337181 RNA, herein designated GAM RNA, and which when bound by GAM337181 RNA causes inhibition of translation of the GAM337181 target mRNA into a corresponding GAM337181 target protein.

The mechanism of the translational inhibition exerted by GAM337181 RNA, herein designated GAM RNA, on one or more GAM337181 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337181 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337181 RNA, herein designated GAM RNA, of GAM337181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337181 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337181 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337181 RNA correlate with, and may be deduced from, the identity of the GAM337181 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337183 6694 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 337183 (GAM337183) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCAC GAM337183 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337183 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGAATCC encoded by the human genome.

GAM337183 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337183 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337183 precursor RNA is designated SEQ ID:6694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6694 is located from position 77738565 to position 77738652 relative to chromosome 1 on the `+` strand.

GAM337183 precursor RNA folds onto itself, forming GAM337183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337183 precursor RNA, designated SEQ ID NO: 6694, and a schematic representation of a predicted secondary folding of GAM337183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337183 folded precursor RNA yielding a GAM337183 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337183 RNA, hereby incorporated herein. Expression of GAM337183 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337183 target RNA, herein designated GAM TARGET RNA.

GAM337183 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337183 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337183 RNA, herein designated GAM RNA, to target binding sites on GAM337183 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337183 target RNA into GAM337183 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337183 target genes. The mRNA of each one of this plurality of GAM337183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337183 RNA, herein designated GAM RNA, and which when bound by GAM337183 RNA causes inhibition of translation of the GAM337183 target mRNA into a corresponding GAM337183 target protein.

The mechanism of the translational inhibition exerted by GAM337183 RNA, herein designated GAM RNA, on one or more GAM337183 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337183 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337183 RNA, herein designated GAM RNA, of GAM337183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337183 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337183 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337183 RNA correlate with, and may be deduced from, the identity of the GAM337183 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337184 6876 GTCCATCCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACATGAC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCCTGGTGTG Messenger 337184 (GAM337184) oligonucleotides modulates expression of respective target

TTAGTCTAGT genes whose function and utility is known in the art.

CTGTTCTCAT GAM337184 is a novel bioinformatically detectable regulatory, non protein
GCTGCTAATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337184 was detected
AAGACATACC is described with additional reference to Figs. 9-15.

TGAGACTGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAATTTATAA encoded by the human genome.

AGGAAAGAGG GAM337184 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTTAATGGAC GAM337184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337184 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337184 precursor RNA is designated SEQ ID:6876, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6876 is located from position 78244320 to position 78244429 relative to chromosome 14 on the `+` strand.

GAM337184 precursor RNA folds onto itself, forming GAM337184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337184 precursor RNA, designated SEQ ID NO: 6876, and a schematic representation of a predicted secondary folding of GAM337184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337184 folded precursor RNA yielding a GAM337184 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337184 RNA, hereby incorporated herein.

GAM337184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337184 target RNA, herein designated GAM TARGET RNA.

GAM337184 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337184 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337184 RNA, herein designated GAM RNA, to target binding sites on GAM337184 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337184 target RNA into GAM337184 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337184 target genes. The mRNA of each one of this plurality of GAM337184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337184 RNA, herein designated GAM RNA, and which when bound by GAM337184 RNA causes inhibition of translation of the GAM337184 target mRNA into a corresponding GAM337184 target protein.

The mechanism of the translational inhibition exerted by GAM337184 RNA, herein designated GAM RNA, on one or more GAM337184 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337184 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337184 RNA, herein designated GAM RNA, of GAM337184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337184 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337184 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337184 RNA correlate with, and may be deduced from, the identity of the GAM337184 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337185 6395 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCGGGAAG Messenger 337185 (GAM337185) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337185 is a novel bioinformatically detectable regulatory, non protein
GATCTTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337185 was detected
TTGTTCTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGTGAA encoded by the human genome.

ACTCCATCTC GAM337185 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337185 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337185 precursor RNA is designated SEQ ID:6395, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6395 is located from position 78245362 to position 78245461 relative to chromosome 16 on the `+` strand.

GAM337185 precursor RNA folds onto itself, forming GAM337185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337185 precursor RNA, designated SEQ ID NO: 6395, and a schematic representation of a predicted secondary folding of GAM337185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337185 folded precursor RNA yielding a GAM337185 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337185 RNA, hereby incorporated herein.

GAM337185 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337185 target RNA, herein designated GAM TARGET RNA.

GAM337185 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337185 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337185 RNA, herein designated GAM RNA, to target binding sites on GAM337185 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337185 target RNA into GAM337185 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337185 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337185 target genes. The mRNA of each one of this plurality of GAM337185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337185 RNA, herein designated GAM RNA, and which when bound by GAM337185 RNA causes inhibition of translation of the GAM337185 target mRNA into a corresponding GAM337185 target protein.

The mechanism of the translational inhibition exerted by GAM337185 RNA, herein designated GAM RNA, on one or more GAM337185 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337185 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337185 RNA, herein designated GAM RNA, of GAM337185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337185 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337185 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337185 RNA correlate with, and may be deduced from, the identity of the GAM337185 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337186 6644 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGTGGAGG Messenger 337186 (GAM337186) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCTT GAM337186 is a novel bioinformatically detectable regulatory, non protein
GCCATTGTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337186 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCGACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAAACTCC encoded by the human genome.

GAM337186 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337186 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337186 precursor RNA is designated SEQ ID:6644, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6644 is located from position 78245368 to position 78245456 relative to chromosome 16 on the `+` strand.

GAM337186 precursor RNA folds onto itself, forming GAM337186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337186 precursor RNA, designated SEQ ID NO: 6644, and a schematic representation of a predicted secondary folding of GAM337186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337186 folded precursor RNA yielding a GAM337186 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337186 RNA, hereby incorporated herein.

GAM337186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337186 target RNA, herein designated GAM TARGET RNA.

GAM337186 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337186 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337186 RNA, herein designated GAM RNA, to target binding sites on GAM337186 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337186 target RNA into GAM337186 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337186 target genes. The mRNA of each one of this plurality of GAM337186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337186 RNA, herein designated GAM RNA, and which when bound by GAM337186 RNA causes inhibition of translation of the GAM337186 target mRNA into a corresponding GAM337186 target protein.

The mechanism of the translational inhibition exerted by GAM337186 RNA, herein designated GAM RNA, on one or more GAM337186 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337186 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337186 RNA, herein designated GAM RNA, of GAM337186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337186 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337186 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337186 RNA correlate with, and may be deduced from, the identity of the GAM337186 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337187 6446 GAGGGAGCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
CGGTCAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCAAGTGGTC Messenger 337187 (GAM337187) oligonucleotides modulates expression of respective target
ATTTCACTCT genes whose function and utility is known in the art.

TTCTCCCTCT GAM337187 is a novel bioinformatically detectable regulatory, non protein
GGGGGACTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337187 was detected
GACATGATTA is described with additional reference to Figs. 9-15.

ACTTGCAATA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTGTGACTC encoded by the human genome.

CCTC GAM337187 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337187 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337187 precursor RNA is designated SEQ ID:6446, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6446 is located from position 78638936 to position 78639029 relative to chromosome 16 on the `+` strand.

GAM337187 precursor RNA folds onto itself, forming GAM337187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337187 precursor RNA, designated SEQ ID NO: 6446, and a schematic representation of a predicted secondary folding of GAM337187 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337187 folded precursor RNA yielding a GAM337187 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337187 RNA, hereby incorporated herein.

GAM337187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337187 target RNA, herein designated GAM TARGET RNA.

GAM337187 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337187 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337187 RNA, herein designated GAM RNA, to target binding sites on GAM337187 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337187 target RNA into GAM337187 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337187 target genes. The mRNA of each one of this plurality of GAM337187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337187 RNA, herein designated GAM RNA, and which when bound by GAM337187 RNA causes inhibition of translation of the GAM337187 target mRNA into a corresponding GAM337187 target protein.

The mechanism of the translational inhibition exerted by GAM337187 RNA, herein designated GAM RNA, on one or more GAM337187 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337187 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337187 RNA, herein designated GAM RNA, of GAM337187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337187 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337187 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337187 RNA correlate with, and may be deduced from, the identity of the GAM337187 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337188 6759 GGCTAAGTCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAGAATTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTGAACCCAG Messenger 337188 (GAM337188) oligonucleotides modulates expression of respective target
GCATCGGAGG genes whose function and utility is known in the art.

TTGCAGTGAG GAM337188 is a novel bioinformatically detectable regulatory, non protein
CCGAGATTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337188 was detected
ACCAATGCAC is described with additional reference to Figs. 9-15.

TCCAGCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCGACAGAGC encoded by the human genome.

GAGACTCCGT GAM337188 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM337188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337188 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337188 precursor RNA is designated SEQ ID:6759, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6759 is located from position 78652714 to position 78652814 relative to chromosome 7 on the `+` strand.

GAM337188 precursor RNA folds onto itself, forming GAM337188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337188 precursor RNA, designated SEQ ID NO: 6759, and a schematic representation of a predicted secondary folding of GAM337188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337188 folded precursor RNA yielding a GAM337188 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337188 RNA, hereby incorporated herein.

GAM337188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337188 target RNA, herein designated GAM TARGET RNA.

GAM337188 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337188 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337188 RNA, herein designated GAM RNA, to target binding sites on GAM337188 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337188 target RNA into GAM337188 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337188 target genes. The mRNA of each one of this plurality of GAM337188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337188 RNA, herein designated GAM RNA, and which when bound by GAM337188 RNA causes inhibition of translation of the GAM337188 target mRNA into a corresponding GAM337188 target protein.

The mechanism of the translational inhibition exerted by GAM337188 RNA, herein designated GAM RNA, on one or more GAM337188 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337188 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337188 RNA, herein designated GAM RNA, of GAM337188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337188 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337188 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337188 RNA correlate with, and may be deduced from, the identity of the GAM337188 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337189 6330 GAGAATTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAACCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CATCGGAGGT Messenger 337189 (GAM337189) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CGAGATTGCA GAM337189 is a novel bioinformatically detectable regulatory, non protein

CCAATGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337189 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CGACAGAGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTC encoded by the human genome.

GAM337189 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337189 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337189 precursor RNA is designated SEQ

ID:6330, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6330 is located from position 78652725 to position 78652810 relative to chromosome 7 on the `+` strand.

GAM337189 precursor RNA folds onto itself, forming GAM337189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337189 precursor RNA, designated SEQ ID NO: 6330, and a schematic representation of a predicted secondary folding of GAM337189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337189 folded precursor RNA yielding a GAM337189 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337189 RNA, hereby incorporated herein.

GAM337189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337189 target RNA, herein designated GAM TARGET RNA.

GAM337189 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337189 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337189 RNA, herein designated GAM RNA, to target binding sites on GAM337189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337189 target RNA into GAM337189 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337189 target genes. The mRNA of each one of this plurality of GAM337189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337189 RNA, herein designated GAM RNA, and which when bound by GAM337189 RNA causes inhibition of translation of the GAM337189 target mRNA into a corresponding GAM337189 target protein.

The mechanism of the translational inhibition exerted by GAM337189 RNA, herein designated GAM RNA, on one or more GAM337189 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337189 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337189 RNA, herein designated GAM RNA, of GAM337189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337189 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337189 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337189 RNA correlate with, and may be deduced from, the identity of the GAM337189 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337190 7306 TTCTGCTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TATTATGAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGACTGGCA Messenger 337190 (GAM337190) oligonucleotides modulates expression of respective target

CAGACATCTG genes whose function and utility is known in the art.

TCAAGGAAGA GAM337190 is a novel bioinformatically detectable regulatory, non protein

AGGATTCTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337190 was detected

GAGCGTATTT is described with additional reference to Figs. 9-15.

GTGTCAGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACTGCATATA encoded by the human genome.

TGGACCACAA GAM337190 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAGAA GAM337190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337190 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337190 precursor RNA is designated SEQ ID:7306, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7306 is located from position 78654888 to position 78654992 relative to chromosome 11 on the `-` strand.

GAM337190 precursor RNA folds onto itself, forming GAM337190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337190 precursor RNA, designated SEQ ID NO: 7306, and a schematic representation of a predicted secondary folding of GAM337190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337190 folded precursor RNA yielding a GAM337190 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337190 RNA, hereby incorporated herein.

GAM337190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337190 target RNA, herein designated GAM TARGET RNA.

GAM337190 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337190 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337190 RNA, herein designated GAM RNA, to target binding sites on GAM337190 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337190 target RNA into GAM337190 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337190 target genes. The mRNA of each one of this plurality of GAM337190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337190 RNA, herein designated GAM RNA, and which when bound by GAM337190 RNA causes inhibition of translation of the GAM337190 target mRNA into a corresponding GAM337190 target protein.

The mechanism of the translational inhibition exerted by GAM337190 RNA, herein designated GAM RNA, on one or more GAM337190 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337190 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337190 RNA, herein designated GAM RNA, of GAM337190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337190 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337190 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337190 RNA correlate with, and may be deduced from, the identity of the GAM337190 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337191 6835 GGTCAGTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAAGTGAAT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTACTCAGAG Messenger 337191 (GAM337191) oligonucleotides modulates expression of respective target

CTGTGAAATC genes whose function and utility is known in the art.

TTGGGGGAAT GAM337191 is a novel bioinformatically detectable regulatory, non protein
TTGACCCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337191 was detected
CACAGTTGAG is described with additional reference to Figs. 9-15.

AGAAGGTTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAAGGATAT encoded by the human genome.

GGGCT GAM337191 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337191 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337191 precursor RNA is designated SEQ ID:6835, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6835 is located from position 79303486 to position 79303580 relative to chromosome 11 on the `-` strand.

GAM337191 precursor RNA folds onto itself, forming GAM337191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337191 precursor RNA, designated SEQ ID NO: 6835, and a schematic representation of a predicted secondary folding of GAM337191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337191 folded precursor RNA yielding a GAM337191 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337191 RNA, hereby incorporated herein.

GAM337191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337191 target RNA, herein designated GAM TARGET RNA.

GAM337191 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337191 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337191 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337191 RNA, herein designated GAM RNA, to target binding sites on GAM337191 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337191 target RNA into GAM337191 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337191 target genes. The mRNA of each one of this plurality of GAM337191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337191 RNA, herein designated GAM RNA, and which when bound by GAM337191 RNA causes inhibition of translation of the GAM337191 target mRNA into a corresponding GAM337191 target protein.

The mechanism of the translational inhibition exerted by GAM337191 RNA, herein designated GAM RNA, on one or more GAM337191 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337191 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337191 RNA, herein designated GAM RNA, of GAM337191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337191 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337191 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337191 RNA correlate with, and may be deduced from, the identity of the GAM337191 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337192 5892 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337192 (GAM337192) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337192 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337192 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337192 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337192 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337192 precursor RNA is designated SEQ ID:5892, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5892 is located from position 79485331 to position 79485412 relative to chromosome 6 on the `+` strand.

GAM337192 precursor RNA folds onto itself, forming GAM337192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337192 precursor RNA, designated SEQ ID NO: 5892, and a schematic representation of a predicted secondary folding of GAM337192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337192 folded precursor RNA yielding a GAM337192 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337192 RNA, hereby incorporated herein.

GAM337192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337192 target RNA, herein designated GAM TARGET RNA.

GAM337192 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337192 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337192 RNA, herein designated GAM RNA, to target binding sites on GAM337192 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337192 target RNA into GAM337192 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337192 target genes. The mRNA of each one of this plurality of GAM337192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337192 RNA, herein designated GAM RNA, and which when bound by GAM337192 RNA causes inhibition of translation of the GAM337192 target mRNA into a corresponding GAM337192 target protein.

The mechanism of the translational inhibition exerted by GAM337192 RNA, herein designated GAM RNA, on one or more GAM337192 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337192 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337192 RNA, herein designated GAM RNA, of GAM337192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337192 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337192 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337192 RNA correlate with, and may be deduced from, the identity of the GAM337192 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337193 7033 TCCCTGTCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTCTTCGAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTTGTTTTT Messenger 337193 (GAM337193) oligonucleotides modulates expression of respective target

AATGCTGGGT genes whose function and utility is known in the art.

GTCGATCGAG GAM337193 is a novel bioinformatically detectable regulatory, non protein

ACAACAAGCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337193 was detected

CTCAGAGCAA is described with additional reference to Figs. 9-15.

AGCAAGGATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CATTACGGGG encoded by the human genome.

G GAM337193 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337193 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337193 precursor RNA is designated SEQ ID:7033, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7033 is located from position 79931894 to position 79931984 relative to chromosome 17 on the `-` strand.

GAM337193 precursor RNA folds onto itself, forming GAM337193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337193 precursor RNA, designated SEQ ID NO: 7033, and a schematic representation of a predicted secondary folding of GAM337193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337193 folded precursor RNA yielding a GAM337193 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337193 RNA, hereby incorporated herein.

GAM337193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337193 target RNA, herein designated GAM TARGET RNA.

GAM337193 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337193 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337193 RNA, herein designated GAM RNA, to target binding sites on GAM337193 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337193 target RNA into GAM337193 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337193 target genes. The mRNA of each one of this plurality of GAM337193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337193 RNA, herein designated GAM RNA, and which when bound by GAM337193 RNA causes inhibition of translation of the GAM337193 target mRNA into a corresponding GAM337193 target protein.

The mechanism of the translational inhibition exerted by GAM337193 RNA, herein designated GAM RNA, on one or more GAM337193 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337193 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337193 RNA, herein designated GAM RNA, of GAM337193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337193 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337193 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337193 RNA correlate with, and may be deduced from, the identity of the GAM337193 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337194 7205 TGCTGCATCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGCCTGGCTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAGGAGGCC Messenger 337194 (GAM337194) oligonucleotides modulates expression of respective target
TCTCTCAGCA genes whose function and utility is known in the art.

TTTTCTGACA GAM337194 is a novel bioinformatically detectable regulatory, non protein
ACAAAGCCGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337194 was detected
GGCTGCAGAT is described with additional reference to Figs. 9-15.

CCCTGGTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATTCCAGGCT encoded by the human genome.

AGCATCAGCA GAM337194 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337194 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337194 precursor RNA is designated SEQ ID:7205, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7205 is located from position 80018909 to position 80019008 relative to chromosome 17 on the `+` strand.

GAM337194 precursor RNA folds onto itself, forming GAM337194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337194 precursor RNA, designated SEQ ID NO: 7205, and a schematic representation of a predicted secondary folding of GAM337194 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337194 folded precursor RNA yielding a GAM337194 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337194 RNA, hereby incorporated herein.

GAM337194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337194 target RNA, herein designated GAM TARGET RNA.

GAM337194 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337194 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337194 RNA, herein designated GAM RNA, to target binding sites on GAM337194 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337194 target RNA into GAM337194 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337194 target genes. The mRNA of each one of this plurality of GAM337194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337194 RNA, herein designated GAM RNA, and which when bound by GAM337194 RNA causes inhibition of translation of the GAM337194 target mRNA into a corresponding GAM337194 target protein.

The mechanism of the translational inhibition exerted by GAM337194 RNA, herein designated GAM RNA, on one or more GAM337194 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337194 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337194 RNA, herein designated GAM RNA, of GAM337194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337194 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337194 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337194 RNA correlate with, and may be deduced from, the identity of the GAM337194 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337195 6542 GCTGCATCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCTGGCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGGAGGCCT Messenger 337195 (GAM337195) oligonucleotides modulates expression of respective target

CTCTCAGCAT genes whose function and utility is known in the art.

TTTCTGACAA GAM337195 is a novel bioinformatically detectable regulatory, non protein

CAAAGCCGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337195 was detected

GCTGCAGATC is described with additional reference to Figs. 9-15.

CCTGGTGAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTCCAGGCTA encoded by the human genome.

GCATCAGC GAM337195 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337195 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337195 precursor RNA is designated SEQ ID:6542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6542 is located from position 80018910 to position 80019007 relative to chromosome 17 on the `+` strand.

GAM337195 precursor RNA folds onto itself, forming GAM337195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337195 precursor RNA, designated SEQ ID NO: 6542, and a schematic representation of a predicted secondary folding of GAM337195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337195 folded precursor RNA yielding a GAM337195 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337195 RNA, hereby incorporated herein.

GAM337195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337195 target RNA, herein designated GAM TARGET RNA.

GAM337195 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337195 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337195 RNA, herein designated GAM RNA, to target binding sites on GAM337195 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337195 target RNA into GAM337195 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337195 target genes. The mRNA of each one of this plurality of GAM337195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337195 RNA, herein designated GAM RNA, and which when bound by GAM337195 RNA causes inhibition of translation of the GAM337195 target mRNA into a corresponding GAM337195 target protein.

The mechanism of the translational inhibition exerted by GAM337195 RNA, herein designated GAM RNA, on one or more GAM337195 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337195 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337195 RNA, herein designated GAM RNA, of GAM337195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337195 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337195 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337195 RNA correlate with, and may be deduced from, the identity of the GAM337195 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337196 5893 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337196 (GAM337196) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337196 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337196 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337196 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337196 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337196 precursor RNA is designated SEQ

ID:5893, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5893 is located from position 80622214 to position 80622295 relative to chromosome 13 on the `+` strand.

GAM337196 precursor RNA folds onto itself, forming GAM337196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337196 precursor RNA, designated SEQ ID NO: 5893, and a schematic representation of a predicted secondary folding of GAM337196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337196 folded precursor RNA yielding a GAM337196 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337196 RNA, hereby incorporated herein.

GAM337196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337196 target RNA, herein designated GAM TARGET RNA.

GAM337196 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337196 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337196 RNA, herein designated GAM RNA, to target binding sites on GAM337196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337196 target RNA into GAM337196 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337196 target genes. The mRNA of each one of this plurality of GAM337196 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337196 RNA, herein designated GAM RNA, and which when bound by GAM337196 RNA causes inhibition of translation of the GAM337196 target mRNA into a corresponding GAM337196 target protein.

The mechanism of the translational inhibition exerted by GAM337196 RNA, herein designated GAM RNA, on one or more GAM337196 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337196 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337196 RNA, herein designated GAM RNA, of GAM337196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337196 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337196 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337196 RNA correlate with, and may be deduced from, the identity of the GAM337196 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337197 6702 GGAGAATTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGGCGGAGA Messenger 337197 (GAM337197) oligonucleotides modulates expression of respective target

CTGCGGTGAG genes whose function and utility is known in the art.

CTGATACCGC GAM337197 is a novel bioinformatically detectable regulatory, non protein

GTCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337197 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAAACTCC encoded by the human genome.

GAM337197 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337197 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337197 precursor RNA is designated SEQ ID:6702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6702 is located from position 81064708 to position 81064796 relative to chromosome 17 on the `+` strand.

GAM337197 precursor RNA folds onto itself, forming GAM337197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337197 precursor RNA, designated SEQ ID NO: 6702, and a schematic representation of a predicted secondary folding of GAM337197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337197 folded precursor RNA yielding a GAM337197 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337197 RNA, hereby incorporated herein. Expression of GAM337197 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337197 target RNA, herein designated GAM TARGET RNA.

GAM337197 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337197 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337197 RNA, herein designated GAM RNA, to target binding sites on GAM337197 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337197 target RNA into GAM337197 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337197 target genes. The mRNA of each one of this plurality of GAM337197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337197 RNA, herein designated GAM RNA, and which when bound by GAM337197 RNA causes inhibition of translation of the GAM337197 target mRNA into a corresponding GAM337197 target protein.

The mechanism of the translational inhibition exerted by GAM337197 RNA, herein designated GAM RNA, on one or more GAM337197 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337197 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337197 RNA, herein designated GAM RNA, of GAM337197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337197 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337197 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337197 RNA correlate with, and may be deduced from, the identity of the GAM337197 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337199 5786 AGGGAAAAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTCATAATTC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGACAGGCTC Messenger 337199 (GAM337199) oligonucleotides modulates expression of respective target

TCGGGGCTTC genes whose function and utility is known in the art.

ACCATACAAC GAM337199 is a novel bioinformatically detectable regulatory, non protein
GCCTTTCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337199 was detected
TATTTGGTTA is described with additional reference to Figs. 9-15.

GTTTTATGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTGGAGTGT encoded by the human genome.

TGACCATGTA GAM337199 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTAATTTTCT GAM337199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
CT GAM337199 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337199 precursor RNA is designated SEQ ID:5786, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5786 is located from position 81438779 to position 81438890 relative to chromosome 16 on the `+` strand.

GAM337199 precursor RNA folds onto itself, forming GAM337199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337199 precursor RNA, designated SEQ ID NO: 5786, and a schematic representation of a predicted secondary folding of GAM337199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337199 folded precursor RNA yielding a GAM337199 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337199 RNA, hereby incorporated herein.

GAM337199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337199 target RNA, herein designated GAM TARGET RNA.

GAM337199 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337199 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337199 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337199 RNA, herein designated GAM RNA, to target binding sites on GAM337199 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337199 target RNA into GAM337199 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337199 target genes. The mRNA of each one of this plurality of GAM337199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337199 RNA, herein designated GAM RNA, and which when bound by GAM337199 RNA causes inhibition of translation of the GAM337199 target mRNA into a corresponding GAM337199 target protein.

The mechanism of the translational inhibition exerted by GAM337199 RNA, herein designated GAM RNA, on one or more GAM337199 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337199 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337199 RNA, herein designated GAM RNA, of GAM337199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337199 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337199 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337199 RNA correlate with, and may be deduced from, the identity of the GAM337199 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337200 5729 AGAGGATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGTCAAG Messenger 337200 (GAM337200) oligonucleotides modulates expression of respective target
GCTGCAGTGA genes whose function and utility is known in the art.

TCCATGATTG GAM337200 is a novel bioinformatically detectable regulatory, non protein
CGCCCCTGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337200 was detected
CTCTGGGCAA is described with additional reference to Figs. 9-15.

CAGAGCAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCCT encoded by the human genome.

GAM337200 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337200 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337200 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337200 precursor RNA is designated SEQ ID:5729, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5729 is located from position 81629047 to position 81629130 relative to chromosome 8 on the `-` strand.

GAM337200 precursor RNA folds onto itself, forming GAM337200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337200 precursor RNA, designated SEQ ID NO: 5729, and a schematic representation of a predicted secondary folding of GAM337200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337200 folded precursor RNA yielding a GAM337200 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337200 RNA, hereby incorporated herein.

GAM337200 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337200 target RNA, herein designated GAM TARGET RNA.

GAM337200 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337200 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337200 RNA, herein designated GAM RNA, to target binding sites on GAM337200 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337200 target RNA into GAM337200 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337200 target genes. The mRNA of each one of this plurality of GAM337200 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337200 RNA, herein designated GAM RNA, and which when bound by GAM337200 RNA causes inhibition of translation of the GAM337200 target mRNA into a corresponding GAM337200 target protein.

The mechanism of the translational inhibition exerted by GAM337200 RNA, herein designated GAM RNA, on one or more GAM337200 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337200 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337200 RNA, herein designated GAM RNA, of GAM337200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337200 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337200 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337200 RNA correlate with, and may be deduced from, the identity of the GAM337200 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337202 6057 CCAGTATTGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GTGGGGAGTG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTTGAGGTC Messenger 337202 (GAM337202) oligonucleotides modulates expression of respective target
ATCTAATGGT genes whose function and utility is known in the art.

GTTGTCTATT GAM337202 is a novel bioinformatically detectable regulatory, non protein
CTTCAGTAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337202 was detected
AACTCCAACA is described with additional reference to Figs. 9-15.

CCCTCTACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGCTATCAC encoded by the human genome.

CACACAACCT GAM337202 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GG GAM337202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337202 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337202 precursor RNA is designated SEQ ID:6057, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6057 is located from position 82178830 to position 82178931 relative to chromosome 7 on the `-` strand.

GAM337202 precursor RNA folds onto itself, forming GAM337202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337202 precursor RNA, designated SEQ ID NO: 6057, and a schematic representation of a predicted secondary folding of GAM337202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337202 folded precursor

RNA yielding a GAM337202 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337202 RNA, hereby incorporated herein.

GAM337202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337202 target RNA, herein designated GAM TARGET RNA.

GAM337202 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337202 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337202 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337202 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337202 RNA, herein designated GAM RNA, to target binding sites on GAM337202 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337202 target RNA into GAM337202 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337202 target genes. The mRNA of each one of this plurality of GAM337202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337202 RNA, herein designated GAM RNA, and which when bound by GAM337202 RNA causes inhibition of translation of the GAM337202 target mRNA into a corresponding GAM337202 target protein.

The mechanism of the translational inhibition exerted by GAM337202 RNA, herein designated GAM RNA, on one or more GAM337202 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337202 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337202 RNA, herein designated GAM RNA, of GAM337202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337202 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337202 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337202 RNA correlate with, and may be deduced from, the identity of the GAM337202 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337203 6648 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCAGAGG Messenger 337203 (GAM337203) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM337203 is a novel bioinformatically detectable regulatory, non protein

ACTACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337203 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337203 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337203 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337203 precursor RNA is designated SEQ ID:6648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6648 is located from position 82201058 to position 82201145 relative to chromosome 9 on the `+` strand.

GAM337203 precursor RNA folds onto itself, forming GAM337203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337203 precursor RNA, designated SEQ ID NO: 6648, and a schematic representation of a predicted secondary folding of GAM337203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337203 folded precursor RNA yielding a GAM337203 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337203 RNA, hereby incorporated herein. Expression of GAM337203 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337203 target RNA, herein designated GAM TARGET RNA.

GAM337203 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337203 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337203 RNA, herein designated GAM RNA, to target binding sites on GAM337203 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337203 target RNA into GAM337203 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337203 target genes. The mRNA of each one of this plurality of GAM337203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337203 RNA, herein designated GAM RNA, and which when bound by GAM337203 RNA causes inhibition of translation of the GAM337203 target mRNA into a corresponding GAM337203 target protein.

The mechanism of the translational inhibition exerted by GAM337203 RNA, herein

designated GAM RNA, on one or more GAM337203 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337203 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337203 RNA, herein designated GAM RNA, of GAM337203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337203 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337203 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337203 RNA correlate with, and may be deduced from, the identity of the GAM337203 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337204 5894 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337204 (GAM337204) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337204 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337204 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337204 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337204 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337204 precursor RNA is designated SEQ ID:5894, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5894 is located from position 82464706 to position 82464787

relative to chromosome 9 on the `+` strand.

GAM337204 precursor RNA folds onto itself, forming GAM337204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337204 precursor RNA, designated SEQ ID NO: 5894, and a schematic representation of a predicted secondary folding of GAM337204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337204 folded precursor RNA yielding a GAM337204 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337204 RNA, hereby incorporated herein.

GAM337204 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337204 target RNA, herein designated GAM TARGET RNA.

GAM337204 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337204 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337204 RNA, herein designated GAM RNA, to target binding sites on GAM337204 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337204 target RNA into GAM337204 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337204 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337204 target genes. The mRNA of each one of this plurality of GAM337204 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337204 RNA, herein designated GAM RNA, and which when bound by GAM337204 RNA causes inhibition of translation of the GAM337204 target mRNA into a corresponding GAM337204 target protein.

The mechanism of the translational inhibition exerted by GAM337204 RNA, herein designated GAM RNA, on one or more GAM337204 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337204 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337204 RNA, herein designated GAM RNA, of GAM337204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337204 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337204 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337204 RNA correlate with, and may be deduced from, the identity of the GAM337204 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337206 5895 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337206 (GAM337206) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337206 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337206 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337206 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337206 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337206 precursor RNA is designated SEQ ID:5895, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5895 is located from position 83433939 to position 83434020 relative to chromosome 9 on the `-` strand.

GAM337206 precursor RNA folds onto itself, forming GAM337206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337206 precursor RNA, designated SEQ ID NO: 5895, and a schematic representation of a predicted secondary folding of GAM337206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337206 folded precursor RNA yielding a GAM337206 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337206 RNA, hereby incorporated herein.

GAM337206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337206 target RNA, herein designated GAM TARGET RNA.

GAM337206 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337206 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337206 RNA, herein designated GAM RNA, to target

binding sites on GAM337206 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337206 target RNA into GAM337206 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337206 target genes. The mRNA of each one of this plurality of GAM337206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337206 RNA, herein designated GAM RNA, and which when bound by GAM337206 RNA causes inhibition of translation of the GAM337206 target mRNA into a corresponding GAM337206 target protein.

The mechanism of the translational inhibition exerted by GAM337206 RNA, herein designated GAM RNA, on one or more GAM337206 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337206 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337206 RNA, herein designated GAM RNA, of GAM337206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337206 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337206 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337206 RNA correlate with, and may be deduced from, the identity of the GAM337206 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337207 7019 TCCACTACTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGTGGCTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCAAATTAC Messenger 337207 (GAM337207) oligonucleotides modulates expression of respective target

TAAATTTCTC genes whose function and utility is known in the art.

TGTGACTACT GAM337207 is a novel bioinformatically detectable regulatory, non protein

TTTCCATTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337207 was detected

TTAAGTAATT is described with additional reference to Figs. 9-15.

TGGTTGGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCAAAAGTCA encoded by the human genome.

ATAATGTGGA GAM337207 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337207 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337207 precursor RNA is designated SEQ ID:7019, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7019 is located from position 84223987 to position 84224086 relative to chromosome 7 on the `+` strand.

GAM337207 precursor RNA folds onto itself, forming GAM337207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337207 precursor RNA, designated SEQ ID NO: 7019, and a schematic representation of a predicted secondary folding of GAM337207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337207 folded precursor RNA yielding a GAM337207 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337207 RNA, hereby incorporated herein.

GAM337207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337207 target RNA, herein designated GAM TARGET RNA.

GAM337207 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337207 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337207 RNA, herein designated GAM RNA, to target binding sites on GAM337207 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337207 target RNA into GAM337207 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337207 target genes. The mRNA of each one of this plurality of GAM337207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337207 RNA, herein designated GAM RNA, and which when bound by GAM337207 RNA causes inhibition of translation of the GAM337207 target mRNA into a corresponding GAM337207 target protein.

The mechanism of the translational inhibition exerted by GAM337207 RNA, herein designated GAM RNA, on one or more GAM337207 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337207 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337207 RNA, herein designated GAM RNA, of GAM337207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337207 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337207 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337207 RNA correlate with, and may be deduced from, the identity of the GAM337207 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337208 6151 CTACTGTTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTTTTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
AATTACTAAA Messenger 337208 (GAM337208) oligonucleotides modulates expression of respective target
TTTCTCTGTG genes whose function and utility is known in the art.

ACTACTTTTC GAM337208 is a novel bioinformatically detectable regulatory, non protein
CATTTCTTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337208 was detected
GTAATTTGGT is described with additional reference to Figs. 9-15.

TGGTTTCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGTCAATAA encoded by the human genome.

TGTGG GAM337208 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337208 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337208 precursor RNA is designated SEQ ID:6151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6151 is located from position 84223991 to position 84224085 relative to chromosome 7 on the `+` strand.

GAM337208 precursor RNA folds onto itself, forming GAM337208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337208 precursor RNA, designated SEQ ID NO: 6151, and a schematic representation of a predicted secondary folding of GAM337208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337208 folded precursor RNA yielding a GAM337208 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337208 RNA, hereby incorporated herein.

GAM337208 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337208 target RNA, herein designated GAM TARGET RNA.

GAM337208 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337208 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337208 RNA, herein designated GAM RNA, to target binding sites on GAM337208 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337208 target RNA into GAM337208 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337208 target genes. The mRNA of each one of this plurality of GAM337208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337208 RNA, herein designated GAM RNA, and which when bound by GAM337208 RNA causes inhibition of translation of the GAM337208 target mRNA into a corresponding GAM337208 target protein.

The mechanism of the translational inhibition exerted by GAM337208 RNA, herein designated GAM RNA, on one or more GAM337208 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337208 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337208 RNA, herein designated GAM RNA, of GAM337208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337208 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337208 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337208 RNA correlate with, and may be deduced from, the identity of the GAM337208 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337209 5896 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337209 (GAM337209) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337209 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337209 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337209 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337209 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337209 precursor RNA is designated SEQ ID:5896, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5896 is located from position 84490971 to position 84491052 relative to chromosome 8 on the `-` strand.

GAM337209 precursor RNA folds onto itself, forming GAM337209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337209 precursor RNA, designated SEQ ID NO: 5896, and a schematic representation of a predicted secondary folding of GAM337209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337209 folded precursor RNA yielding a GAM337209 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337209 RNA, hereby incorporated herein.

GAM337209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337209 target RNA, herein designated GAM TARGET RNA.

GAM337209 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337209 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337209 RNA, herein designated GAM RNA, to target binding sites on GAM337209 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337209 target RNA into GAM337209 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337209 target genes. The mRNA of each one of this plurality of GAM337209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337209 RNA, herein designated GAM RNA, and which when bound by GAM337209 RNA causes inhibition of translation of the GAM337209 target mRNA into a corresponding GAM337209 target protein.

The mechanism of the translational inhibition exerted by GAM337209 RNA, herein designated GAM RNA, on one or more GAM337209 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337209 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337209 RNA, herein designated GAM RNA, of GAM337209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337209 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337209 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337209 RNA correlate with, and may be deduced from, the identity of the GAM337209 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337210 5897 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337210 (GAM337210) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337210 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337210 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337210 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337210 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337210 precursor RNA is designated SEQ ID:5897, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5897 is located from position 84536421 to position 84536502 relative to chromosome 5 on the `+` strand.

GAM337210 precursor RNA folds onto itself, forming GAM337210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337210 precursor RNA, designated SEQ ID NO: 5897, and a schematic representation of a predicted secondary folding of GAM337210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337210 folded precursor RNA yielding a GAM337210 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337210 RNA, hereby incorporated herein.

GAM337210 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337210 target RNA, herein designated GAM TARGET RNA.

GAM337210 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337210 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337210 RNA, herein designated GAM RNA, to target binding sites on GAM337210 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337210 target RNA into GAM337210 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337210 target genes. The mRNA of each one of this plurality of GAM337210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337210 RNA, herein designated GAM RNA, and which when bound by GAM337210 RNA causes inhibition of translation of the GAM337210 target mRNA into a corresponding GAM337210 target protein.

The mechanism of the translational inhibition exerted by GAM337210 RNA, herein designated GAM RNA, on one or more GAM337210 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337210 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337210 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337210 RNA, herein designated GAM RNA, of GAM337210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337210 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337210 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337210 RNA correlate with, and may be deduced from, the identity of the GAM337210 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337211 5898 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337211 (GAM337211) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337211 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337211 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337211 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337211 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337211 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337211 precursor RNA is designated SEQ ID:5898, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5898 is located from position 84648170 to position 84648251 relative to chromosome 12 on the `-` strand.

GAM337211 precursor RNA folds onto itself, forming GAM337211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337211 precursor RNA, designated SEQ ID NO: 5898, and a schematic representation of a predicted secondary folding of GAM337211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337211 folded precursor RNA yielding a GAM337211 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337211 RNA, hereby incorporated herein.

GAM337211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337211 target RNA, herein designated GAM TARGET RNA.

GAM337211 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337211 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337211 RNA, herein designated GAM RNA, to target binding sites on GAM337211 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337211 target RNA into GAM337211 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337211 target genes. The mRNA of each one of this plurality of GAM337211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337211 RNA, herein designated GAM RNA, and which when bound by GAM337211 RNA causes inhibition of translation of the GAM337211 target mRNA into a corresponding GAM337211 target protein.

The mechanism of the translational inhibition exerted by GAM337211 RNA, herein

designated GAM RNA, on one or more GAM337211 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337211 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337211 RNA, herein designated GAM RNA, of GAM337211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337211 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337211 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337211 RNA correlate with, and may be deduced from, the identity of the GAM337211 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337212 5899 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337212 (GAM337212) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337212 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337212 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337212 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337212 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337212 precursor RNA is designated SEQ ID:5899, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5899 is located from position 84939391 to position 84939472

relative to chromosome 12 on the `+` strand.

GAM337212 precursor RNA folds onto itself, forming GAM337212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337212 precursor RNA, designated SEQ ID NO: 5899, and a schematic representation of a predicted secondary folding of GAM337212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337212 folded precursor RNA yielding a GAM337212 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337212 RNA, hereby incorporated herein.

GAM337212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337212 target RNA, herein designated GAM TARGET RNA.

GAM337212 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337212 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337212 RNA, herein designated GAM RNA, to target binding sites on GAM337212 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337212 target RNA into GAM337212 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337212 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337212 target genes. The mRNA of each one of this plurality of GAM337212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337212 RNA, herein designated GAM RNA, and which when bound by GAM337212 RNA causes inhibition of translation of the GAM337212 target mRNA into a corresponding GAM337212 target protein.

The mechanism of the translational inhibition exerted by GAM337212 RNA, herein designated GAM RNA, on one or more GAM337212 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337212 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337212 RNA, herein designated GAM RNA, of GAM337212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337212 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337212 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337212 RNA correlate with, and may be deduced from, the identity of the GAM337212 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337213 5772 AGGCAGGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATCACGTGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCAGGAGGT Messenger 337213 (GAM337213) oligonucleotides modulates expression of respective target
GAAGGCTACA genes whose function and utility is known in the art.

GTGAAGTGAG GAM337213 is a novel bioinformatically detectable regulatory, non protein
ATCATGCAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337213 was detected
TGTACTTCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGCAAGAT encoded by the human genome.

TCTCTTTCT GAM337213 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337213 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337213 precursor RNA is designated SEQ ID:5772, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5772 is located from position 85256084 to position 85256182 relative to chromosome 12 on the `+` strand.

GAM337213 precursor RNA folds onto itself, forming GAM337213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337213 precursor RNA, designated SEQ ID NO: 5772, and a schematic representation of a predicted secondary folding of GAM337213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337213 folded precursor RNA yielding a GAM337213 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337213 RNA, hereby incorporated herein.

GAM337213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337213 target RNA, herein designated GAM TARGET RNA.

GAM337213 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337213 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337213 RNA, herein designated GAM RNA, to target binding sites on GAM337213 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337213 target RNA into GAM337213 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337213 target genes. The mRNA of each one of this plurality of GAM337213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337213 RNA, herein designated GAM RNA, and which when bound by GAM337213 RNA causes inhibition of translation of the GAM337213 target mRNA into a corresponding GAM337213 target protein.

The mechanism of the translational inhibition exerted by GAM337213 RNA, herein designated GAM RNA, on one or more GAM337213 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337213 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337213 RNA, herein designated GAM RNA, of GAM337213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337213 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337213 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337213 RNA correlate with, and may be deduced from, the identity of the GAM337213 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337214 6710 GGAGGATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGAGCCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGAAGG Messenger 337214 (GAM337214) oligonucleotides modulates expression of respective target

CTACAGTGAA genes whose function and utility is known in the art.

GTGAGATCAT GAM337214 is a novel bioinformatically detectable regulatory, non protein

GCAACTGTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337214 was detected

TTCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGATTCTCT encoded by the human genome.

GAM337214 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337214 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337214 precursor RNA is designated SEQ ID:6710, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6710 is located from position 85256089 to position 85256178 relative to chromosome 12 on the `+` strand.

GAM337214 precursor RNA folds onto itself, forming GAM337214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337214 precursor RNA, designated SEQ ID NO: 6710, and a schematic representation of a predicted secondary folding of GAM337214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337214 folded precursor RNA yielding a GAM337214 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337214 RNA, hereby incorporated herein.

GAM337214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337214 target RNA, herein designated GAM TARGET RNA.

GAM337214 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337214 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337214 RNA, herein designated GAM RNA, to target binding sites on GAM337214 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337214 target RNA into GAM337214 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337214 target genes. The mRNA of each one of this plurality of GAM337214 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337214 RNA, herein designated GAM RNA, and which when bound by GAM337214 RNA causes inhibition of translation of the GAM337214 target mRNA into a corresponding GAM337214 target protein.

The mechanism of the translational inhibition exerted by GAM337214 RNA, herein designated GAM RNA, on one or more GAM337214 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337214 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337214 RNA, herein designated GAM RNA, of GAM337214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337214 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337214 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337214 RNA correlate with, and may be deduced from, the identity of the GAM337214 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337215 6366 GAGGATCACG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAGCCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTGAAGGC Messenger 337215 (GAM337215) oligonucleotides modulates expression of respective target
TACAGTGAAG genes whose function and utility is known in the art.

TGAGATCATG GAM337215 is a novel bioinformatically detectable regulatory, non protein
CAACTGTACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337215 was detected
TCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGATTCTC encoded by the human genome.

GAM337215 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337215 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337215 precursor RNA is designated SEQ ID:6366, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6366 is located from position 85256090 to position 85256177 relative to chromosome 12 on the `+` strand.

GAM337215 precursor RNA folds onto itself, forming GAM337215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337215 precursor RNA, designated SEQ ID NO: 6366, and a schematic representation of a predicted secondary folding of GAM337215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337215 folded precursor RNA yielding a GAM337215 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337215 RNA, hereby incorporated herein.

GAM337215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337215 target RNA, herein designated GAM TARGET RNA.

GAM337215 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337215 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337215 RNA, herein designated GAM RNA, to target binding sites on GAM337215 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337215 target RNA into GAM337215 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337215 target genes. The mRNA of each one of this plurality of GAM337215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337215 RNA, herein designated GAM RNA, and which when bound by GAM337215 RNA causes inhibition of translation of the GAM337215 target mRNA into a corresponding GAM337215 target protein.

The mechanism of the translational inhibition exerted by GAM337215 RNA, herein designated GAM RNA, on one or more GAM337215 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337215 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337215 RNA, herein designated GAM RNA, of GAM337215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337215 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337215 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337215

RNA correlate with, and may be deduced from, the identity of the GAM337215 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337216 5900 AGTTTTAGGG TACATGTGCA CAACATGCAG GTTTGTTACA TATGTATACA TGTGCCATGT TGGTGTGCTG CACCCATTAA CT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337216 (GAM337216) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337216 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337216 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337216 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337216 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337216 precursor RNA is designated SEQ ID:5900, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5900 is located from position 85369298 to position 85369379 relative to chromosome 7 on the `-` strand.

GAM337216 precursor RNA folds onto itself, forming GAM337216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337216 precursor RNA, designated SEQ ID NO: 5900, and a schematic representation of a predicted secondary folding of GAM337216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337216 folded precursor RNA yielding a GAM337216 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337216 RNA, hereby incorporated herein.

GAM337216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337216 target RNA, herein designated GAM TARGET RNA.

GAM337216 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337216 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337216 RNA, herein designated GAM RNA, to target binding sites on GAM337216 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337216 target RNA into GAM337216 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337216 target genes. The mRNA of each one of this plurality of GAM337216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337216 RNA, herein designated GAM RNA, and which when bound by GAM337216 RNA causes inhibition of translation of the GAM337216 target mRNA into a corresponding GAM337216 target protein.

The mechanism of the translational inhibition exerted by GAM337216 RNA, herein designated GAM RNA, on one or more GAM337216 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337216 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337216 RNA, herein designated GAM RNA, of GAM337216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337216 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337216 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337216 RNA correlate with, and may be deduced from, the identity of the GAM337216 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337217 6091 CCCTGTCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTCTCCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATATGCTTGT Messenger 337217 (GAM337217) oligonucleotides modulates expression of respective target
TGGAGATCCT genes whose function and utility is known in the art.

TCAGGCAGTA GAM337217 is a novel bioinformatically detectable regulatory, non protein
AGGGAGAGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337217 was detected
TTGCCTCCTT is described with additional reference to Figs. 9-15.

ACACAGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337217 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337217 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337217 precursor RNA is designated SEQ ID:6091, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6091 is located from position 86608510 to position 86608588 relative to chromosome 15 on the `+` strand.

GAM337217 precursor RNA folds onto itself, forming GAM337217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337217 precursor RNA, designated SEQ ID NO: 6091, and a schematic representation of a predicted secondary folding of GAM337217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337217 folded precursor RNA yielding a GAM337217 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337217 RNA, hereby incorporated herein.

GAM337217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337217 target RNA, herein designated GAM TARGET RNA.

GAM337217 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337217 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337217 RNA, herein designated GAM RNA, to target binding sites on GAM337217 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337217 target RNA into GAM337217 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337217 target genes. The mRNA of each one of this plurality of GAM337217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337217 RNA, herein designated GAM RNA, and which when bound by GAM337217 RNA causes inhibition of translation of the GAM337217 target mRNA into a corresponding GAM337217 target protein.

The mechanism of the translational inhibition exerted by GAM337217 RNA, herein designated GAM RNA, on one or more GAM337217 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337217 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337217 RNA, herein designated GAM RNA, of GAM337217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337217 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337217 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337217 RNA correlate with, and may be deduced from, the identity of the GAM337217 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337218 5774 AGGCCATCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGGGGCC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAGATGACA Messenger 337218 (GAM337218) oligonucleotides modulates expression of respective target

CTCTCCCCCT genes whose function and utility is known in the art.

GTAACTCAGC GAM337218 is a novel bioinformatically detectable regulatory, non protein

CTGGCTCTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337218 was detected

CTATTGGGAT is described with additional reference to Figs. 9-15.

GTGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337218 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337218 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337218 precursor RNA is designated SEQ ID:5774, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5774 is located from position 86923030 to position 86923105 relative to chromosome 14 on the `+` strand.

GAM337218 precursor RNA folds onto itself, forming GAM337218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337218 precursor RNA, designated SEQ ID NO: 5774, and a schematic representation of a predicted secondary folding of GAM337218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337218 folded precursor RNA yielding a GAM337218 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337218 RNA, hereby incorporated herein.

GAM337218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337218 target RNA, herein designated GAM TARGET RNA.

GAM337218 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337218 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337218 RNA, herein designated GAM RNA, to target binding sites on GAM337218 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337218 target RNA into GAM337218 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337218 target genes. The mRNA of each one of this plurality of GAM337218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337218 RNA, herein designated GAM RNA, and which when bound by GAM337218 RNA causes inhibition of translation of the GAM337218 target mRNA into a corresponding GAM337218 target protein.

The mechanism of the translational inhibition exerted by GAM337218 RNA, herein designated GAM RNA, on one or more GAM337218 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337218 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337218 RNA, herein designated GAM RNA, of GAM337218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337218 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337218 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337218 RNA correlate with, and may be deduced from, the identity of the GAM337218 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337220 6315 GACCTCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGCTGGGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGCTGGGCT Messenger 337220 (GAM337220) oligonucleotides modulates expression of respective target

GAGACAATTA genes whose function and utility is known in the art.

ATGTCTGTCA GAM337220 is a novel bioinformatically detectable regulatory, non protein

GCCCAAACCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337220 was detected

GGCACTCTGA is described with additional reference to Figs. 9-15.

CCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337220 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337220 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337220 precursor RNA is designated SEQ ID:6315, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6315 is located from position 87035430 to position 87035503 relative to chromosome 15 on the `+` strand.

GAM337220 precursor RNA folds onto itself, forming GAM337220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337220 precursor RNA, designated SEQ ID NO: 6315, and a schematic representation of a predicted secondary folding of GAM337220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337220 folded precursor RNA yielding a GAM337220 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337220 RNA, hereby incorporated herein.

GAM337220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337220 target RNA, herein designated GAM TARGET RNA.

GAM337220 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337220 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337220 RNA, herein designated GAM RNA, to target binding sites on GAM337220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337220 target RNA into GAM337220 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337220 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337220 target genes. The mRNA of each one of this

plurality of GAM337220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337220 RNA, herein designated GAM RNA, and which when bound by GAM337220 RNA causes inhibition of translation of the GAM337220 target mRNA into a corresponding GAM337220 target protein.

The mechanism of the translational inhibition exerted by GAM337220 RNA, herein designated GAM RNA, on one or more GAM337220 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337220 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337220 RNA, herein designated GAM RNA, of GAM337220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337220 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337220 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337220 RNA correlate with, and may be deduced from, the identity of the GAM337220 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337221 6830 GGTACATGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ACTACTGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATAGTCTCTT Messenger 337221 (GAM337221) oligonucleotides modulates expression of respective target

TGCTGGAACT genes whose function and utility is known in the art.

TGGTCCTATG GAM337221 is a novel bioinformatically detectable regulatory, non protein

GCCCTACTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337221 was detected

CAGAGAGGAA is described with additional reference to Figs. 9-15.

GGCTATGAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCAGTCTAG encoded by the human genome.

GCCTGCGCC GAM337221 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337221 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337221 precursor RNA is designated SEQ ID:6830, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6830 is located from position 87449030 to position 87449128 relative to chromosome 10 on the `-` strand.

GAM337221 precursor RNA folds onto itself, forming GAM337221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337221 precursor RNA, designated SEQ ID NO: 6830, and a schematic representation of a predicted secondary folding of GAM337221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337221 folded precursor RNA yielding a GAM337221 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337221 RNA, hereby incorporated herein.

GAM337221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337221 target RNA, herein designated GAM TARGET RNA.

GAM337221 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337221 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337221 RNA, herein designated GAM RNA, to target binding sites on GAM337221 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337221 target RNA into GAM337221 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337221 target genes. The mRNA of each one of this plurality of GAM337221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337221 RNA, herein designated GAM RNA, and which when bound by GAM337221 RNA causes inhibition of translation of the GAM337221 target mRNA into a corresponding GAM337221 target protein.

The mechanism of the translational inhibition exerted by GAM337221 RNA, herein designated GAM RNA, on one or more GAM337221 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337221 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337221 RNA, herein designated GAM RNA, of GAM337221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337221 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337221 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337221 RNA correlate with, and may be deduced from, the identity of the GAM337221 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337224 5901 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337224 (GAM337224) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337224 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337224 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337224 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337224 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337224 precursor RNA is designated SEQ ID:5901, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5901 is located from position 88198417 to position 88198498 relative to chromosome 7 on the `-` strand.

GAM337224 precursor RNA folds onto itself, forming GAM337224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337224 precursor RNA, designated SEQ ID NO: 5901, and a schematic representation of a predicted secondary folding of GAM337224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337224 folded precursor RNA yielding a GAM337224 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337224 RNA, hereby incorporated herein.

GAM337224 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337224 target RNA, herein designated GAM TARGET RNA.

GAM337224 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337224 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337224 RNA, herein designated GAM RNA, to target binding sites on GAM337224 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337224 target RNA into GAM337224 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337224 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337224 target genes. The mRNA of each one of this plurality of GAM337224 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337224 RNA, herein designated GAM RNA, and which when bound by GAM337224 RNA causes inhibition of translation of the GAM337224 target mRNA into a corresponding GAM337224 target protein.

The mechanism of the translational inhibition exerted by GAM337224 RNA, herein designated GAM RNA, on one or more GAM337224 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337224 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337224 RNA, herein designated GAM RNA, of GAM337224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337224 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337224 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337224 RNA correlate with, and may be deduced from, the identity of the GAM337224 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337225 6196 CTGAGAGGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAGGCTTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAGCCGAGG Messenger 337225 (GAM337225) oligonucleotides modulates expression of respective target

CCACACCACT genes whose function and utility is known in the art.

GCACTCCGGC GAM337225 is a novel bioinformatically detectable regulatory, non protein
CTTGGTGACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337225 was detected
GAGACTCTGC is described with additional reference to Figs. 9-15.

CTCGAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337225 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337225 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337225 precursor RNA is designated SEQ ID:6196, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6196 is located from position 88408163 to position 88408240 relative to chromosome 15 on the `+` strand.

GAM337225 precursor RNA folds onto itself, forming GAM337225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337225 precursor RNA, designated SEQ ID NO: 6196, and a schematic representation of a predicted secondary folding of GAM337225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337225 folded precursor RNA yielding a GAM337225 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337225 RNA, hereby incorporated herein.

GAM337225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337225 target RNA, herein designated GAM TARGET RNA.

GAM337225 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337225 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337225 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337225 RNA, herein designated GAM RNA, to target binding sites on GAM337225 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337225 target RNA into GAM337225 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337225 target genes. The mRNA of each one of this plurality of GAM337225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337225 RNA, herein designated GAM RNA, and which when bound by GAM337225 RNA causes inhibition of translation of the GAM337225 target mRNA into a corresponding GAM337225 target protein.

The mechanism of the translational inhibition exerted by GAM337225 RNA, herein designated GAM RNA, on one or more GAM337225 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337225 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337225 RNA, herein designated GAM RNA, of GAM337225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337225 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337225 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337225 RNA correlate with, and may be deduced from, the identity of the GAM337225 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337226 6868 GTATAACGCA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAACACAATT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTAAATAGT Messenger 337226 (GAM337226) oligonucleotides modulates expression of respective target
CAAAAGTTTT genes whose function and utility is known in the art.

TCCTGGCAAG GAM337226 is a novel bioinformatically detectable regulatory, non protein
GAGACTTTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337226 was detected
TAGACACCTA is described with additional reference to Figs. 9-15.

CCCTGTGATC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATCTGTGTGC encoded by the human genome.

GAM337226 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337226 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337226 precursor RNA is designated SEQ ID:6868, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6868 is located from position 88578225 to position 88578314 relative to chromosome 9 on the `+` strand.

GAM337226 precursor RNA folds onto itself, forming GAM337226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337226 precursor RNA, designated SEQ ID NO: 6868, and a schematic representation of a predicted secondary folding of GAM337226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337226 folded precursor RNA yielding a GAM337226 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337226 RNA, hereby incorporated herein.

GAM337226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337226 target RNA, herein designated GAM TARGET RNA.

GAM337226 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337226 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337226 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337226 RNA, herein designated GAM RNA, to target binding sites on GAM337226 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337226 target RNA into GAM337226 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337226 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337226 target genes. The mRNA of each one of this plurality of GAM337226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337226 RNA, herein designated GAM RNA, and which when bound by GAM337226 RNA causes inhibition of translation of the GAM337226 target mRNA into a corresponding GAM337226 target protein.

The mechanism of the translational inhibition exerted by GAM337226 RNA, herein designated GAM RNA, on one or more GAM337226 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337226 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337226 RNA, herein designated GAM RNA, of GAM337226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337226 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337226 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337226 RNA correlate with, and may be deduced from, the identity of the GAM337226 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337227 7122 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCCCAGGAG Messenger 337227 (GAM337227) oligonucleotides modulates expression of respective target
GTGGAGGCTG genes whose function and utility is known in the art.

CAGTGACCCA GAM337227 is a novel bioinformatically detectable regulatory, non protein
TATTCATGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337227 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACCCTCTCTC GAM337227 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337227 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337227 precursor RNA is designated SEQ ID:7122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7122 is located from position 88903075 to position 88903175 relative to chromosome 10 on the `+` strand.

GAM337227 precursor RNA folds onto itself, forming GAM337227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337227 precursor RNA, designated SEQ ID NO: 7122, and a schematic representation of a predicted secondary folding of GAM337227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337227 folded precursor RNA yielding a GAM337227 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337227 RNA, hereby incorporated herein. Expression of GAM337227 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337227 target RNA, herein designated GAM TARGET RNA.

GAM337227 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337227 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337227 RNA, herein designated GAM RNA, to target binding sites on GAM337227 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337227 target RNA into GAM337227 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337227 target genes. The mRNA of each one of this plurality of GAM337227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337227 RNA, herein designated GAM RNA, and which when bound by GAM337227 RNA causes inhibition of translation of the GAM337227 target mRNA into a corresponding GAM337227 target protein.

The mechanism of the translational inhibition exerted by GAM337227 RNA, herein designated GAM RNA, on one or more GAM337227 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337227 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337227 RNA, herein designated GAM RNA, of GAM337227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337227 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337227 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337227 RNA correlate with, and may be deduced from, the identity of the GAM337227 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337228 5902 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337228 (GAM337228) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337228 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337228 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337228 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337228 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337228 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337228 precursor RNA is designated SEQ ID:5902, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5902 is located from position 88997770 to position 88997851 relative to chromosome 3 on the `+` strand.

GAM337228 precursor RNA folds onto itself, forming GAM337228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337228 precursor RNA, designated SEQ ID NO: 5902, and a schematic representation of a predicted secondary folding of GAM337228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337228 folded precursor RNA yielding a GAM337228 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337228 RNA, hereby incorporated herein.

GAM337228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337228 target RNA, herein designated GAM TARGET RNA.

GAM337228 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337228 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337228 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337228 RNA, herein designated GAM RNA, to target binding sites on GAM337228 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337228 target RNA into GAM337228 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337228 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337228 target genes. The mRNA of each one of this plurality of GAM337228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337228 RNA, herein designated GAM RNA, and which when bound by GAM337228 RNA causes inhibition of translation of the GAM337228 target mRNA into a corresponding GAM337228 target protein.

The mechanism of the translational inhibition exerted by GAM337228 RNA, herein designated GAM RNA, on one or more GAM337228 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337228 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337228 RNA, herein designated GAM RNA, of GAM337228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337228 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337228 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337228 RNA correlate with, and may be deduced from, the identity of the GAM337228 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337229 7211 TGCTTCTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AACCTCCATC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCATGCCATG Messenger 337229 (GAM337229) oligonucleotides modulates expression of respective target
GTGCTTCGAG genes whose function and utility is known in the art.

GAGCGTACCA GAM337229 is a novel bioinformatically detectable regulatory, non protein
GCCTTGCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337229 was detected
ACCACAACAG is described with additional reference to Figs. 9-15.

GGACTGGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAGGCA encoded by the human genome.

GAM337229 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337229 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337229 precursor RNA is designated SEQ ID:7211, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7211 is located from position 89060884 to position 89060970 relative to chromosome 16 on the `+` strand.

GAM337229 precursor RNA folds onto itself, forming GAM337229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337229 precursor RNA, designated SEQ ID NO: 7211, and a schematic representation of a predicted secondary folding of GAM337229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337229 folded precursor RNA yielding a GAM337229 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337229 RNA, hereby incorporated herein.

GAM337229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337229 target RNA, herein designated GAM TARGET RNA.

GAM337229 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337229 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337229 RNA, herein designated GAM RNA, to target binding sites on GAM337229 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337229 target RNA into GAM337229 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337229 target genes. The mRNA of each one of this plurality of GAM337229 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM337229 RNA, herein designated GAM RNA, and which when bound by GAM337229 RNA causes inhibition of translation of the GAM337229 target mRNA into a corresponding GAM337229 target protein.

The mechanism of the translational inhibition exerted by GAM337229 RNA, herein designated GAM RNA, on one or more GAM337229 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337229 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337229 RNA, herein designated GAM RNA, of GAM337229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337229 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337229 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337229 RNA correlate with, and may be deduced from, the identity of the GAM337229 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337230 6118 CCTGCCCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
AACTCCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CTTATTCACC Messenger 337230 (GAM337230) oligonucleotides modulates expression of respective target
AACCACTCCA genes whose function and utility is known in the art.

CCAGCTCTGA GAM337230 is a novel bioinformatically detectable regulatory, non protein
CCCTGACTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337230 was detected
TGGGGTTCCC is described with additional reference to Figs. 9-15.

ATCTCAGTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAGCCTGTG encoded by the human genome.

CTGCTGCCCC GAM337230 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTGAAGAGCA GAM337230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

TCCTTCCAGG GAM337230 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337230 precursor RNA is designated SEQ ID:6118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6118 is located from position 89181165 to position 89181284 relative to chromosome 9 on the `-` strand.

GAM337230 precursor RNA folds onto itself, forming GAM337230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337230 precursor RNA, designated SEQ ID NO: 6118, and a schematic representation of a predicted secondary folding of GAM337230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337230 folded precursor RNA yielding a GAM337230 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337230 RNA, hereby incorporated herein.

GAM337230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337230 target RNA, herein designated GAM TARGET RNA.

GAM337230 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337230 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337230 RNA, herein designated GAM RNA, to target

binding sites on GAM337230 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337230 target RNA into GAM337230 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337230 target genes. The mRNA of each one of this plurality of GAM337230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337230 RNA, herein designated GAM RNA, and which when bound by GAM337230 RNA causes inhibition of translation of the GAM337230 target mRNA into a corresponding GAM337230 target protein.

The mechanism of the translational inhibition exerted by GAM337230 RNA, herein designated GAM RNA, on one or more GAM337230 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337230 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337230 RNA, herein designated GAM RNA, of GAM337230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337230 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337230 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337230 RNA correlate with, and may be deduced from, the identity of the GAM337230 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337232 6207 CTGAGTTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATAGGGAACT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGGGTTTA Messenger 337232 (GAM337232) oligonucleotides modulates expression of respective target

AAGTCACCGT genes whose function and utility is known in the art.

TGGAACTACA GAM337232 is a novel bioinformatically detectable regulatory, non protein

CTGTGTGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337232 was detected

TTATAAACTT is described with additional reference to Figs. 9-15.

ATGTTCCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTATCATAT encoded by the human genome.

TCTTGGCTCA GAM337232 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

G GAM337232 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337232 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337232 precursor RNA is designated SEQ ID:6207, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6207 is located from position 89243160 to position 89243260 relative to chromosome 11 on the `-` strand.

GAM337232 precursor RNA folds onto itself, forming GAM337232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337232 precursor RNA, designated SEQ ID NO: 6207, and a schematic representation of a predicted secondary folding of GAM337232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337232 folded precursor RNA yielding a GAM337232 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337232 RNA, hereby incorporated herein.

GAM337232 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337232 target RNA, herein designated GAM TARGET RNA.

GAM337232 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337232 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337232 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337232 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337232 RNA, herein designated GAM RNA, to target binding sites on GAM337232 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337232 target RNA into GAM337232 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337232 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337232 target genes. The mRNA of each one of this plurality of GAM337232 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337232 RNA, herein designated GAM RNA, and which when bound by GAM337232 RNA causes inhibition of translation of the GAM337232 target mRNA into a corresponding GAM337232 target protein.

The mechanism of the translational inhibition exerted by GAM337232 RNA, herein designated GAM RNA, on one or more GAM337232 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337232 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337232 RNA, herein designated GAM RNA, of GAM337232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337232 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337232 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337232 RNA correlate with, and may be deduced from, the identity of the GAM337232 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337233 6719 GGATCGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCGAGGCTG Messenger 337233 (GAM337233) oligonucleotides modulates expression of respective target
CAGTGAGCTG genes whose function and utility is known in the art.

TGATCACACC GAM337233 is a novel bioinformatically detectable regulatory, non protein
ACTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337233 was detected
AGCCTGGGCA is described with additional reference to Figs. 9-15.

ACAGAGCGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACC encoded by the human genome.

GAM337233 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337233 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337233 precursor RNA is designated SEQ ID:6719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6719 is located from position 89325453 to position 89325535 relative to chromosome 14 on the `-` strand.

GAM337233 precursor RNA folds onto itself, forming GAM337233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337233 precursor RNA, designated SEQ ID NO: 6719, and a schematic representation of a predicted secondary folding of GAM337233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337233 folded precursor RNA yielding a GAM337233 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337233 RNA, hereby incorporated herein. Expression of GAM337233 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337233 target RNA, herein designated GAM TARGET RNA.

GAM337233 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337233 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337233 RNA, herein designated GAM RNA, to target binding sites on GAM337233 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337233 target RNA into GAM337233 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337233 target genes. The mRNA of each one of this plurality of GAM337233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337233 RNA, herein designated GAM RNA, and which when bound by GAM337233 RNA causes inhibition of translation of the GAM337233 target mRNA into a corresponding GAM337233 target protein.

The mechanism of the translational inhibition exerted by GAM337233 RNA, herein designated GAM RNA, on one or more GAM337233 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337233 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337233 RNA, herein designated GAM RNA, of GAM337233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337233 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337233 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337233 RNA correlate with, and may be deduced from, the identity of the GAM337233 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337234 7060 TCGCTTGAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGAGTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCTGCAG Messenger 337234 (GAM337234) oligonucleotides modulates expression of respective target
TGAGCTGTGA genes whose function and utility is known in the art.

TCACACCACT GAM337234 is a novel bioinformatically detectable regulatory, non protein
GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337234 was detected
CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGCGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337234 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337234 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337234 precursor RNA is designated SEQ ID:7060, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7060 is located from position 89325457 to position 89325532 relative to chromosome 14 on the `-` strand.

GAM337234 precursor RNA folds onto itself, forming GAM337234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337234 precursor RNA, designated SEQ ID NO: 7060, and a schematic representation of a predicted secondary folding of GAM337234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337234 folded precursor RNA yielding a GAM337234 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337234 RNA, hereby incorporated herein. Expression of GAM337234 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337234 target RNA, herein designated GAM TARGET RNA.

GAM337234 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337234 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337234 RNA, herein designated GAM RNA, to target binding sites on GAM337234 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337234 target RNA into GAM337234 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337234 target genes. The mRNA of each one of this plurality of GAM337234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337234 RNA, herein designated GAM RNA, and which when bound by GAM337234 RNA causes inhibition of translation of the GAM337234 target mRNA into a corresponding GAM337234 target protein.

The mechanism of the translational inhibition exerted by GAM337234 RNA, herein designated GAM RNA, on one or more GAM337234 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337234 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337234 RNA, herein designated GAM RNA, of

GAM337234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337234 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337234 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337234 RNA correlate with, and may be deduced from, the identity of the GAM337234 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337235 6142 CGCTTGAGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGAGTTCG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337235 (GAM337235) oligonucleotides modulates expression of respective target

GAGCTGTGAT genes whose function and utility is known in the art.

CACACCACTG GAM337235 is a novel bioinformatically detectable regulatory, non protein

CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337235 was detected

TGGGCAACAG is described with additional reference to Figs. 9-15.

AGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337235 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337235 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337235 precursor RNA is designated SEQ ID:6142, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6142 is located from position 89325458 to position 89325531 relative to chromosome 14 on the `-` strand.

GAM337235 precursor RNA folds onto itself, forming GAM337235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337235 precursor RNA, designated SEQ ID NO: 6142, and

a schematic representation of a predicted secondary folding of GAM337235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337235 folded precursor RNA yielding a GAM337235 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337235 RNA, hereby incorporated herein. Expression of GAM337235 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337235 target RNA, herein designated GAM TARGET RNA.

GAM337235 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337235 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337235 RNA, herein designated GAM RNA, to target binding sites on GAM337235 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337235 target RNA into GAM337235 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337235 target genes. The mRNA of each one of this plurality of GAM337235 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337235 RNA, herein designated GAM RNA, and which when bound by GAM337235 RNA causes inhibition of translation of the GAM337235 target mRNA into a corresponding GAM337235 target protein.

The mechanism of the translational inhibition exerted by GAM337235 RNA, herein designated GAM RNA, on one or more GAM337235 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337235 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337235 RNA, herein designated GAM RNA, of GAM337235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337235 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337235 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337235 RNA correlate with, and may be deduced from, the identity of the GAM337235 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337237 6415 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAAG Messenger 337237 (GAM337237) oligonucleotides modulates expression of respective target

CAGAGGTTGC genes whose function and utility is known in the art.

GGTGAGCTGA GAM337237 is a novel bioinformatically detectable regulatory, non protein

ATCATGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337237 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGCAGCAC encoded by the human genome.

TTCGTCTC GAM337237 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337237 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337237 precursor RNA is designated SEQ ID:6415, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6415 is located from position 89368234 to position 89368331 relative to chromosome 4 on the `+` strand.

GAM337237 precursor RNA folds onto itself, forming GAM337237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337237 precursor RNA, designated SEQ ID NO: 6415, and a schematic representation of a predicted secondary folding of GAM337237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337237 folded precursor RNA yielding a GAM337237 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337237 RNA, hereby incorporated herein. Expression of GAM337237 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337237 target RNA, herein designated GAM TARGET RNA.

GAM337237 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337237 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337237 RNA, herein designated GAM RNA, to target binding sites on GAM337237 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337237 target RNA into GAM337237 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337237 target genes. The mRNA of each one of this plurality of GAM337237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337237 RNA, herein designated GAM RNA, and which when bound by GAM337237 RNA causes inhibition of translation of the GAM337237 target mRNA into a corresponding GAM337237 target protein.

The mechanism of the translational inhibition exerted by GAM337237 RNA, herein designated GAM RNA, on one or more GAM337237 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337237 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337237 RNA, herein designated GAM RNA, of GAM337237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337237 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337237 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337237 RNA correlate with, and may be deduced from, the identity of the GAM337237 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337238 6681 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGCAGAGG Messenger 337238 (GAM337238) oligonucleotides modulates expression of respective target
TTGCGGTGAG genes whose function and utility is known in the art.

CTGAATCATG GAM337238 is a novel bioinformatically detectable regulatory, non protein
CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337238 was detected
CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCACTTC encoded by the human genome.

GAM337238 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337238 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337238 precursor RNA is designated SEQ ID:6681, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6681 is located from position 89368240 to position 89368326 relative to chromosome 4 on the `+` strand.

GAM337238 precursor RNA folds onto itself, forming GAM337238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337238 precursor RNA, designated SEQ ID NO: 6681, and a schematic representation of a predicted secondary folding of GAM337238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337238 folded precursor RNA yielding a GAM337238 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337238 RNA, hereby incorporated herein. Expression of GAM337238 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337238 target RNA, herein designated GAM TARGET RNA.

GAM337238 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337238 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337238 RNA, herein designated GAM RNA, to target binding sites on GAM337238 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337238 target RNA into GAM337238 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337238 target genes. The mRNA of each one of this plurality of GAM337238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337238 RNA, herein designated GAM RNA, and which when bound by GAM337238 RNA causes inhibition of translation of the GAM337238 target mRNA into a corresponding GAM337238 target protein.

The mechanism of the translational inhibition exerted by GAM337238 RNA, herein designated GAM RNA, on one or more GAM337238 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337238 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337238 RNA, herein designated GAM RNA, of GAM337238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337238 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337238 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337238 RNA correlate with, and may be deduced from, the identity of the GAM337238 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337242 7196 TGCATGCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAAATCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

CTGTCTCATT Messenger 337242 (GAM337242) oligonucleotides modulates expression of respective target

TGTCTGTTGG genes whose function and utility is known in the art.

AAATACAGTT GAM337242 is a novel bioinformatically detectable regulatory, non protein
CTGGCACTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337242 was detected
GATATGGTGA is described with additional reference to Figs. 9-15.

ACAGACAGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAGGCCACA encoded by the human genome.

ACATTCA GAM337242 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337242 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337242 precursor RNA is designated SEQ ID:7196, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7196 is located from position 89742768 to position 89742864 relative to chromosome 7 on the `+` strand.

GAM337242 precursor RNA folds onto itself, forming GAM337242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337242 precursor RNA, designated SEQ ID NO: 7196, and a schematic representation of a predicted secondary folding of GAM337242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337242 folded precursor RNA yielding a GAM337242 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337242 RNA, hereby incorporated herein.

GAM337242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337242 target RNA, herein designated GAM TARGET RNA.

GAM337242 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337242 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337242 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337242 RNA, herein designated GAM RNA, to target binding sites on GAM337242 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337242 target RNA into GAM337242 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337242 target genes. The mRNA of each one of this plurality of GAM337242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337242 RNA, herein designated GAM RNA, and which when bound by GAM337242 RNA causes inhibition of translation of the GAM337242 target mRNA into a corresponding GAM337242 target protein.

The mechanism of the translational inhibition exerted by GAM337242 RNA, herein designated GAM RNA, on one or more GAM337242 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337242 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337242 RNA, herein designated GAM RNA, of GAM337242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337242 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337242 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337242 RNA correlate with, and may be deduced from, the identity of the GAM337242 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337243 6940 GTTCTCTATG Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTAGGCAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAAGAAACAG Messenger 337243 (GAM337243) oligonucleotides modulates expression of respective target
CACCCTTCAT genes whose function and utility is known in the art.

ATTTTAAGGG GAM337243 is a novel bioinformatically detectable regulatory, non protein
ACTGTGCTAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337243 was detected
ATTTCTTCAT is described with additional reference to Figs. 9-15.

TCTTGGCGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTGAGAAT encoded by the human genome.

GAM337243 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337243 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337243 precursor RNA is designated SEQ ID:6940, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6940 is located from position 89931751 to position 89931839 relative to chromosome 14 on the `+` strand.

GAM337243 precursor RNA folds onto itself, forming GAM337243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337243 precursor RNA, designated SEQ ID NO: 6940, and a schematic representation of a predicted secondary folding of GAM337243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337243 folded precursor RNA yielding a GAM337243 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337243 RNA, hereby incorporated herein.

GAM337243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337243 target RNA, herein designated GAM TARGET RNA.

GAM337243 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337243 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337243 RNA, herein designated GAM RNA, to target binding sites on GAM337243 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337243 target RNA into GAM337243 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337243 target genes. The mRNA of each one of this plurality of GAM337243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337243 RNA, herein designated GAM RNA, and which when bound by GAM337243 RNA causes inhibition of translation of the GAM337243 target mRNA into a corresponding GAM337243 target protein.

The mechanism of the translational inhibition exerted by GAM337243 RNA, herein designated GAM RNA, on one or more GAM337243 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337243 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337243 RNA, herein designated GAM RNA, of GAM337243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337243 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337243 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337243 RNA correlate with, and may be deduced from, the identity of the GAM337243 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337245 6950 GTTTTTACTA Fig. 8 further provides a conceptual description of another novel bioinformatically
TAACATATTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TAGAAAGCTA Messenger 337245 (GAM337245) oligonucleotides modulates expression of respective target
ACAAGCTAGA genes whose function and utility is known in the art.

GAGAGCGGTG GAM337245 is a novel bioinformatically detectable regulatory, non protein
AAGGGCTCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337245 was detected
TCAGCATGTT is described with additional reference to Figs. 9-15.

CCTCTCTGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTGTGTTAG encoded by the human genome.

TTTTGC GAM337245 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337245 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337245 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337245 precursor RNA is designated SEQ ID:6950, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6950 is located from position 90083877 to position 90083972 relative to chromosome 11 on the `+` strand.

GAM337245 precursor RNA folds onto itself, forming GAM337245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337245 precursor RNA, designated SEQ ID NO: 6950, and a schematic representation of a predicted secondary folding of GAM337245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337245 folded precursor RNA yielding a GAM337245 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337245 RNA, hereby incorporated herein.

GAM337245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337245 target RNA, herein designated GAM TARGET RNA.

GAM337245 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337245 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337245 RNA, herein designated GAM RNA, to target binding sites on GAM337245 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337245 target RNA into GAM337245 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337245 target genes. The mRNA of each one of this plurality of GAM337245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337245 RNA, herein designated GAM RNA, and which when bound by GAM337245 RNA causes inhibition of translation of the GAM337245 target mRNA into a corresponding GAM337245 target protein.

The mechanism of the translational inhibition exerted by GAM337245 RNA, herein designated GAM RNA, on one or more GAM337245 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337245 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337245 RNA, herein designated GAM RNA, of

GAM337245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337245 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337245 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337245 RNA correlate with, and may be deduced from, the identity of the GAM337245 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337246 6955 TAACATATTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TAGAAAGCTA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAAGCTAGA Messenger 337246 (GAM337246) oligonucleotides modulates expression of respective target

GAGAGCGGTG genes whose function and utility is known in the art.

AAGGGCTCTC GAM337246 is a novel bioinformatically detectable regulatory, non protein

TCAGCATGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337246 was detected

CCTCTCTGTC is described with additional reference to Figs. 9-15.

TGTGTGTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337246 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337246 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337246 precursor RNA is designated SEQ ID:6955, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6955 is located from position 90083887 to position 90083965 relative to chromosome 11 on the `+` strand.

GAM337246 precursor RNA folds onto itself, forming GAM337246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337246 precursor RNA, designated SEQ ID NO: 6955, and

a schematic representation of a predicted secondary folding of GAM337246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337246 folded precursor RNA yielding a GAM337246 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337246 RNA, hereby incorporated herein.

GAM337246 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337246 target RNA, herein designated GAM TARGET RNA.

GAM337246 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337246 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337246 RNA, herein designated GAM RNA, to target binding sites on GAM337246 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337246 target RNA into GAM337246 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337246 target genes. The mRNA of each one of this plurality of GAM337246 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337246 RNA, herein designated GAM RNA, and which when bound by GAM337246 RNA causes inhibition of translation of the GAM337246 target mRNA into a corresponding GAM337246 target protein.

The mechanism of the translational inhibition exerted by GAM337246 RNA, herein designated GAM RNA, on one or more GAM337246 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337246 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337246 RNA, herein designated GAM RNA, of GAM337246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337246 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337246 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337246 RNA correlate with, and may be deduced from, the identity of the GAM337246 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337247 6879 GTCCCCTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTTTCTACC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATACCCCCAG Messenger 337247 (GAM337247) oligonucleotides modulates expression of respective target

TAAAGCTACT genes whose function and utility is known in the art.

TAAAATCCTC GAM337247 is a novel bioinformatically detectable regulatory, non protein

TGTAGGAAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337247 was detected

AGCTGAGTAA is described with additional reference to Figs. 9-15.

TTGGGGGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGATGGAGGA encoded by the human genome.

C GAM337247 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337247 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337247 precursor RNA is designated SEQ ID:6879, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6879 is located from position 90114587 to position 90114677 relative to chromosome 11 on the `-` strand.

GAM337247 precursor RNA folds onto itself, forming GAM337247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337247 precursor RNA, designated SEQ ID NO: 6879, and a schematic representation of a predicted secondary folding of GAM337247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337247 folded precursor RNA yielding a GAM337247 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337247 RNA, hereby incorporated herein.

GAM337247 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337247 target RNA, herein designated GAM TARGET RNA.

GAM337247 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337247 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337247 RNA, herein designated GAM RNA, to target binding sites on GAM337247 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337247 target RNA into GAM337247 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337247 target genes. The mRNA of each one of this plurality of GAM337247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337247 RNA, herein designated GAM RNA, and which when bound by GAM337247 RNA causes inhibition of translation of the GAM337247 target mRNA into a corresponding GAM337247 target protein.

The mechanism of the translational inhibition exerted by GAM337247 RNA, herein designated GAM RNA, on one or more GAM337247 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337247 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337247 RNA, herein designated GAM RNA, of GAM337247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337247 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337247 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337247 RNA correlate with, and may be deduced from, the identity of the GAM337247 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337248 5903 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337248 (GAM337248) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337248 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337248 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337248 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337248 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337248 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337248 precursor RNA is designated SEQ

ID:5903, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5903 is located from position 90495199 to position 90495280 relative to chromosome 11 on the `+` strand.

GAM337248 precursor RNA folds onto itself, forming GAM337248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337248 precursor RNA, designated SEQ ID NO: 5903, and a schematic representation of a predicted secondary folding of GAM337248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337248 folded precursor RNA yielding a GAM337248 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337248 RNA, hereby incorporated herein.

GAM337248 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337248 target RNA, herein designated GAM TARGET RNA.

GAM337248 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337248 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337248 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337248 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337248 RNA, herein designated GAM RNA, to target binding sites on GAM337248 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337248 target RNA into GAM337248 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337248 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337248 target genes. The mRNA of each one of this plurality of GAM337248 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337248 RNA, herein designated GAM RNA, and which when bound by GAM337248 RNA causes inhibition of translation of the GAM337248 target mRNA into a corresponding GAM337248 target protein.

The mechanism of the translational inhibition exerted by GAM337248 RNA, herein designated GAM RNA, on one or more GAM337248 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337248 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337248 RNA, herein designated GAM RNA, of GAM337248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337248 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337248 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337248 RNA correlate with, and may be deduced from, the identity of the GAM337248 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337250 5904 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337250 (GAM337250) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337250 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337250 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337250 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337250 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337250 precursor RNA is designated SEQ ID:5904, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5904 is located from position 91509421 to position 91509502 relative to chromosome 14 on the `-` strand.

GAM337250 precursor RNA folds onto itself, forming GAM337250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337250 precursor RNA, designated SEQ ID NO: 5904, and a schematic representation of a predicted secondary folding of GAM337250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337250 folded precursor RNA yielding a GAM337250 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337250 RNA, hereby incorporated herein.

GAM337250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337250 target RNA, herein designated GAM TARGET RNA.

GAM337250 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337250 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337250 RNA, herein designated GAM RNA, to target binding sites on GAM337250 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337250 target RNA into GAM337250 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337250 target genes. The mRNA of each one of this plurality of GAM337250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337250 RNA, herein designated GAM RNA, and which when bound by GAM337250 RNA causes inhibition of translation of the GAM337250 target mRNA into a corresponding GAM337250 target protein.

The mechanism of the translational inhibition exerted by GAM337250 RNA, herein designated GAM RNA, on one or more GAM337250 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337250 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337250 RNA, herein designated GAM RNA, of GAM337250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337250 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337250 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337250 RNA correlate with, and may be deduced from, the identity of the GAM337250 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337251 6837 GGTCGAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGTATCGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGAGCCCAG Messenger 337251 (GAM337251) oligonucleotides modulates expression of respective target

GAGTTTGAGT genes whose function and utility is known in the art.

CCAGCCTGGG GAM337251 is a novel bioinformatically detectable regulatory, non protein
CAACATAGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337251 was detected
AGACCTTGTC is described with additional reference to Figs. 9-15.

TTGACC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337251 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337251 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337251 precursor RNA is designated SEQ ID:6837, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6837 is located from position 91699065 to position 91699140 relative to chromosome 10 on the `+` strand.

GAM337251 precursor RNA folds onto itself, forming GAM337251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337251 precursor RNA, designated SEQ ID NO: 6837, and a schematic representation of a predicted secondary folding of GAM337251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337251 folded precursor RNA yielding a GAM337251 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337251 RNA, hereby incorporated herein.

GAM337251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337251 target RNA, herein designated GAM TARGET RNA.

GAM337251 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337251 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337251 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337251 RNA, herein designated GAM RNA, to target binding sites on GAM337251 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337251 target RNA into GAM337251 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337251 target genes. The mRNA of each one of this plurality of GAM337251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337251 RNA, herein designated GAM RNA, and which when bound by GAM337251 RNA causes inhibition of translation of the GAM337251 target mRNA into a corresponding GAM337251 target protein.

The mechanism of the translational inhibition exerted by GAM337251 RNA, herein designated GAM RNA, on one or more GAM337251 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337251 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337251 RNA, herein designated GAM RNA, of GAM337251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337251 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337251 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337251 RNA correlate with, and may be deduced from, the identity of the GAM337251 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337254 5757 AGGAATTTGT Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGAAACTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCCTGTTTT Messenger 337254 (GAM337254) oligonucleotides modulates expression of respective target
GGTTTGGAGA genes whose function and utility is known in the art.

GTAGTTCTCT GAM337254 is a novel bioinformatically detectable regulatory, non protein
CTAACTAGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337254 was detected
ACAGGAGTGG is described with additional reference to Figs. 9-15.

CCTTGAAATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTCCT encoded by the human genome.

GAM337254 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337254 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337254 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337254 precursor RNA is designated SEQ ID:5757, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5757 is located from position 91841622 to position 91841706 relative to chromosome 7 on the `-` strand.

GAM337254 precursor RNA folds onto itself, forming GAM337254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337254 precursor RNA, designated SEQ ID NO: 5757, and a schematic representation of a predicted secondary folding of GAM337254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337254 folded precursor RNA yielding a GAM337254 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337254 RNA, hereby incorporated herein.

GAM337254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337254 target RNA, herein designated GAM TARGET RNA.

GAM337254 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337254 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337254 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337254 RNA, herein designated GAM RNA, to target binding sites on GAM337254 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337254 target RNA into GAM337254 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337254 target genes. The mRNA of each one of this plurality of GAM337254 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337254 RNA, herein designated GAM RNA, and which when bound by GAM337254 RNA causes inhibition of translation of the GAM337254 target mRNA into a corresponding GAM337254 target protein.

The mechanism of the translational inhibition exerted by GAM337254 RNA, herein designated GAM RNA, on one or more GAM337254 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337254 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337254 RNA, herein designated GAM RNA, of GAM337254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337254 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337254 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337254 RNA correlate with, and may be deduced from, the identity of the GAM337254 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337255 6961 TACCTTCTTT Fig. 8 further provides a conceptual description of another novel bioinformatically
GCTGCCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATGCTGCT Messenger 337255 (GAM337255) oligonucleotides modulates expression of respective target
ATGGGCGTTT genes whose function and utility is known in the art.

ATTTGATCTG GAM337255 is a novel bioinformatically detectable regulatory, non protein
CTTGTGGCTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337255 was detected
AGTTTGCTCA is described with additional reference to Figs. 9-15.

GCAGTGAAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAGGTG encoded by the human genome.

GAM337255 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337255 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337255 precursor RNA is designated SEQ ID:6961, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6961 is located from position 92455725 to position 92455811 relative to chromosome 14 on the `+` strand.

GAM337255 precursor RNA folds onto itself, forming GAM337255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337255 precursor RNA, designated SEQ ID NO: 6961, and a schematic representation of a predicted secondary folding of GAM337255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337255 folded precursor RNA yielding a GAM337255 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337255 RNA, hereby incorporated herein.

GAM337255 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337255 target RNA, herein designated GAM TARGET RNA.

GAM337255 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337255 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337255 RNA, herein designated GAM RNA, to target binding sites on GAM337255 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337255 target RNA into GAM337255 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337255 target genes. The mRNA of each one of this plurality of GAM337255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337255 RNA, herein designated GAM RNA, and which when bound by GAM337255 RNA causes inhibition of translation of the GAM337255 target mRNA into a corresponding GAM337255 target protein.

The mechanism of the translational inhibition exerted by GAM337255 RNA, herein designated GAM RNA, on one or more GAM337255 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337255 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337255 RNA, herein designated GAM RNA, of GAM337255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337255 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337255 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337255 RNA correlate with, and may be deduced from, the identity of the GAM337255 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337256 5700 ACCTTCTTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
CTGCCTGGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GATGCTGCTA Messenger 337256 (GAM337256) oligonucleotides modulates expression of respective target
TGGGCGTTTA genes whose function and utility is known in the art.

TTTGATCTGC GAM337256 is a novel bioinformatically detectable regulatory, non protein
TTGTGGCTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337256 was detected
GTTTGCTCAG is described with additional reference to Figs. 9-15.

CAGTGAAATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGGT encoded by the human genome.

GAM337256 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337256 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337256 precursor RNA is designated SEQ ID:5700, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5700 is located from position 92455726 to position 92455810 relative to chromosome 14 on the `+` strand.

GAM337256 precursor RNA folds onto itself, forming GAM337256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337256 precursor RNA, designated SEQ ID NO: 5700, and a schematic representation of a predicted secondary folding of GAM337256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337256 folded precursor RNA yielding a GAM337256 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337256 RNA, hereby incorporated herein.

GAM337256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337256 target RNA, herein designated GAM TARGET RNA.

GAM337256 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337256 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337256 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337256 RNA, herein designated GAM RNA, to target binding sites on GAM337256 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337256 target RNA into GAM337256 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337256 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337256 target genes. The mRNA of each one of this plurality of GAM337256 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337256 RNA, herein designated GAM RNA, and which when bound by GAM337256 RNA causes inhibition of translation of the GAM337256 target mRNA into a corresponding GAM337256 target protein.

The mechanism of the translational inhibition exerted by GAM337256 RNA, herein designated GAM RNA, on one or more GAM337256 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337256 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337256 RNA, herein designated GAM RNA, of GAM337256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337256 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337256 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337256 RNA correlate with, and may be deduced from, the identity of the GAM337256 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337257 6251 CTTACCCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTCATGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATACAAAGGA Messenger 337257 (GAM337257) oligonucleotides modulates expression of respective target

AGATGGCTGT genes whose function and utility is known in the art.

TTGGGGTTGC GAM337257 is a novel bioinformatically detectable regulatory, non protein

CGTGTCTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337257 was detected

AGCAATTAAG is described with additional reference to Figs. 9-15.

GAGATGGCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGCCAAGCA encoded by the human genome.

GTGTGAAGTG GAM337257 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

ACAGCACCAG GAM337257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337257 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337257 precursor RNA is designated SEQ ID:6251, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6251 is located from position 92938874 to position 92938983 relative to chromosome 10 on the `+` strand.

GAM337257 precursor RNA folds onto itself, forming GAM337257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337257 precursor RNA, designated SEQ ID NO: 6251, and a schematic representation of a predicted secondary folding of GAM337257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337257 folded precursor RNA yielding a GAM337257 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337257 RNA, hereby incorporated herein.

GAM337257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337257 target RNA, herein designated GAM TARGET RNA.

GAM337257 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337257 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337257 RNA, herein designated GAM RNA, to target binding sites on GAM337257 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337257 target RNA into GAM337257 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337257 target genes. The mRNA of each one of this plurality of GAM337257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337257 RNA, herein designated GAM RNA, and which when bound by GAM337257 RNA causes inhibition of translation of the GAM337257 target mRNA into a corresponding GAM337257 target protein.

The mechanism of the translational inhibition exerted by GAM337257 RNA, herein designated GAM RNA, on one or more GAM337257 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337257 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337257 RNA, herein designated GAM RNA, of GAM337257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337257 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337257 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337257 RNA correlate with, and may be deduced from, the identity of the GAM337257 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337258 6238 CTGTATTTCA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCAATACAA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGAAGATGG Messenger 337258 (GAM337258) oligonucleotides modulates expression of respective target

CTGTTTGGGG genes whose function and utility is known in the art.

TTGCCGTGTC GAM337258 is a novel bioinformatically detectable regulatory, non protein

TCTTAGCAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337258 was detected

TAAGGAGATG is described with additional reference to Figs. 9-15.

GCTACAGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCAGTGTGA encoded by the human genome.

AGTGACAG GAM337258 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337258 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337258 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337258 precursor RNA is designated SEQ ID:6238, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6238 is located from position 92938880 to position 92938977 relative to chromosome 10 on the `+` strand.

GAM337258 precursor RNA folds onto itself, forming GAM337258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337258 precursor RNA, designated SEQ ID NO: 6238, and a schematic representation of a predicted secondary folding of GAM337258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337258 folded precursor RNA yielding a GAM337258 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337258 RNA, hereby incorporated herein.

GAM337258 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337258 target RNA, herein designated GAM TARGET RNA.

GAM337258 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337258 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337258 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337258 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337258 RNA, herein designated GAM RNA, to target binding sites on GAM337258 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337258 target RNA into GAM337258 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM337258 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337258 target genes. The mRNA of each one of this plurality of GAM337258 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337258 RNA, herein designated GAM RNA, and which when bound by GAM337258 RNA causes inhibition of translation of the GAM337258 target mRNA into a corresponding GAM337258 target protein.

The mechanism of the translational inhibition exerted by GAM337258 RNA, herein designated GAM RNA, on one or more GAM337258 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337258 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337258 RNA, herein designated GAM RNA, of GAM337258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337258 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337258 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337258 RNA correlate with, and may be deduced from, the identity of the GAM337258 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337263 5905 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337263 (GAM337263) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337263 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337263 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337263 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337263 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337263 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337263 precursor RNA is designated SEQ ID:5905, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5905 is located from position 93264106 to position 93264187 relative to chromosome 10 on the `-` strand.

GAM337263 precursor RNA folds onto itself, forming GAM337263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337263 precursor RNA, designated SEQ ID NO: 5905, and a schematic representation of a predicted secondary folding of GAM337263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337263 folded precursor RNA yielding a GAM337263 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337263 RNA, hereby incorporated herein.

GAM337263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337263 target RNA, herein designated GAM TARGET RNA.

GAM337263 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337263 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337263 RNA, herein designated GAM RNA, to target binding sites on GAM337263 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337263 target RNA into GAM337263 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337263 target genes. The mRNA of each one of this plurality of GAM337263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337263 RNA, herein designated GAM RNA, and which when bound by GAM337263 RNA causes inhibition of translation of the GAM337263 target mRNA into a corresponding GAM337263 target protein.

The mechanism of the translational inhibition exerted by GAM337263 RNA, herein designated GAM RNA, on one or more GAM337263 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337263 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337263 RNA, herein designated GAM RNA, of GAM337263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337263 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337263 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337263 RNA correlate with, and may be deduced from, the identity of the GAM337263 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337264 7199 TGCCTCTCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCACTTCCAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTCCTACCT Messenger 337264 (GAM337264) oligonucleotides modulates expression of respective target

GTGATAGACG genes whose function and utility is known in the art.

TCTAAGTGAA GAM337264 is a novel bioinformatically detectable regulatory, non protein
AGTACTAGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337264 was detected
TAGTTGTTTG is described with additional reference to Figs. 9-15.

GGATTGGTAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGACAGAGAA encoded by the human genome.

AACAGCA GAM337264 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337264 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337264 precursor RNA is designated SEQ ID:7199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7199 is located from position 93648456 to position 93648552 relative to chromosome 9 on the `+` strand.

GAM337264 precursor RNA folds onto itself, forming GAM337264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337264 precursor RNA, designated SEQ ID NO: 7199, and a schematic representation of a predicted secondary folding of GAM337264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337264 folded precursor RNA yielding a GAM337264 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337264 RNA, hereby incorporated herein.

GAM337264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337264 target RNA, herein designated GAM TARGET RNA.

GAM337264 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337264 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337264 RNA, herein designated GAM RNA, to target binding sites on GAM337264 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337264 target RNA into GAM337264 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337264 target genes. The mRNA of each one of this plurality of GAM337264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337264 RNA, herein designated GAM RNA, and which when bound by GAM337264 RNA causes inhibition of translation of the GAM337264 target mRNA into a corresponding GAM337264 target protein.

The mechanism of the translational inhibition exerted by GAM337264 RNA, herein designated GAM RNA, on one or more GAM337264 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337264 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337264 RNA, herein designated GAM RNA, of GAM337264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337264 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337264 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337264 RNA correlate with, and may be deduced from, the identity of the GAM337264 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337265 7068 TCTCTGGCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCCAATCTC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTACCTGTGA Messenger 337265 (GAM337265) oligonucleotides modulates expression of respective target
TAGACGTCTA genes whose function and utility is known in the art.

AGTGAAAGTA GAM337265 is a novel bioinformatically detectable regulatory, non protein
CTAGCTTAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337265 was detected
TGTTTGGGAT is described with additional reference to Figs. 9-15.

TGGTAGTGAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGA encoded by the human genome.

GAM337265 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337265 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337265 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337265 precursor RNA is designated SEQ ID:7068, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7068 is located from position 93648460 to position 93648544 relative to chromosome 9 on the `+` strand.

GAM337265 precursor RNA folds onto itself, forming GAM337265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337265 precursor RNA, designated SEQ ID NO: 7068, and a schematic representation of a predicted secondary folding of GAM337265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337265 folded precursor RNA yielding a GAM337265 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337265 RNA, hereby incorporated herein.

GAM337265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337265 target RNA, herein designated GAM TARGET RNA.

GAM337265 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337265 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337265 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337265 RNA, herein designated GAM RNA, to target binding sites on GAM337265 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337265 target RNA into GAM337265 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337265 target genes. The mRNA of each one of this plurality of GAM337265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337265 RNA, herein designated GAM RNA, and which when bound by GAM337265 RNA causes inhibition of translation of the GAM337265 target mRNA into a corresponding GAM337265 target protein.

The mechanism of the translational inhibition exerted by GAM337265 RNA, herein designated GAM RNA, on one or more GAM337265 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337265 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337265 RNA, herein designated GAM RNA, of GAM337265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337265 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337265 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337265 RNA correlate with, and may be deduced from, the identity of the GAM337265 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337266 6176 CTCTGGCACT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCCAATCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TACCTGTGAT Messenger 337266 (GAM337266) oligonucleotides modulates expression of respective target
AGACGTCTAA genes whose function and utility is known in the art.

GTGAAAGTAC GAM337266 is a novel bioinformatically detectable regulatory, non protein
TAGCTTAGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337266 was detected
GTTTGGGATT is described with additional reference to Figs. 9-15.

GGTAGTGACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAG encoded by the human genome.

GAM337266 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337266 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337266 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337266 precursor RNA is designated SEQ ID:6176, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6176 is located from position 93648461 to position 93648543 relative to chromosome 9 on the `+` strand.

GAM337266 precursor RNA folds onto itself, forming GAM337266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337266 precursor RNA, designated SEQ ID NO: 6176, and a schematic representation of a predicted secondary folding of GAM337266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337266 folded precursor RNA yielding a GAM337266 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337266 RNA, hereby incorporated herein.

GAM337266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337266 target RNA, herein designated GAM TARGET RNA.

GAM337266 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337266 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337266 RNA, herein designated GAM RNA, to target binding sites on GAM337266 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337266 target RNA into GAM337266 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337266 target genes. The mRNA of each one of this plurality of GAM337266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337266 RNA, herein designated GAM RNA, and which when bound by GAM337266 RNA causes inhibition of translation of the GAM337266 target mRNA into a corresponding GAM337266 target protein.

The mechanism of the translational inhibition exerted by GAM337266 RNA, herein designated GAM RNA, on one or more GAM337266 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337266 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337266 RNA, herein designated GAM RNA, of GAM337266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337266 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337266 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337266 RNA correlate with, and may be deduced from, the identity of the GAM337266 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337267 6155 CTATGCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
CATTGGAAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGTAGAGGCC Messenger 337267 (GAM337267) oligonucleotides modulates expression of respective target
CTTACTAGCA genes whose function and utility is known in the art.

CACCTCAAAT GAM337267 is a novel bioinformatically detectable regulatory, non protein
CAAACTGGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337267 was detected
TTGCAGCAGA is described with additional reference to Figs. 9-15.

CCTTTTGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTTTAGAGG encoded by the human genome.

CTGGAAATAG GAM337267 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337267 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337267 precursor RNA is designated SEQ ID:6155, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6155 is located from position 93666704 to position 93666803 relative to chromosome X on the `+` strand.

GAM337267 precursor RNA folds onto itself, forming GAM337267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337267 precursor RNA, designated SEQ ID NO: 6155, and a schematic representation of a predicted secondary folding of GAM337267 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337267 folded precursor RNA yielding a GAM337267 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337267 RNA, hereby incorporated herein.

GAM337267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337267 target RNA, herein designated GAM TARGET RNA.

GAM337267 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337267 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337267 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337267 RNA, herein designated GAM RNA, to target binding sites on GAM337267 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337267 target RNA into GAM337267 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337267 target genes. The mRNA of each one of this plurality of GAM337267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337267 RNA, herein designated GAM RNA, and which when bound by GAM337267 RNA causes inhibition of translation of the GAM337267 target mRNA into a corresponding GAM337267 target protein.

The mechanism of the translational inhibition exerted by GAM337267 RNA, herein designated GAM RNA, on one or more GAM337267 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337267 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337267 RNA, herein designated GAM RNA, of GAM337267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337267 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337267 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337267 RNA correlate with, and may be deduced from, the identity of the GAM337267 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337269 7072 TCTGATCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GAACTGCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTTGGTGGT Messenger 337269 (GAM337269) oligonucleotides modulates expression of respective target

CAGGAGGGGT genes whose function and utility is known in the art.

TCTTAGTAAG GAM337269 is a novel bioinformatically detectable regulatory, non protein

CAAACTCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337269 was detected

TTAATCCCAG is described with additional reference to Figs. 9-15.

AGTCGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337269 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337269 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337269 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337269 precursor RNA is designated SEQ ID:7072, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7072 is located from position 94289451 to position 94289527 relative to chromosome 15 on the `-` strand.

GAM337269 precursor RNA folds onto itself, forming GAM337269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337269 precursor RNA, designated SEQ ID NO: 7072, and a schematic representation of a predicted secondary folding of GAM337269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337269 folded precursor RNA yielding a GAM337269 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337269 RNA, hereby incorporated herein.

GAM337269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337269 target RNA, herein designated GAM TARGET RNA.

GAM337269 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337269 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337269 RNA, herein designated GAM RNA, to target binding sites on GAM337269 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337269 target RNA into GAM337269 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337269 target genes. The mRNA of each one of this plurality of GAM337269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337269 RNA, herein designated GAM RNA, and which when bound by GAM337269 RNA causes inhibition of translation of the GAM337269 target mRNA into a corresponding GAM337269 target protein.

The mechanism of the translational inhibition exerted by GAM337269 RNA, herein designated GAM RNA, on one or more GAM337269 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337269 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337269 RNA, herein designated GAM RNA, of GAM337269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337269 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337269 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337269 RNA correlate with, and may be deduced from, the identity of the GAM337269 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337270 6515 GCGATCTCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

AACAATTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGCTGAACA Messenger 337270 (GAM337270) oligonucleotides modulates expression of respective target

GCCTCACCAG genes whose function and utility is known in the art.

CATGCCATGT GAM337270 is a novel bioinformatically detectable regulatory, non protein

ACTACCTCCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337270 was detected

CTTGCTGATG is described with additional reference to Figs. 9-15.

ACTGAAGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTGGACTAA encoded by the human genome.

AGATGAGTTA GAM337270 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAAGAAGC GAM337270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337270 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337270 precursor RNA is designated SEQ ID:6515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6515 is located from position 94365822 to position 94365929 relative to chromosome 10 on the `-` strand.

GAM337270 precursor RNA folds onto itself, forming GAM337270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337270 precursor RNA, designated SEQ ID NO: 6515, and a schematic representation of a predicted secondary folding of GAM337270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337270 folded precursor RNA yielding a GAM337270 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337270 RNA, hereby incorporated herein.

GAM337270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337270 target RNA, herein designated GAM TARGET RNA.

GAM337270 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337270 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337270 RNA, herein designated GAM RNA, to target binding sites on GAM337270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337270 target RNA into GAM337270 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM337270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337270 target genes. The mRNA of each one of this plurality of GAM337270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337270 RNA, herein designated GAM RNA, and which when bound by GAM337270 RNA causes inhibition of translation of the GAM337270 target mRNA into a corresponding GAM337270 target protein.

The mechanism of the translational inhibition exerted by GAM337270 RNA, herein designated GAM RNA, on one or more GAM337270 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337270 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337270 RNA, herein designated GAM RNA, of GAM337270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337270 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337270 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337270 RNA correlate with, and may be deduced from, the identity of the GAM337270 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337271 7070 TCTCTTAACA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTCCGGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGAACAGCCT Messenger 337271 (GAM337271) oligonucleotides modulates expression of respective target

CACCAGCATG genes whose function and utility is known in the art.

CCATGTACTA GAM337271 is a novel bioinformatically detectable regulatory, non protein

CCTCCGCTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337271 was detected

CTGATGACTG is described with additional reference to Figs. 9-15.

AAGTGGCCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACTAAAGAT encoded by the human genome.

GAGTTAAAAG GAM337271 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337271 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337271 precursor RNA is designated SEQ ID:7070, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7070 is located from position 94365825 to position 94365925 relative to chromosome 10 on the `-` strand.

GAM337271 precursor RNA folds onto itself, forming GAM337271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337271 precursor RNA, designated SEQ ID NO: 7070, and a schematic representation of a predicted secondary folding of GAM337271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337271 folded precursor RNA yielding a GAM337271 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337271 RNA, hereby incorporated herein.

GAM337271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337271 target RNA, herein designated GAM TARGET RNA.

GAM337271 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337271 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337271 RNA, herein designated GAM RNA, to target binding sites on GAM337271 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337271 target RNA into GAM337271 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337271 target genes. The mRNA of each one of this plurality of GAM337271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337271 RNA, herein designated GAM RNA, and which when bound by GAM337271 RNA causes inhibition of translation of the GAM337271 target mRNA into a corresponding GAM337271 target protein.

The mechanism of the translational inhibition exerted by GAM337271 RNA, herein designated GAM RNA, on one or more GAM337271 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337271 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337271 RNA, herein designated GAM RNA, of GAM337271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337271 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337271 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337271 RNA correlate with, and may be deduced from, the identity of the GAM337271 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337273 6141 CGCTTGAGCC Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGGAGGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTTGCAGT Messenger 337273 (GAM337273) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

GGCACCACTG GAM337273 is a novel bioinformatically detectable regulatory, non protein CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337273 was detected TGGGCAACAG is described with additional reference to Figs. 9-15.

TG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337273 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337273 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337273 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337273 precursor RNA is designated SEQ ID:6141, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6141 is located from position 94706874 to position 94706945 relative to chromosome 1 on the `+` strand.

GAM337273 precursor RNA folds onto itself, forming GAM337273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337273 precursor RNA, designated SEQ ID NO: 6141, and a schematic representation of a predicted secondary folding of GAM337273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337273 folded precursor RNA yielding a GAM337273 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337273 RNA, hereby incorporated herein. Expression of GAM337273 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337273 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337273 target RNA, herein designated GAM TARGET RNA.

GAM337273 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337273 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337273 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337273 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337273 RNA, herein designated GAM RNA, to target binding sites on GAM337273 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337273 target RNA into GAM337273 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337273 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337273 target genes. The mRNA of each one of this plurality of GAM337273 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337273 RNA, herein designated GAM RNA, and which when bound by GAM337273 RNA causes inhibition of translation of the GAM337273 target mRNA into a corresponding GAM337273 target protein.

The mechanism of the translational inhibition exerted by GAM337273 RNA, herein designated GAM RNA, on one or more GAM337273 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337273 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337273 RNA, herein designated GAM RNA, of GAM337273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337273 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337273 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337273 RNA correlate with, and may be deduced from, the identity of the GAM337273 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337274 6350 GAGACTCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
CGTTCTACTG detected oligonucleotides of the present invention, referred to here as Genomic Address
GCAACTGGAG Messenger 337274 (GAM337274) oligonucleotides modulates expression of respective target
TTTGTTCAAG genes whose function and utility is known in the art.

AAATACCTGA GAM337274 is a novel bioinformatically detectable regulatory, non protein
GTTGGTTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337274 was detected
TAACTGTCGA is described with additional reference to Figs. 9-15.

GTTCGATTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCAAGTGGAA encoded by the human genome.

GGGTGGGAGT GAM337274 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTC GAM337274 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337274 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337274 precursor RNA is designated SEQ ID:6350, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6350 is located from position 94819576 to position 94819678 relative to chromosome 15 on the `-` strand.

GAM337274 precursor RNA folds onto itself, forming GAM337274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337274 precursor RNA, designated SEQ ID NO: 6350, and a schematic representation of a predicted secondary folding of GAM337274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337274 folded precursor RNA yielding a GAM337274 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337274 RNA, hereby incorporated herein.

GAM337274 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337274 target RNA, herein designated GAM TARGET RNA.

GAM337274 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337274 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337274 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337274 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337274 RNA, herein designated GAM RNA, to target binding sites on GAM337274 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337274 target RNA into GAM337274 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337274 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337274 target genes. The mRNA of each one of this plurality of GAM337274 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337274 RNA, herein designated GAM RNA, and which when bound by GAM337274 RNA causes inhibition of translation of the GAM337274 target mRNA into a corresponding GAM337274 target protein.

The mechanism of the translational inhibition exerted by GAM337274 RNA, herein designated GAM RNA, on one or more GAM337274 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337274 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337274 RNA, herein designated GAM RNA, of GAM337274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337274 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337274 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337274 RNA correlate with, and may be deduced from, the identity of the GAM337274 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337275 6156 CTCACCCGTT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTACTGGCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGAGTTTG Messenger 337275 (GAM337275) oligonucleotides modulates expression of respective target
TTCAAGAAAT genes whose function and utility is known in the art.

ACCTGAGTTG GAM337275 is a novel bioinformatically detectable regulatory, non protein
GTTCTTTAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337275 was detected
TGTCGAGTTC is described with additional reference to Figs. 9-15.

GATTGTCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGGAAGGGT encoded by the human genome.

GGG GAM337275 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337275 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337275 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337275 precursor RNA is designated SEQ ID:6156, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6156 is located from position 94819582 to position 94819674 relative to chromosome 15 on the `-` strand.

GAM337275 precursor RNA folds onto itself, forming GAM337275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337275 precursor RNA, designated SEQ ID NO: 6156, and a schematic representation of a predicted secondary folding of GAM337275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337275 folded precursor RNA yielding a GAM337275 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337275 RNA, hereby incorporated herein.

GAM337275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337275 target RNA, herein designated GAM TARGET RNA.

GAM337275 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337275 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337275 RNA, herein designated GAM RNA, to target binding sites on GAM337275 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337275 target RNA into GAM337275 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337275 target genes. The mRNA of each one of this plurality of GAM337275 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337275 RNA, herein designated GAM RNA, and which when bound by GAM337275 RNA causes inhibition of translation of the GAM337275 target mRNA into a corresponding GAM337275 target protein.

The mechanism of the translational inhibition exerted by GAM337275 RNA, herein designated GAM RNA, on one or more GAM337275 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337275 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337275 RNA, herein designated GAM RNA, of GAM337275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337275 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337275 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337275 RNA correlate with, and may be deduced from, the identity of the GAM337275 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337277 6121 CCTGGAGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTCCATATT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGATATGTCC Messenger 337277 (GAM337277) oligonucleotides modulates expression of respective target
CCTTCTATAA genes whose function and utility is known in the art.

GTGCAATACA GAM337277 is a novel bioinformatically detectable regulatory, non protein
CTTAATGGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337277 was detected
CCCTCTGTGC is described with additional reference to Figs. 9-15.

TTAGGGAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGTAATCTA encoded by the human genome.

AGCAGAAGGT GAM337277 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TTTTAAGG GAM337277 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337277 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337277 precursor RNA is designated SEQ ID:6121, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6121 is located from position 94888202 to position 94888309 relative to chromosome 11 on the `-` strand.

GAM337277 precursor RNA folds onto itself, forming GAM337277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337277 precursor RNA, designated SEQ ID NO: 6121, and a schematic representation of a predicted secondary folding of GAM337277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337277 folded precursor RNA yielding a GAM337277 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337277 RNA, hereby incorporated herein.

GAM337277 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337277 target RNA, herein designated GAM TARGET RNA.

GAM337277 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337277 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337277 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337277 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337277 RNA, herein designated GAM RNA, to target binding sites on GAM337277 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337277 target RNA into GAM337277 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337277 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337277 target genes. The mRNA of each one of this plurality of GAM337277 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337277 RNA, herein designated GAM RNA, and which when bound by GAM337277 RNA causes inhibition of translation of the GAM337277 target mRNA into a corresponding GAM337277 target protein.

The mechanism of the translational inhibition exerted by GAM337277 RNA, herein

designated GAM RNA, on one or more GAM337277 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337277 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337277 RNA, herein designated GAM RNA, of GAM337277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337277 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337277 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337277 RNA correlate with, and may be deduced from, the identity of the GAM337277 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337278 6000 CACGGCTATT Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGTAGCAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTGGGCTTG Messenger 337278 (GAM337278) oligonucleotides modulates expression of respective target
AATTCAGATC genes whose function and utility is known in the art.

TGCTTCTCAG GAM337278 is a novel bioinformatically detectable regulatory, non protein
TCCAGTGTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337278 was detected
TCTGCTCTGT is described with additional reference to Figs. 9-15.

AACTGGCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
G encoded by the human genome.

GAM337278 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337278 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337278 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337278 precursor RNA is designated SEQ ID:6000, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6000 is located from position 94917186 to position 94917266

relative to chromosome 8 on the `-` strand.

GAM337278 precursor RNA folds onto itself, forming GAM337278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337278 precursor RNA, designated SEQ ID NO: 6000, and a schematic representation of a predicted secondary folding of GAM337278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337278 folded precursor RNA yielding a GAM337278 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337278 RNA, hereby incorporated herein.

GAM337278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337278 target RNA, herein designated GAM TARGET RNA.

GAM337278 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337278 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337278 RNA, herein designated GAM RNA, to target binding sites on GAM337278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337278 target RNA into GAM337278 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337278 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337278 target genes. The mRNA of each one of this plurality of GAM337278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337278 RNA, herein designated GAM RNA, and which when bound by GAM337278 RNA causes inhibition of translation of the GAM337278 target mRNA into a corresponding GAM337278 target protein.

The mechanism of the translational inhibition exerted by GAM337278 RNA, herein designated GAM RNA, on one or more GAM337278 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337278 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337278 RNA, herein designated GAM RNA, of GAM337278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337278 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337278 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337278 RNA correlate with, and may be deduced from, the identity of the GAM337278 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337279 5794 AGGTGATGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGGCATGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGAGGTCAC Messenger 337279 (GAM337279) oligonucleotides modulates expression of respective target

TGTTGGATGT genes whose function and utility is known in the art.

CAGACTGGAG GAM337279 is a novel bioinformatically detectable regulatory, non protein

CCCGACCTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337279 was detected

GTGACTCTCA is described with additional reference to Figs. 9-15.

CCAGGGCCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTGTGAG encoded by the human genome.

CCTGGCACCT GAM337279 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337279 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337279 precursor RNA is designated SEQ ID:5794, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5794 is located from position 95196288 to position 95196387 relative to chromosome 9 on the `+` strand.

GAM337279 precursor RNA folds onto itself, forming GAM337279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337279 precursor RNA, designated SEQ ID NO: 5794, and a schematic representation of a predicted secondary folding of GAM337279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337279 folded precursor RNA yielding a GAM337279 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337279 RNA, hereby incorporated herein.

GAM337279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337279 target RNA, herein designated GAM TARGET RNA.

GAM337279 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337279 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337279 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337279 RNA, herein designated GAM RNA, to target binding sites on GAM337279 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337279 target RNA into GAM337279 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337279 target genes. The mRNA of each one of this plurality of GAM337279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337279 RNA, herein designated GAM RNA, and which when bound by GAM337279 RNA causes inhibition of translation of the GAM337279 target mRNA into a corresponding GAM337279 target protein.

The mechanism of the translational inhibition exerted by GAM337279 RNA, herein designated GAM RNA, on one or more GAM337279 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337279 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337279 RNA, herein designated GAM RNA, of GAM337279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337279 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337279 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337279 RNA correlate with, and may be deduced from, the identity of the GAM337279 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337281 7129 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAA Messenger 337281 (GAM337281) oligonucleotides modulates expression of respective target

GAGGAGGTTG genes whose function and utility is known in the art.

CAGTAAGCCG GAM337281 is a novel bioinformatically detectable regulatory, non protein

AGATCGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337281 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAAGTGAG encoded by the human genome.

ATTCCCTCTC GAM337281 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337281 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337281 precursor RNA is designated SEQ ID:7129, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7129 is located from position 95469300 to position 95469400 relative to chromosome 10 on the `+` strand.

GAM337281 precursor RNA folds onto itself, forming GAM337281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337281 precursor RNA, designated SEQ ID NO: 7129, and a schematic representation of a predicted secondary folding of GAM337281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337281 folded precursor RNA yielding a GAM337281 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337281 RNA, hereby incorporated herein. Expression of GAM337281 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337281 target RNA, herein designated GAM TARGET RNA.

GAM337281 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337281 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337281 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337281 RNA, herein designated GAM RNA, to target binding sites on GAM337281 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337281 target RNA into GAM337281 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337281 target genes. The mRNA of each one of this plurality of GAM337281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337281 RNA, herein designated GAM RNA, and which when bound by GAM337281 RNA causes inhibition of translation of the GAM337281 target mRNA into a corresponding GAM337281 target protein.

The mechanism of the translational inhibition exerted by GAM337281 RNA, herein designated GAM RNA, on one or more GAM337281 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337281 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337281 RNA, herein designated GAM RNA, of GAM337281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337281 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337281 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337281 RNA correlate with, and may be deduced from, the identity of the GAM337281 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337282 6604 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGAGGAGG Messenger 337282 (GAM337282) oligonucleotides modulates expression of respective target
TTGCAGTAAG genes whose function and utility is known in the art.

CCGAGATCGT GAM337282 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337282 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGATTCC encoded by the human genome.

GAM337282 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337282 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337282 precursor RNA is designated SEQ ID:6604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6604 is located from position 95469307 to position 95469394 relative to chromosome 10 on the `+` strand.

GAM337282 precursor RNA folds onto itself, forming GAM337282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337282 precursor RNA, designated SEQ ID NO: 6604, and a schematic representation of a predicted secondary folding of GAM337282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337282 folded precursor RNA yielding a GAM337282 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337282 RNA, hereby incorporated herein. Expression of GAM337282 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337282 target RNA, herein designated GAM TARGET RNA.

GAM337282 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337282 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337282 RNA, herein designated GAM RNA, to target binding sites on GAM337282 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337282 target RNA into GAM337282 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337282 target genes. The mRNA of each one of this plurality of GAM337282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337282 RNA, herein designated GAM RNA, and which when bound by GAM337282 RNA causes inhibition of translation of the GAM337282 target mRNA into a corresponding GAM337282 target protein.

The mechanism of the translational inhibition exerted by GAM337282 RNA, herein designated GAM RNA, on one or more GAM337282 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337282 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337282 RNA, herein designated GAM RNA, of GAM337282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337282 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337282 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337282 RNA correlate with, and may be deduced from, the identity of the GAM337282 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337283 6818 GGGGTATAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
CACTGAGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAAACAGGAT Messenger 337283 (GAM337283) oligonucleotides modulates expression of respective target
TCATCTGAGA genes whose function and utility is known in the art.

ACATCGGTTG GAM337283 is a novel bioinformatically detectable regulatory, non protein
CATGTCTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337283 was detected
TGCTTCAGTG is described with additional reference to Figs. 9-15.

TTCAAGTCTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CC encoded by the human genome.

GAM337283 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337283 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337283 precursor RNA is designated SEQ ID:6818, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6818 is located from position 96090585 to position 96090666 relative to chromosome 14 on the `+` strand.

GAM337283 precursor RNA folds onto itself, forming GAM337283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337283 precursor RNA, designated SEQ ID NO: 6818, and a schematic representation of a predicted secondary folding of GAM337283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337283 folded precursor

RNA yielding a GAM337283 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337283 RNA, hereby incorporated herein.

GAM337283 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337283 target RNA, herein designated GAM TARGET RNA.

GAM337283 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337283 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337283 RNA, herein designated GAM RNA, to target binding sites on GAM337283 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337283 target RNA into GAM337283 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337283 target genes. The mRNA of each one of this plurality of GAM337283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337283 RNA, herein designated GAM RNA, and which when bound by GAM337283 RNA causes inhibition of translation of the GAM337283 target mRNA into a corresponding GAM337283 target protein.

The mechanism of the translational inhibition exerted by GAM337283 RNA, herein designated GAM RNA, on one or more GAM337283 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337283 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337283 RNA, herein designated GAM RNA, of GAM337283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337283 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337283 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337283 RNA correlate with, and may be deduced from, the identity of the GAM337283 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337285 7208 TGCTGTGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TAACAGTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
TTTCTGAGTA Messenger 337285 (GAM337285) oligonucleotides modulates expression of respective target
TATTTTCATG genes whose function and utility is known in the art.

TCAAATAGCA GAM337285 is a novel bioinformatically detectable regulatory, non protein
AAAGTAGAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337285 was detected
TTTTGGAGGA is described with additional reference to Figs. 9-15.

GGTGTGAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATGAAGAGT encoded by the human genome.

GACTAGAGGA GAM337285 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AAATAGAGAG GAM337285 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TCAGAAGTTG GAM337285 precursor RNA does not encode a protein. A nucleotide sequence identical or

CAGTA highly similar to the nucleotide sequence of GAM337285 precursor RNA is designated SEQ ID:7208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7208 is located from position 96668219 to position 96668343 relative to chromosome 13 on the `-` strand.

GAM337285 precursor RNA folds onto itself, forming GAM337285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337285 precursor RNA, designated SEQ ID NO: 7208, and a schematic representation of a predicted secondary folding of GAM337285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337285 folded precursor RNA yielding a GAM337285 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337285 RNA, hereby incorporated herein.

GAM337285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337285 target RNA, herein designated GAM TARGET RNA.

GAM337285 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337285 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337285 RNA, herein designated GAM RNA, to target binding sites on GAM337285 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337285 target RNA into GAM337285 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337285 target genes. The mRNA of each one of this plurality of GAM337285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337285 RNA, herein designated GAM RNA, and which when bound by GAM337285 RNA causes inhibition of translation of the GAM337285 target mRNA into a corresponding GAM337285 target protein.

The mechanism of the translational inhibition exerted by GAM337285 RNA, herein

designated GAM RNA, on one or more GAM337285 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337285 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337285 RNA, herein designated GAM RNA, of GAM337285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337285 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337285 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337285 RNA correlate with, and may be deduced from, the identity of the GAM337285 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337286 6103 CCTAACAGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTTTTCTGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TATATTTTCA Messenger 337286 (GAM337286) oligonucleotides modulates expression of respective target

TGTCAAATAG genes whose function and utility is known in the art.

CAAAAGTAGA GAM337286 is a novel bioinformatically detectable regulatory, non protein

ACTTTTGGAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337286 was detected

GAGGTGTGAA is described with additional reference to Figs. 9-15.

GAAATGAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGACTAGAG encoded by the human genome.

G GAM337286 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337286 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337286 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337286 precursor RNA is designated SEQ ID:6103, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6103 is located from position 96668245 to position 96668335

relative to chromosome 13 on the `-` strand.

GAM337286 precursor RNA folds onto itself, forming GAM337286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337286 precursor RNA, designated SEQ ID NO: 6103, and a schematic representation of a predicted secondary folding of GAM337286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337286 folded precursor RNA yielding a GAM337286 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337286 RNA, hereby incorporated herein.

GAM337286 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337286 target RNA, herein designated GAM TARGET RNA.

GAM337286 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337286 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337286 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337286 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337286 RNA, herein designated GAM RNA, to target binding sites on GAM337286 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337286 target RNA into GAM337286 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337286 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337286 target genes. The mRNA of each one of this plurality of GAM337286 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337286 RNA, herein designated GAM RNA, and which when bound by GAM337286 RNA causes inhibition of translation of the GAM337286 target mRNA into a corresponding GAM337286 target protein.

The mechanism of the translational inhibition exerted by GAM337286 RNA, herein designated GAM RNA, on one or more GAM337286 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337286 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337286 RNA, herein designated GAM RNA, of GAM337286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337286 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337286 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337286 RNA correlate with, and may be deduced from, the identity of the GAM337286 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337288 6081 CCCGCCTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCTCGAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CACTGGGATT Messenger 337288 (GAM337288) oligonucleotides modulates expression of respective target

ACAGATGTGA genes whose function and utility is known in the art.

GCCACCATGC GAM337288 is a novel bioinformatically detectable regulatory, non protein

CCAGTTGGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337288 was detected

GCTCTAAACA is described with additional reference to Figs. 9-15.

TTAAATTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCAAAGAGA encoded by the human genome.

TGATGAGGCT GAM337288 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGG GAM337288 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337288 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337288 precursor RNA is designated SEQ ID:6081, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6081 is located from position 96681277 to position 96681379 relative to chromosome 12 on the `-` strand.

GAM337288 precursor RNA folds onto itself, forming GAM337288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337288 precursor RNA, designated SEQ ID NO: 6081, and a schematic representation of a predicted secondary folding of GAM337288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337288 folded precursor RNA yielding a GAM337288 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337288 RNA, hereby incorporated herein.

GAM337288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337288 target RNA, herein designated GAM TARGET RNA.

GAM337288 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337288 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337288 RNA, herein designated GAM RNA, to target binding sites on GAM337288 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337288 target RNA into GAM337288 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337288 target genes. The mRNA of each one of this plurality of GAM337288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337288 RNA, herein designated GAM RNA, and which when bound by GAM337288 RNA causes inhibition of translation of the GAM337288 target mRNA into a corresponding GAM337288 target protein.

The mechanism of the translational inhibition exerted by GAM337288 RNA, herein designated GAM RNA, on one or more GAM337288 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337288 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337288 RNA, herein designated GAM RNA, of GAM337288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337288 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337288 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337288 RNA correlate with, and may be deduced from, the identity of the GAM337288 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337289 6080 CCCGCCTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCTCGAGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CACTGGGATT Messenger 337289 (GAM337289) oligonucleotides modulates expression of respective target

ACAGATGTGA genes whose function and utility is known in the art.

GCCACCATGC GAM337289 is a novel bioinformatically detectable regulatory, non protein

CCAGTTGGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337289 was detected

GCTCTAAACA is described with additional reference to Figs. 9-15.

TTAAATTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGCAAAGAGA encoded by the human genome.

TGATGAGGCT GAM337289 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GG GAM337289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337289 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337289 precursor RNA is designated SEQ ID:6080, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6080 is located from position 96681278 to position 96681379 relative to chromosome 12 on the `-` strand.

GAM337289 precursor RNA folds onto itself, forming GAM337289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337289 precursor RNA, designated SEQ ID NO: 6080, and a schematic representation of a predicted secondary folding of GAM337289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337289 folded precursor RNA yielding a GAM337289 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337289 RNA, hereby incorporated herein.

GAM337289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337289 target RNA, herein designated GAM TARGET RNA.

GAM337289 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337289 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337289 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337289 RNA, herein designated GAM RNA, to target binding sites on GAM337289 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337289 target RNA into GAM337289 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337289 target genes. The mRNA of each one of this plurality of GAM337289 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337289 RNA, herein designated GAM RNA, and which when bound by GAM337289 RNA causes inhibition of translation of the GAM337289 target mRNA into a corresponding GAM337289 target protein.

The mechanism of the translational inhibition exerted by GAM337289 RNA, herein designated GAM RNA, on one or more GAM337289 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337289 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337289 RNA, herein designated GAM RNA, of GAM337289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337289 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337289 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337289 RNA correlate with, and may be deduced from, the identity of the GAM337289 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337290 7014 TCATAGTCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

CGTTTGTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGCCCATCTT Messenger 337290 (GAM337290) oligonucleotides modulates expression of respective target

TTTTGGGAAG genes whose function and utility is known in the art.

TCTTTCCAGG GAM337290 is a novel bioinformatically detectable regulatory, non protein

TATTCACAGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337290 was detected

GACTTGGGCC is described with additional reference to Figs. 9-15.

TCAAACTGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGATGCTGTG encoded by the human genome.

G GAM337290 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337290 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337290 precursor RNA is designated SEQ ID:7014, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7014 is located from position 96688012 to position 96688102 relative to chromosome X on the `+` strand.

GAM337290 precursor RNA folds onto itself, forming GAM337290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337290 precursor RNA, designated SEQ ID NO: 7014, and a schematic representation of a predicted secondary folding of GAM337290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337290 folded precursor RNA yielding a GAM337290 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337290 RNA, hereby incorporated herein.

GAM337290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337290 target RNA, herein designated GAM TARGET RNA.

GAM337290 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337290 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337290 RNA, herein designated GAM RNA, to target binding sites on GAM337290 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337290 target RNA into GAM337290 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337290 target genes. The mRNA of each one of this plurality of GAM337290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337290 RNA, herein designated GAM RNA, and which when bound by GAM337290 RNA causes inhibition of translation of the GAM337290 target mRNA into a corresponding GAM337290 target protein.

The mechanism of the translational inhibition exerted by GAM337290 RNA, herein designated GAM RNA, on one or more GAM337290 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337290 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337290 RNA, herein designated GAM RNA, of GAM337290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337290 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337290 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337290 RNA correlate with, and may be deduced from, the identity of the GAM337290 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337291 6213 CTGCATCACC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGAGAGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
AAGAACCTTG Messenger 337291 (GAM337291) oligonucleotides modulates expression of respective target
TTTTTATAGC genes whose function and utility is known in the art.

AGAGAAATAT GAM337291 is a novel bioinformatically detectable regulatory, non protein
AAGCACAGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337291 was detected
AGGTTCTGTC is described with additional reference to Figs. 9-15.

ACTTGCCAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GATGATCCCA encoded by the human genome.

G GAM337291 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337291 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337291 precursor RNA is designated SEQ ID:6213, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6213 is located from position 97011857 to position 97011947 relative to chromosome 8 on the `+` strand.

GAM337291 precursor RNA folds onto itself, forming GAM337291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337291 precursor RNA, designated SEQ ID NO: 6213, and a schematic representation of a predicted secondary folding of GAM337291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337291 folded precursor RNA yielding a GAM337291 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337291 RNA, hereby incorporated herein.

GAM337291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337291 target RNA, herein designated GAM TARGET RNA.

GAM337291 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337291 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337291 RNA, herein designated GAM RNA, to target binding sites on GAM337291 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337291 target RNA into GAM337291 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337291 target genes. The mRNA of each one of this plurality of GAM337291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337291 RNA, herein designated GAM RNA, and which when bound by GAM337291 RNA causes inhibition of translation of the GAM337291 target mRNA into a corresponding GAM337291 target protein.

The mechanism of the translational inhibition exerted by GAM337291 RNA, herein designated GAM RNA, on one or more GAM337291 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337291 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337291 RNA, herein designated GAM RNA, of GAM337291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337291 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337291 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337291 RNA correlate with, and may be deduced from, the identity of the GAM337291 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337292 5906 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337292 (GAM337292) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337292 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337292 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337292 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337292 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337292 precursor RNA is designated SEQ ID:5906, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5906 is located from position 97029751 to position 97029832 relative to chromosome 5 on the `+` strand.

GAM337292 precursor RNA folds onto itself, forming GAM337292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337292 precursor RNA, designated SEQ ID NO: 5906, and a schematic representation of a predicted secondary folding of GAM337292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337292 folded precursor RNA yielding a GAM337292 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337292 RNA, hereby incorporated herein.

GAM337292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337292 target RNA, herein designated GAM TARGET RNA.

GAM337292 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337292 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337292 RNA, herein designated GAM RNA, to target binding sites on GAM337292 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337292 target RNA into GAM337292 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337292 target genes. The mRNA of each one of this plurality of GAM337292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337292 RNA, herein designated GAM RNA, and which when bound by GAM337292 RNA causes inhibition of translation of the GAM337292 target mRNA into a corresponding GAM337292 target protein.

The mechanism of the translational inhibition exerted by GAM337292 RNA, herein designated GAM RNA, on one or more GAM337292 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337292 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337292 RNA, herein designated GAM RNA, of GAM337292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337292 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337292 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337292 RNA correlate with, and may be deduced from, the identity of the GAM337292 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337293 6929 GTGTGTCTGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TTTCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCAGGCGTGC Messenger 337293 (GAM337293) oligonucleotides modulates expression of respective target

TGTCTGAAGA genes whose function and utility is known in the art.

GGCTTTGGAA GAM337293 is a novel bioinformatically detectable regulatory, non protein

GTACCCCAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337293 was detected

TAATTCAGTT is described with additional reference to Figs. 9-15.

CTTGACCTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCCAGGGCCA encoded by the human genome.

CACACAT GAM337293 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337293 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337293 precursor RNA is designated SEQ ID:6929, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6929 is located from position 97153223 to position 97153319 relative to chromosome 15 on the `+` strand.

GAM337293 precursor RNA folds onto itself, forming GAM337293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337293 precursor RNA, designated SEQ ID NO: 6929, and a schematic representation of a predicted secondary folding of GAM337293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337293 folded precursor RNA yielding a GAM337293 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337293 RNA, hereby incorporated herein.

GAM337293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337293 target RNA, herein designated GAM TARGET RNA.

GAM337293 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337293 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337293 RNA, herein designated GAM RNA, to target binding sites on GAM337293 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337293 target RNA into GAM337293 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337293 target genes. The mRNA of each one of this plurality of GAM337293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337293 RNA, herein designated GAM RNA, and which when bound by GAM337293 RNA causes inhibition of translation of the GAM337293 target mRNA into a corresponding GAM337293 target protein.

The mechanism of the translational inhibition exerted by GAM337293 RNA, herein designated GAM RNA, on one or more GAM337293 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337293 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337293 RNA, herein designated GAM RNA, of GAM337293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337293 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337293 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337293 RNA correlate with, and may be deduced from, the identity of the GAM337293 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337294 6924 GTGTCTGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCAGGAGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCGTGCTG Messenger 337294 (GAM337294) oligonucleotides modulates expression of respective target

TCTGAAGAGG genes whose function and utility is known in the art.

CTTTGGAAGT GAM337294 is a novel bioinformatically detectable regulatory, non protein

ACCCCAAATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337294 was detected

ATTCAGTTCT is described with additional reference to Figs. 9-15.

TGACCTGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGGGCCACA encoded by the human genome.

CAC GAM337294 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337294 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337294 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337294 precursor RNA is designated SEQ

ID:6924, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6924 is located from position 97153225 to position 97153317 relative to chromosome 15 on the `+` strand.

GAM337294 precursor RNA folds onto itself, forming GAM337294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337294 precursor RNA, designated SEQ ID NO: 6924, and a schematic representation of a predicted secondary folding of GAM337294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337294 folded precursor RNA yielding a GAM337294 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337294 RNA, hereby incorporated herein.

GAM337294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337294 target RNA, herein designated GAM TARGET RNA.

GAM337294 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337294 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337294 RNA, herein designated GAM RNA, to target binding sites on GAM337294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337294 target RNA into GAM337294 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337294 target genes. The mRNA of each one of this plurality of GAM337294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337294 RNA, herein designated GAM RNA, and which when bound by GAM337294 RNA causes inhibition of translation of the GAM337294 target mRNA into a corresponding GAM337294 target protein.

The mechanism of the translational inhibition exerted by GAM337294 RNA, herein designated GAM RNA, on one or more GAM337294 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337294 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337294 RNA, herein designated GAM RNA, of GAM337294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337294 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337294 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337294 RNA correlate with, and may be deduced from, the identity of the GAM337294 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337296 6281 GAAAGGGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCACGGAAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGAGAATGG Messenger 337296 (GAM337296) oligonucleotides modulates expression of respective target

AGGAAGAACA genes whose function and utility is known in the art.

GTGCTTTGAG GAM337296 is a novel bioinformatically detectable regulatory, non protein

TGACTGCTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337296 was detected

AGGGTCTTCC is described with additional reference to Figs. 9-15.

TATTATTTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTTCTGAGG encoded by the human genome.

ATTCTCGTTC GAM337296 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337296 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337296 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337296 precursor RNA is designated SEQ ID:6281, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6281 is located from position 97963174 to position 97963273 relative to chromosome 13 on the `-` strand.

GAM337296 precursor RNA folds onto itself, forming GAM337296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337296 precursor RNA, designated SEQ ID NO: 6281, and a schematic representation of a predicted secondary folding of GAM337296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337296 folded precursor RNA yielding a GAM337296 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337296 RNA, hereby incorporated herein.

GAM337296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337296 target RNA, herein designated GAM TARGET RNA.

GAM337296 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337296 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337296 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337296 RNA, herein designated GAM RNA, to target binding sites on GAM337296 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337296 target RNA into GAM337296 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337296 target genes. The mRNA of each one of this plurality of GAM337296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337296 RNA, herein designated GAM RNA, and which when bound by GAM337296 RNA causes inhibition of translation of the GAM337296 target mRNA into a corresponding GAM337296 target protein.

The mechanism of the translational inhibition exerted by GAM337296 RNA, herein designated GAM RNA, on one or more GAM337296 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337296 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337296 RNA, herein designated GAM RNA, of GAM337296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337296 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337296 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337296 RNA correlate with, and may be deduced from, the identity of the GAM337296 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337297 6795 GGGAGTCCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAGCGTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAATGGAGGA Messenger 337297 (GAM337297) oligonucleotides modulates expression of respective target

AGAACAGTGC genes whose function and utility is known in the art.

TTTGAGTGAC GAM337297 is a novel bioinformatically detectable regulatory, non protein
TGCTGCAGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337297 was detected
TCTTCCTATT is described with additional reference to Figs. 9-15.

ATTTTTAGTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTGAGGATTC encoded by the human genome.

TC GAM337297 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337297 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337297 precursor RNA is designated SEQ ID:6795, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6795 is located from position 97963178 to position 97963269 relative to chromosome 13 on the `-` strand.

GAM337297 precursor RNA folds onto itself, forming GAM337297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337297 precursor RNA, designated SEQ ID NO: 6795, and a schematic representation of a predicted secondary folding of GAM337297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337297 folded precursor RNA yielding a GAM337297 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337297 RNA, hereby incorporated herein.

GAM337297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337297 target RNA, herein designated GAM TARGET RNA.

GAM337297 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337297 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337297 RNA, herein designated GAM RNA, to target binding sites on GAM337297 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337297 target RNA into GAM337297 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337297 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337297 target genes. The mRNA of each one of this plurality of GAM337297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337297 RNA, herein designated GAM RNA, and which when bound by GAM337297 RNA causes inhibition of translation of the GAM337297 target mRNA into a corresponding GAM337297 target protein.

The mechanism of the translational inhibition exerted by GAM337297 RNA, herein designated GAM RNA, on one or more GAM337297 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337297 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337297 RNA, herein designated GAM RNA, of GAM337297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337297 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337297 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337297 RNA correlate with, and may be deduced from, the identity of the GAM337297 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337298 6747 GGCCATGCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGTCACCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
AAATACTGCA Messenger 337298 (GAM337298) oligonucleotides modulates expression of respective target
CGGCCATGCC genes whose function and utility is known in the art.

TTTGTCAGGC GAM337298 is a novel bioinformatically detectable regulatory, non protein
AGGCTGAGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337298 was detected
ACTGGGAGTT is described with additional reference to Figs. 9-15.

AGGAGGGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CC encoded by the human genome.

GAM337298 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337298 precursor RNA is designated SEQ ID:6747, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6747 is located from position 98182570 to position 98182651 relative to chromosome 15 on the `+` strand.

GAM337298 precursor RNA folds onto itself, forming GAM337298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337298 precursor RNA, designated SEQ ID NO: 6747, and a schematic representation of a predicted secondary folding of GAM337298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337298 folded precursor RNA yielding a GAM337298 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337298 RNA, hereby incorporated herein.

GAM337298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337298 target RNA, herein designated GAM TARGET RNA.

GAM337298 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337298 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337298 RNA, herein designated GAM RNA, to target binding sites on GAM337298 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337298 target RNA into GAM337298 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337298 target genes. The mRNA of each one of this plurality of GAM337298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337298 RNA, herein designated GAM RNA, and which when bound by GAM337298 RNA causes inhibition of translation of the GAM337298 target mRNA into a corresponding GAM337298 target protein.

The mechanism of the translational inhibition exerted by GAM337298 RNA, herein designated GAM RNA, on one or more GAM337298 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337298 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337298 RNA, herein designated GAM RNA, of GAM337298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337298 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337298 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337298 RNA correlate with, and may be deduced from, the identity of the GAM337298 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337299 7094 TGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 337299 (GAM337299) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGT GAM337299 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337299 was detected
TCCATCCTGA is described with additional reference to Figs. 9-15.

GTGACAAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AAGACTGTCT encoded by the human genome.

CA GAM337299 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337299 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337299 precursor RNA is designated SEQ ID:7094, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7094 is located from position 98227794 to position 98227885 relative to chromosome 7 on the `+` strand.

GAM337299 precursor RNA folds onto itself, forming GAM337299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337299 precursor RNA, designated SEQ ID NO: 7094, and a schematic representation of a predicted secondary folding of GAM337299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337299 folded precursor RNA yielding a GAM337299 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337299 RNA, hereby incorporated herein.

GAM337299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337299 target RNA, herein designated GAM TARGET RNA.

GAM337299 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337299 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337299 RNA, herein designated GAM RNA, to target binding sites on GAM337299 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337299 target RNA into GAM337299 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337299 target genes. The mRNA of each one of this plurality of GAM337299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337299 RNA, herein designated GAM RNA, and which when bound by GAM337299 RNA causes inhibition of translation of the GAM337299 target mRNA into a corresponding GAM337299 target protein.

The mechanism of the translational inhibition exerted by GAM337299 RNA, herein designated GAM RNA, on one or more GAM337299 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337299 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337299 RNA, herein designated GAM RNA, of GAM337299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337299 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337299 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337299 RNA correlate with, and may be deduced from, the identity of the GAM337299 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337300 7315 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTTGCAG Messenger 337300 (GAM337300) oligonucleotides modulates expression of respective target
TGAGCCGAGA genes whose function and utility is known in the art.

TCGTGCCACT GAM337300 is a novel bioinformatically detectable regulatory, non protein
GCACTCCATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337300 was detected
CTGAGTGACA is described with additional reference to Figs. 9-15.

AAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337300 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337300 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337300 precursor RNA is designated SEQ ID:7315, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7315 is located from position 98227800 to position 98227875 relative to chromosome 7 on the `+` strand.

GAM337300 precursor RNA folds onto itself, forming GAM337300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337300 precursor RNA, designated SEQ ID NO: 7315, and a schematic representation of a predicted secondary folding of GAM337300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337300 folded precursor RNA yielding a GAM337300 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337300 RNA, hereby incorporated herein.

GAM337300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337300 target RNA, herein designated GAM TARGET RNA.

GAM337300 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337300 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337300 RNA, herein designated GAM RNA, to target binding sites on GAM337300 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337300 target RNA into GAM337300 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337300 target genes. The mRNA of each one of this plurality of GAM337300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337300 RNA, herein designated GAM RNA, and which when bound by GAM337300 RNA causes inhibition of translation of the GAM337300 target mRNA into a corresponding GAM337300 target protein.

The mechanism of the translational inhibition exerted by GAM337300 RNA, herein designated GAM RNA, on one or more GAM337300 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337300 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337300 RNA, herein designated GAM RNA, of GAM337300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337300 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337300 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337300 RNA correlate with, and may be deduced from, the identity of the GAM337300 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337301 5907 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337301 (GAM337301) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337301 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337301 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337301 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337301 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337301 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337301 precursor RNA is designated SEQ ID:5907, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5907 is located from position 98287751 to position 98287832 relative to chromosome 1 on the `-` strand.

GAM337301 precursor RNA folds onto itself, forming GAM337301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337301 precursor RNA, designated SEQ ID NO: 5907, and a schematic representation of a predicted secondary folding of GAM337301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337301 folded precursor RNA yielding a GAM337301 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337301 RNA, hereby incorporated herein.

GAM337301 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337301 target RNA, herein designated GAM TARGET RNA.

GAM337301 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337301 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337301 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337301 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337301 RNA, herein designated GAM RNA, to target binding sites on GAM337301 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337301 target RNA into GAM337301 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337301 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337301 target genes. The mRNA of each one of this plurality of GAM337301 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337301 RNA, herein designated GAM RNA, and which when bound by GAM337301 RNA causes inhibition of translation of the GAM337301 target mRNA into a corresponding GAM337301 target protein.

The mechanism of the translational inhibition exerted by GAM337301 RNA, herein designated GAM RNA, on one or more GAM337301 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337301 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337301 RNA, herein designated GAM RNA, of GAM337301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337301 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337301 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337301 RNA correlate with, and may be deduced from, the identity of the GAM337301 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337302 5908 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337302 (GAM337302) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337302 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337302 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337302 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337302 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337302 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337302 precursor RNA is designated SEQ ID:5908, and is provided hereinbelow with reference to the sequence listing part.

Nucleotide sequence SEQ ID:5908 is located from position 98298734 to position 98298815 relative to chromosome 2 on the `-` strand.

GAM337302 precursor RNA folds onto itself, forming GAM337302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337302 precursor RNA, designated SEQ ID NO: 5908, and a schematic representation of a predicted secondary folding of GAM337302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337302 folded precursor RNA yielding a GAM337302 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337302 RNA, hereby incorporated herein.

GAM337302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337302 target RNA, herein designated GAM TARGET RNA.

GAM337302 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337302 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337302 RNA, herein designated GAM RNA, to target binding sites on GAM337302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337302 target RNA into GAM337302 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337302 target genes. The mRNA of each one of this plurality of GAM337302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337302 RNA, herein designated GAM RNA, and which when bound by GAM337302 RNA causes inhibition of translation of the GAM337302 target mRNA into a corresponding GAM337302 target protein.

The mechanism of the translational inhibition exerted by GAM337302 RNA, herein designated GAM RNA, on one or more GAM337302 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337302 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337302 RNA, herein designated GAM RNA, of GAM337302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337302 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337302 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337302 RNA correlate with, and may be deduced from, the identity of the GAM337302 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337303 6688 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTGGAGG Messenger 337303 (GAM337303) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCGC GAM337303 is a novel bioinformatically detectable regulatory, non protein

CCACTGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337303 was detected

CCAGCCTGGG is described with additional reference to Figs. 9-15.

CAACAGAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGACTCT encoded by the human genome.

GAM337303 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337303 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337303 precursor RNA is designated SEQ ID:6688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6688 is located from position 98459191 to position 98459277 relative to chromosome X on the `+` strand.

GAM337303 precursor RNA folds onto itself, forming GAM337303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337303 precursor RNA, designated SEQ ID NO: 6688, and a schematic representation of a predicted secondary folding of GAM337303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337303 folded precursor RNA yielding a GAM337303 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337303 RNA, hereby incorporated herein. Expression of GAM337303 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337303 target RNA, herein designated GAM TARGET RNA.

GAM337303 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337303 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337303 RNA, herein designated GAM RNA, to target binding sites on GAM337303 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337303 target RNA into GAM337303 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337303 target genes. The mRNA of each one of this plurality of GAM337303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337303 RNA, herein designated GAM RNA, and which when bound by GAM337303 RNA causes inhibition of translation of the GAM337303 target mRNA into a corresponding GAM337303 target protein.

The mechanism of the translational inhibition exerted by GAM337303 RNA, herein designated GAM RNA, on one or more GAM337303 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337303 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337303 RNA, herein designated GAM RNA, of GAM337303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337303 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337303 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337303 RNA correlate with, and may be deduced from, the identity of the GAM337303 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337304 7319 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 337304 (GAM337304) oligonucleotides modulates expression of respective target

TGAGCCGAGA genes whose function and utility is known in the art.

TCGCCCACTG GAM337304 is a novel bioinformatically detectable regulatory, non protein
CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337304 was detected
TGGGCAACAG is described with additional reference to Figs. 9-15.

AGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337304 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337304 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337304 precursor RNA is designated SEQ ID:7319, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7319 is located from position 98459197 to position 98459271 relative to chromosome X on the `+` strand.

GAM337304 precursor RNA folds onto itself, forming GAM337304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337304 precursor RNA, designated SEQ ID NO: 7319, and a schematic representation of a predicted secondary folding of GAM337304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337304 folded precursor RNA yielding a GAM337304 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337304 RNA, hereby incorporated herein. Expression of GAM337304 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337304 target RNA, herein designated GAM TARGET RNA.

GAM337304 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337304 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337304 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337304 RNA, herein designated GAM RNA, to target binding sites on GAM337304 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337304 target RNA into GAM337304 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337304 target genes. The mRNA of each one of this plurality of GAM337304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337304 RNA, herein designated GAM RNA, and which when bound by GAM337304 RNA causes inhibition of translation of the GAM337304 target mRNA into a corresponding GAM337304 target protein.

The mechanism of the translational inhibition exerted by GAM337304 RNA, herein designated GAM RNA, on one or more GAM337304 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337304 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337304 RNA, herein designated GAM RNA, of GAM337304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337304 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337304 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337304 RNA correlate with, and may be deduced from, the identity of the GAM337304 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337305 7288 TTATGAATCC Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTTTTATGA detected oligonucleotides of the present invention, referred to here as Genomic Address
AATGTCCAAA Messenger 337305 (GAM337305) oligonucleotides modulates expression of respective target
ATAGGCAAAT genes whose function and utility is known in the art.

CTATGGACAG GAM337305 is a novel bioinformatically detectable regulatory, non protein
AAAGTAGAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337305 was detected
GCAGATTCGT is described with additional reference to Figs. 9-15.

GG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337305 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337305 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337305 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337305 precursor RNA is designated SEQ ID:7288, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7288 is located from position 98645765 to position 98645836 relative to chromosome 10 on the `+` strand.

GAM337305 precursor RNA folds onto itself, forming GAM337305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337305 precursor RNA, designated SEQ ID NO: 7288, and a schematic representation of a predicted secondary folding of GAM337305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337305 folded precursor RNA yielding a GAM337305 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337305 RNA, hereby incorporated herein.

GAM337305 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337305 target RNA, herein designated GAM TARGET RNA.

GAM337305 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337305 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337305 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337305 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337305 RNA, herein designated GAM RNA, to target binding sites on GAM337305 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337305 target RNA into GAM337305 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337305 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337305 target genes. The mRNA of each one of this plurality of GAM337305 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337305 RNA, herein designated GAM RNA, and which when bound by GAM337305 RNA causes inhibition of translation of the GAM337305 target mRNA into a corresponding GAM337305 target protein.

The mechanism of the translational inhibition exerted by GAM337305 RNA, herein designated GAM RNA, on one or more GAM337305 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337305 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337305 RNA, herein designated GAM RNA, of GAM337305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337305 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337305 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337305 RNA correlate with, and may be deduced from, the identity of the GAM337305 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337306 5963 ATGAATCCGT TTTTATGAAA TGTCCAAAAT AGGCAAATCT ATGGACAGAA AGTAGAAAGC AGATTCGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337306 (GAM337306) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337306 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337306 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337306 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337306 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337306 precursor RNA is designated SEQ ID:5963, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5963 is located from position 98645767 to position 98645834 relative to chromosome 10 on the `+` strand.

GAM337306 precursor RNA folds onto itself, forming GAM337306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337306 precursor RNA, designated SEQ ID NO: 5963, and a schematic representation of a predicted secondary folding of GAM337306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337306 folded precursor RNA yielding a GAM337306 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337306 RNA, hereby incorporated herein.

GAM337306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337306 target RNA, herein designated GAM TARGET RNA.

GAM337306 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337306 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337306 RNA, herein designated GAM RNA, to target binding sites on GAM337306 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337306 target RNA into GAM337306 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337306 target genes. The mRNA of each one of this plurality of GAM337306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337306 RNA, herein designated GAM RNA, and which when bound by GAM337306 RNA causes inhibition of translation of the GAM337306 target mRNA into a corresponding GAM337306 target protein.

The mechanism of the translational inhibition exerted by GAM337306 RNA, herein designated GAM RNA, on one or more GAM337306 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337306 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337306 RNA, herein designated GAM RNA, of GAM337306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337306 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337306 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337306 RNA correlate with, and may be deduced from, the identity of the GAM337306 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337310 5909 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337310 (GAM337310) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337310 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337310 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337310 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337310 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337310 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337310 precursor RNA is designated SEQ ID:5909, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5909 is located from position 98924324 to position 98924405 relative to chromosome 5 on the `+` strand.

GAM337310 precursor RNA folds onto itself, forming GAM337310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337310 precursor RNA, designated SEQ ID NO: 5909, and a schematic representation of a predicted secondary folding of GAM337310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337310 folded precursor RNA yielding a GAM337310 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337310 RNA, hereby incorporated herein.

GAM337310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337310 target RNA, herein designated GAM TARGET RNA.

GAM337310 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337310 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337310 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337310 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337310 RNA, herein designated GAM RNA, to target binding sites on GAM337310 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337310 target RNA into GAM337310 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337310 target genes. The mRNA of each one of this plurality of GAM337310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337310 RNA, herein designated GAM RNA, and which when bound by GAM337310 RNA causes inhibition of translation of the GAM337310 target mRNA into a corresponding GAM337310 target protein.

The mechanism of the translational inhibition exerted by GAM337310 RNA, herein designated GAM RNA, on one or more GAM337310 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337310 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337310 RNA, herein designated GAM RNA, of GAM337310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337310 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337310 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337310 RNA correlate with, and may be deduced from, the identity of the GAM337310 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337311 6397 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 337311 (GAM337311) oligonucleotides modulates expression of respective target

CGGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCAA GAM337311 is a novel bioinformatically detectable regulatory, non protein

GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337311 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAACAGCGAA encoded by the human genome.

ACTCTGTCTC GAM337311 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337311 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337311 precursor RNA is designated SEQ ID:6397, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6397 is located from position 98930879 to position 98930978 relative to chromosome 12 on the `+` strand.

GAM337311 precursor RNA folds onto itself, forming GAM337311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337311 precursor RNA, designated SEQ ID NO: 6397, and a schematic representation of a predicted secondary folding of GAM337311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337311 folded precursor RNA yielding a GAM337311 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337311 RNA, hereby incorporated herein. Expression of GAM337311 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337311 target RNA, herein designated GAM TARGET RNA.

GAM337311 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337311 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337311 RNA, herein designated GAM RNA, to target binding sites on GAM337311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337311 target RNA into GAM337311 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337311 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337311 target genes. The mRNA of each one of this plurality of GAM337311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337311 RNA, herein designated GAM RNA, and which when bound by GAM337311 RNA causes inhibition of translation of the GAM337311 target mRNA into a corresponding GAM337311 target protein.

The mechanism of the translational inhibition exerted by GAM337311 RNA, herein designated GAM RNA, on one or more GAM337311 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337311 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337311 RNA, herein designated GAM RNA, of GAM337311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337311 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337311 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337311 RNA correlate with, and may be deduced from, the identity of the GAM337311 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337312 6733 GGCAGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCGGGAGGCG Messenger 337312 (GAM337312) oligonucleotides modulates expression of respective target

GAGGTTGTGG genes whose function and utility is known in the art.

TGAGCCAAGA GAM337312 is a novel bioinformatically detectable regulatory, non protein

TTGCGCCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337312 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGCGAAAC encoded by the human genome.

TCTGTC GAM337312 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337312 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337312 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337312 precursor RNA is designated SEQ ID:6733, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6733 is located from position 98930881 to position 98930976 relative to chromosome 12 on the `+` strand.

GAM337312 precursor RNA folds onto itself, forming GAM337312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337312 precursor RNA, designated SEQ ID NO: 6733, and a schematic representation of a predicted secondary folding of GAM337312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337312 folded precursor RNA yielding a GAM337312 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337312 RNA, hereby incorporated herein. Expression of GAM337312 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337312 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337312 target RNA, herein designated GAM TARGET RNA.

GAM337312 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337312 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337312 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337312 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337312 RNA, herein designated GAM RNA, to target binding sites on GAM337312 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337312 target RNA into GAM337312 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337312 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337312 target genes. The mRNA of each one of this plurality of GAM337312 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337312 RNA, herein designated GAM RNA, and which when bound by GAM337312 RNA causes inhibition of translation of the GAM337312 target mRNA into a corresponding GAM337312 target protein.

The mechanism of the translational inhibition exerted by GAM337312 RNA, herein designated GAM RNA, on one or more GAM337312 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337312 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337312 RNA, herein designated GAM RNA, of GAM337312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337312 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337312 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337312 RNA correlate with, and may be deduced from, the identity of the GAM337312 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337313 6650 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 337313 (GAM337313) oligonucleotides modulates expression of respective target

TTGTGGTGAG genes whose function and utility is known in the art.

CCAAGATTGC GAM337313 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337313 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAAACTCT encoded by the human genome.

GAM337313 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337313 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337313 precursor RNA is designated SEQ ID:6650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6650 is located from position 98930885 to position 98930973 relative to chromosome 12 on the `+` strand.

GAM337313 precursor RNA folds onto itself, forming GAM337313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337313 precursor RNA, designated SEQ ID NO: 6650, and a schematic representation of a predicted secondary folding of GAM337313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337313 folded precursor RNA yielding a GAM337313 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337313 RNA, hereby incorporated herein. Expression of GAM337313 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337313 target RNA, herein designated GAM TARGET RNA.

GAM337313 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337313 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337313 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337313 RNA, herein designated GAM RNA, to target binding sites on GAM337313 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337313 target RNA into GAM337313 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337313 target genes. The mRNA of each one of this plurality of GAM337313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337313 RNA, herein designated GAM RNA, and which when bound by GAM337313 RNA causes inhibition of translation of the GAM337313 target mRNA into a corresponding GAM337313 target protein.

The mechanism of the translational inhibition exerted by GAM337313 RNA, herein designated GAM RNA, on one or more GAM337313 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337313 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337313 RNA, herein designated GAM RNA, of GAM337313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337313 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337313 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337313 RNA correlate with, and may be deduced from, the identity of the GAM337313 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337314 6643 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGCAGAAG Messenger 337314 (GAM337314) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATCAC GAM337314 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337314 was detected
TTCAGCCTGG is described with additional reference to Figs. 9-15.

GTGACAGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGACTCC encoded by the human genome.

GAM337314 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337314 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337314 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337314 precursor RNA is designated SEQ ID:6643, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6643 is located from position 98985382 to position 98985469 relative to chromosome 15 on the `+` strand.

GAM337314 precursor RNA folds onto itself, forming GAM337314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337314 precursor RNA, designated SEQ ID NO: 6643, and a schematic representation of a predicted secondary folding of GAM337314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337314 folded precursor RNA yielding a GAM337314 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337314 RNA, hereby incorporated herein.

GAM337314 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337314 target RNA, herein designated GAM TARGET RNA.

GAM337314 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337314 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337314 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337314 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337314 RNA, herein designated GAM RNA, to target binding sites on GAM337314 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337314 target RNA into GAM337314 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337314 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337314 target genes. The mRNA of each one of this plurality of GAM337314 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337314 RNA, herein designated GAM RNA, and which when bound by GAM337314 RNA causes inhibition of translation of the GAM337314 target mRNA into a corresponding GAM337314 target protein.

The mechanism of the translational inhibition exerted by GAM337314 RNA, herein designated GAM RNA, on one or more GAM337314 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337314 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337314 RNA, herein designated GAM RNA, of GAM337314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337314 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337314 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337314 RNA correlate with, and may be deduced from, the identity of the GAM337314 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337315 7250 TGGTCCACAT Fig. 8 further provides a conceptual description of another novel bioinformatically
TCTACATAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCACCCTCC Messenger 337315 (GAM337315) oligonucleotides modulates expression of respective target
ACACAGTGGA genes whose function and utility is known in the art.

CAATGTCAAG GAM337315 is a novel bioinformatically detectable regulatory, non protein
AGGTGGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337315 was detected
GTGTGGGGTG is described with additional reference to Figs. 9-15.

GGGCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337315 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337315 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337315 precursor RNA is designated SEQ ID:7250, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7250 is located from position 99006060 to position 99006135 relative to chromosome 14 on the `+` strand.

GAM337315 precursor RNA folds onto itself, forming GAM337315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337315 precursor RNA, designated SEQ ID NO: 7250, and a schematic representation of a predicted secondary folding of GAM337315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337315 folded precursor RNA yielding a GAM337315 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337315 RNA, hereby incorporated herein.

GAM337315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337315 target RNA, herein designated GAM TARGET RNA.

GAM337315 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337315 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337315 RNA, herein designated GAM RNA, to target binding sites on GAM337315 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337315 target RNA into GAM337315 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337315 target genes. The mRNA of each one of this plurality of GAM337315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337315 RNA, herein designated GAM RNA, and which when bound by GAM337315 RNA causes inhibition of translation of the GAM337315 target mRNA into a corresponding GAM337315 target protein.

The mechanism of the translational inhibition exerted by GAM337315 RNA, herein designated GAM RNA, on one or more GAM337315 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337315 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337315 RNA, herein designated GAM RNA, of GAM337315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337315 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337315 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337315 RNA correlate with, and may be deduced from, the identity of the GAM337315 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337317 6493 GCAGGCAGGG AGAGGGAGGA GGTGAAGGAA CAAATGCTGA ACACCTGTTA TTTATGAAGC ACTCTACATA TGTTCTTTCA TTTCACTCCT GGTGAAAACC TGC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337317 (GAM337317) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337317 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337317 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337317 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337317 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337317 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337317 precursor RNA is designated SEQ ID:6493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6493 is located from position 99096789 to position 99096891 relative to chromosome 12 on the `+` strand.

GAM337317 precursor RNA folds onto itself, forming GAM337317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337317 precursor RNA, designated SEQ ID NO: 6493, and a schematic representation of a predicted secondary folding of GAM337317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337317 folded precursor RNA yielding a GAM337317 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337317 RNA, hereby incorporated herein.

GAM337317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337317 target RNA, herein designated GAM TARGET RNA.

GAM337317 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337317 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337317 RNA, herein designated GAM RNA, to target binding sites on GAM337317 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337317 target RNA into GAM337317 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337317 target genes. The mRNA of each one of this plurality of GAM337317 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337317 RNA, herein designated GAM RNA, and which when bound by GAM337317 RNA causes inhibition of translation of the GAM337317 target mRNA into a corresponding GAM337317 target protein.

The mechanism of the translational inhibition exerted by GAM337317 RNA, herein designated GAM RNA, on one or more GAM337317 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337317 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337317 RNA, herein designated GAM RNA, of GAM337317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337317 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337317 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337317 RNA correlate with, and may be deduced from, the identity of the GAM337317 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337318 6495 GCAGGGAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAGGAGGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGAACAAA Messenger 337318 (GAM337318) oligonucleotides modulates expression of respective target

TGCTGAACAC genes whose function and utility is known in the art.

CTGTTATTTA GAM337318 is a novel bioinformatically detectable regulatory, non protein

TGAAGCACTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337318 was detected

TACATATGTT is described with additional reference to Figs. 9-15.

CTTTCATTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACTCCTGGTG encoded by the human genome.

AAAACCTGC GAM337318 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337318 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337318 precursor RNA is designated SEQ ID:6495, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6495 is located from position 99096793 to position 99096891 relative to chromosome 12 on the `+` strand.

GAM337318 precursor RNA folds onto itself, forming GAM337318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337318 precursor RNA, designated SEQ ID NO: 6495, and a schematic representation of a predicted secondary folding of GAM337318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337318 folded precursor RNA yielding a GAM337318 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337318 RNA, hereby incorporated herein.

GAM337318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337318 target RNA, herein designated GAM TARGET RNA.

GAM337318 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337318 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337318 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337318 RNA, herein designated GAM RNA, to target binding sites on GAM337318 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337318 target RNA into GAM337318 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337318 target genes. The mRNA of each one of this

plurality of GAM337318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337318 RNA, herein designated GAM RNA, and which when bound by GAM337318 RNA causes inhibition of translation of the GAM337318 target mRNA into a corresponding GAM337318 target protein.

The mechanism of the translational inhibition exerted by GAM337318 RNA, herein designated GAM RNA, on one or more GAM337318 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337318 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337318 RNA, herein designated GAM RNA, of GAM337318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337318 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337318 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337318 RNA correlate with, and may be deduced from, the identity of the GAM337318 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337319 6790 GGGAGGAGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GAAGGAACAA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGCTGAACA Messenger 337319 (GAM337319) oligonucleotides modulates expression of respective target

CCTGTTATTT genes whose function and utility is known in the art.

ATGAAGCACT GAM337319 is a novel bioinformatically detectable regulatory, non protein

CTACATATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337319 was detected

TCTTTCATTT is described with additional reference to Figs. 9-15.

CACTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337319 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337319 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337319 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337319 precursor RNA is designated SEQ ID:6790, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6790 is located from position 99096802 to position 99096878 relative to chromosome 12 on the `+` strand.

GAM337319 precursor RNA folds onto itself, forming GAM337319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337319 precursor RNA, designated SEQ ID NO: 6790, and a schematic representation of a predicted secondary folding of GAM337319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337319 folded precursor RNA yielding a GAM337319 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337319 RNA, hereby incorporated herein.

GAM337319 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337319 target RNA, herein designated GAM TARGET RNA.

GAM337319 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337319 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337319 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337319 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337319 RNA, herein designated GAM RNA, to target binding sites on GAM337319 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337319 target RNA into GAM337319 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337319 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337319 target genes. The mRNA of each one of this plurality of GAM337319 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337319 RNA, herein designated GAM RNA, and which when bound by GAM337319 RNA causes inhibition of translation of the GAM337319 target mRNA into a corresponding GAM337319 target protein.

The mechanism of the translational inhibition exerted by GAM337319 RNA, herein designated GAM RNA, on one or more GAM337319 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337319 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337319 RNA, herein designated GAM RNA, of GAM337319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337319 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337319 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337319 RNA correlate with, and may be deduced from, the identity of the GAM337319 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337320 5657 AACGTGTGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GATTGATGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCATGGACT Messenger 337320 (GAM337320) oligonucleotides modulates expression of respective target

CTGTTGCCCC genes whose function and utility is known in the art.

AAGTCCCCAA GAM337320 is a novel bioinformatically detectable regulatory, non protein

GCCTTGTACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337320 was detected

AGCGTT is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337320 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337320 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337320 precursor RNA is designated SEQ ID:5657, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5657 is located from position 99149261 to position 99149326 relative to chromosome 13 on the `+` strand.

GAM337320 precursor RNA folds onto itself, forming GAM337320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337320 precursor RNA, designated SEQ ID NO: 5657, and a schematic representation of a predicted secondary folding of GAM337320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337320 folded precursor RNA yielding a GAM337320 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337320 RNA, hereby incorporated herein.

GAM337320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337320 target RNA, herein designated GAM TARGET RNA.

GAM337320 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337320 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337320 RNA, herein designated GAM RNA, to target binding sites on GAM337320 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337320 target RNA into GAM337320 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337320 target genes. The mRNA of each one of this plurality of GAM337320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337320 RNA, herein designated GAM RNA, and which when bound by GAM337320 RNA causes inhibition of translation of the GAM337320 target mRNA into a corresponding GAM337320 target protein.

The mechanism of the translational inhibition exerted by GAM337320 RNA, herein designated GAM RNA, on one or more GAM337320 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337320 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337320 RNA, herein designated GAM RNA, of GAM337320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337320 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337320 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337320 RNA correlate with, and may be deduced from, the identity of the GAM337320 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337321 6664 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAATCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGTTGGAGG Messenger 337321 (GAM337321) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGGTCAC GAM337321 is a novel bioinformatically detectable regulatory, non protein
CTGCATTCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337321 was detected
GCCTGCTGAC is described with additional reference to Figs. 9-15.

AGCGAGACTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
C encoded by the human genome.

GAM337321 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337321 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337321 precursor RNA is designated SEQ ID:6664, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6664 is located from position 99258727 to position 99258807 relative to chromosome 7 on the `+` strand.

GAM337321 precursor RNA folds onto itself, forming GAM337321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337321 precursor RNA, designated SEQ ID NO: 6664, and a schematic representation of a predicted secondary folding of GAM337321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337321 folded precursor RNA yielding a GAM337321 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337321 RNA, hereby incorporated herein.

GAM337321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337321 target RNA, herein designated GAM TARGET RNA.

GAM337321 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337321 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337321 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337321 RNA, herein designated GAM RNA, to target binding sites on GAM337321 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337321 target RNA into GAM337321 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337321 target genes. The mRNA of each one of this plurality of GAM337321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337321 RNA, herein designated GAM RNA, and which when bound by GAM337321 RNA causes inhibition of translation of the GAM337321 target mRNA into a corresponding GAM337321 target protein.

The mechanism of the translational inhibition exerted by GAM337321 RNA, herein designated GAM RNA, on one or more GAM337321 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337321 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337321 RNA, herein designated GAM RNA, of GAM337321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337321 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337321 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337321 RNA correlate with, and may be deduced from, the identity of the GAM337321 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337324 6645 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGCCGGAGG Messenger 337324 (GAM337324) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

TCGAGATCAT GAM337324 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337324 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACTCC encoded by the human genome.

GAM337324 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337324 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337324 precursor RNA is designated SEQ ID:6645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6645 is located from position 99463318 to position 99463406 relative to chromosome 14 on the `+` strand.

GAM337324 precursor RNA folds onto itself, forming GAM337324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337324 precursor RNA, designated SEQ ID NO: 6645, and a schematic representation of a predicted secondary folding of GAM337324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337324 folded precursor RNA yielding a GAM337324 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337324 RNA, hereby incorporated herein. Expression of GAM337324 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337324 target RNA, herein designated GAM TARGET RNA.

GAM337324 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337324 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337324 RNA, herein designated GAM RNA, to target binding sites on GAM337324 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337324 target RNA into GAM337324 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337324 target genes. The mRNA of each one of this plurality of GAM337324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337324 RNA, herein designated GAM RNA, and which when bound by GAM337324 RNA causes inhibition of translation of the GAM337324 target mRNA into a corresponding GAM337324 target protein.

The mechanism of the translational inhibition exerted by GAM337324 RNA, herein designated GAM RNA, on one or more GAM337324 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337324 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337324 RNA, herein designated GAM RNA, of GAM337324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337324 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337324 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337324 RNA correlate with, and may be deduced from, the identity of the GAM337324 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337326 7016 TCATGGTTCC Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGAAGGTAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GATTGGTGGC Messenger 337326 (GAM337326) oligonucleotides modulates expression of respective target
CACCACATTC genes whose function and utility is known in the art.

AGTCTCCTTC GAM337326 is a novel bioinformatically detectable regulatory, non protein
ACAGCTAAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337326 was detected
GTAGCCACAT is described with additional reference to Figs. 9-15.

AACTATGCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGCCACGGG encoded by the human genome.

GATATGAATG GAM337326 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CTACTACTAA GAM337326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TTTTTTCCCT GAM337326 precursor RNA does not encode a protein. A nucleotide sequence identical or

TGAAACAATG highly similar to the nucleotide sequence of GAM337326 precursor RNA is designated SEQ
G ID:7016, and is provided hereinbelow with reference to the sequence listing part.
Nucleotide sequence SEQ ID:7016 is located from position 99654607 to position 99654737 relative to chromosome 11 on the `+` strand.

GAM337326 precursor RNA folds onto itself, forming GAM337326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337326 precursor RNA, designated SEQ ID NO: 7016, and a schematic representation of a predicted secondary folding of GAM337326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337326 folded precursor RNA yielding a GAM337326 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337326 RNA, hereby incorporated herein.

GAM337326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337326 target RNA, herein designated GAM TARGET RNA.

GAM337326 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337326 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337326 RNA, herein designated GAM RNA, to target binding sites on GAM337326 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337326 target RNA into GAM337326 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337326 target genes. The mRNA of each one of this plurality of GAM337326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337326 RNA, herein designated GAM RNA, and which when bound by GAM337326 RNA causes inhibition of translation of the GAM337326 target mRNA into a corresponding GAM337326 target protein.

The mechanism of the translational inhibition exerted by GAM337326 RNA, herein designated GAM RNA, on one or more GAM337326 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337326 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337326 RNA, herein designated GAM RNA, of GAM337326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337326 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337326 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337326 RNA correlate with, and may be deduced from, the identity of the GAM337326 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337327 6829 GGTAAGATTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGGCCACCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTCAGTCT Messenger 337327 (GAM337327) oligonucleotides modulates expression of respective target

CCTTCACAGC genes whose function and utility is known in the art.

TAAGTGTAGC GAM337327 is a novel bioinformatically detectable regulatory, non protein

CACATAACTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337327 was detected

TGCTTTGGCC is described with additional reference to Figs. 9-15.

ACGGGGATAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAATGCTACT encoded by the human genome.

ACTAATTTTT GAM337327 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCC GAM337327 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337327 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337327 precursor RNA is designated SEQ ID:6829, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6829 is located from position 99654622 to position 99654724 relative to chromosome 11 on the `+` strand.

GAM337327 precursor RNA folds onto itself, forming GAM337327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337327 precursor RNA, designated SEQ ID NO: 6829, and a schematic representation of a predicted secondary folding of GAM337327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337327 folded precursor RNA yielding a GAM337327 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337327 RNA, hereby incorporated herein.

GAM337327 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337327 target RNA, herein designated GAM TARGET RNA.

GAM337327 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337327 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337327 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337327 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337327 RNA, herein designated GAM RNA, to target binding sites on GAM337327 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337327 target RNA into GAM337327 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337327 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337327 target genes. The mRNA of each one of this plurality of GAM337327 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337327 RNA, herein designated GAM RNA, and which when bound by GAM337327 RNA causes inhibition of translation of the GAM337327 target mRNA into a corresponding GAM337327 target protein.

The mechanism of the translational inhibition exerted by GAM337327 RNA, herein designated GAM RNA, on one or more GAM337327 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337327 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337327 RNA, herein designated GAM RNA, of GAM337327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337327 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337327 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337327 RNA correlate with, and may be deduced from, the identity of the GAM337327 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337328 5664 AAGATTGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCCACCACAT detected oligonucleotides of the present invention, referred to here as Genomic Address

TCAGTCTCCT Messenger 337328 (GAM337328) oligonucleotides modulates expression of respective target

TCACAGCTAA genes whose function and utility is known in the art.

GTGTAGCCAC GAM337328 is a novel bioinformatically detectable regulatory, non protein

ATAACTATGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337328 was detected

TTTGGCCACG is described with additional reference to Figs. 9-15.

GGGATATGAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCTACTACT encoded by the human genome.

AATTTT GAM337328 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337328 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337328 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337328 precursor RNA is designated SEQ ID:5664, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5664 is located from position 99654625 to position 99654720 relative to chromosome 11 on the `+` strand.

GAM337328 precursor RNA folds onto itself, forming GAM337328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337328 precursor RNA, designated SEQ ID NO: 5664, and a schematic representation of a predicted secondary folding of GAM337328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337328 folded precursor RNA yielding a GAM337328 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337328 RNA, hereby incorporated herein.

GAM337328 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337328 target RNA, herein designated GAM TARGET RNA.

GAM337328 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337328 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337328 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337328 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337328 RNA, herein designated GAM RNA, to target binding sites on GAM337328 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337328 target RNA into GAM337328 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM337328 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337328 target genes. The mRNA of each one of this plurality of GAM337328 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337328 RNA, herein designated GAM RNA, and which when bound by GAM337328 RNA causes inhibition of translation of the GAM337328 target mRNA into a corresponding GAM337328 target protein.

The mechanism of the translational inhibition exerted by GAM337328 RNA, herein designated GAM RNA, on one or more GAM337328 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337328 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337328 RNA, herein designated GAM RNA, of GAM337328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337328 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337328 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337328 RNA correlate with, and may be deduced from, the identity of the GAM337328 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337329 5659 AAGAAGAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGCTGGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGGACCTCA Messenger 337329 (GAM337329) oligonucleotides modulates expression of respective target

GGATCTCAAG genes whose function and utility is known in the art.

AACATCATGG GAM337329 is a novel bioinformatically detectable regulatory, non protein

AATTGAGTTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337329 was detected

CCTGGGTTTT is described with additional reference to Figs. 9-15.

CTTTTTGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

T encoded by the human genome.

GAM337329 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337329 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337329 precursor RNA is designated SEQ ID:5659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5659 is located from position 99733672 to position 99733752 relative to chromosome 14 on the `+` strand.

GAM337329 precursor RNA folds onto itself, forming GAM337329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337329 precursor RNA, designated SEQ ID NO: 5659, and a schematic representation of a predicted secondary folding of GAM337329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337329 folded precursor RNA yielding a GAM337329 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337329 RNA, hereby incorporated herein.

GAM337329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337329 target RNA, herein designated GAM TARGET RNA.

GAM337329 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337329 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337329 RNA, herein designated GAM RNA, to target binding sites on GAM337329 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337329 target RNA into GAM337329 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337329 target genes. The mRNA of each one of this plurality of GAM337329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337329 RNA, herein designated GAM RNA, and which when bound by GAM337329 RNA causes inhibition of translation of the GAM337329 target mRNA into a corresponding GAM337329 target protein.

The mechanism of the translational inhibition exerted by GAM337329 RNA, herein designated GAM RNA, on one or more GAM337329 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337329 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337329 RNA, herein designated GAM RNA, of GAM337329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337329 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337329 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337329 RNA correlate with, and may be deduced from, the identity of the GAM337329 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337330 5910 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337330 (GAM337330) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337330 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337330 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337330 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337330 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337330 precursor RNA is designated SEQ ID:5910, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5910 is located from position 100140600 to position 100140681 relative to chromosome 6 on the `-` strand.

GAM337330 precursor RNA folds onto itself, forming GAM337330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337330 precursor RNA, designated SEQ ID NO: 5910, and a schematic representation of a predicted secondary folding of GAM337330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337330 folded precursor RNA yielding a GAM337330 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337330 RNA, hereby incorporated herein.

GAM337330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337330 target RNA, herein designated GAM TARGET RNA.

GAM337330 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337330 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337330 RNA, herein designated GAM RNA, to target binding sites on GAM337330 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337330 target RNA into GAM337330 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337330 target genes. The mRNA of each one of this plurality of GAM337330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337330 RNA, herein designated GAM RNA, and which when bound by GAM337330 RNA causes inhibition of translation of the GAM337330 target mRNA into a corresponding GAM337330 target protein.

The mechanism of the translational inhibition exerted by GAM337330 RNA, herein designated GAM RNA, on one or more GAM337330 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337330 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337330 RNA, herein designated GAM RNA, of GAM337330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337330 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337330 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337330 RNA correlate with, and may be deduced from, the identity of the GAM337330 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337331 7135 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCATTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337331 (GAM337331) oligonucleotides modulates expression of respective target
GTGGAAGTTG genes whose function and utility is known in the art.

CAGTGAGCTC GAM337331 is a novel bioinformatically detectable regulatory, non protein
AGATCGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337331 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAATGA encoded by the human genome.

AACTCCATCT GAM337331 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM337331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337331 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337331 precursor RNA is designated SEQ ID:7135, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7135 is located from position 100281287 to position 100281388 relative to chromosome 7 on the `+` strand.

GAM337331 precursor RNA folds onto itself, forming GAM337331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337331 precursor RNA, designated SEQ ID NO: 7135, and a schematic representation of a predicted secondary folding of GAM337331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337331 folded precursor RNA yielding a GAM337331 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337331 RNA, hereby incorporated herein.

GAM337331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337331 target RNA, herein designated GAM TARGET RNA.

GAM337331 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337331 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337331 RNA, herein designated GAM RNA, to target binding sites on GAM337331 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337331 target RNA into GAM337331 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337331 target genes. The mRNA of each one of this plurality of GAM337331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337331 RNA, herein designated GAM RNA, and which when bound by GAM337331 RNA causes inhibition of translation of the GAM337331 target mRNA into a corresponding GAM337331 target protein.

The mechanism of the translational inhibition exerted by GAM337331 RNA, herein designated GAM RNA, on one or more GAM337331 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337331 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337331 RNA, herein designated GAM RNA, of GAM337331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337331 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337331 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337331 RNA correlate with, and may be deduced from, the identity of the GAM337331 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337333 5911 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337333 (GAM337333) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337333 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337333 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337333 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337333 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337333 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337333 precursor RNA is designated SEQ ID:5911, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5911 is located from position 100558408 to position 100558489 relative to chromosome 1 on the `+` strand.

GAM337333 precursor RNA folds onto itself, forming GAM337333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337333 precursor RNA, designated SEQ ID NO: 5911, and a schematic representation of a predicted secondary folding of GAM337333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337333 folded precursor RNA yielding a GAM337333 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337333 RNA, hereby incorporated herein.

GAM337333 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337333 target RNA, herein designated GAM TARGET RNA.

GAM337333 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337333 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337333 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337333 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337333 RNA, herein designated GAM RNA, to target binding sites on GAM337333 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337333 target RNA into GAM337333 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337333 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337333 target genes. The mRNA of each one of this plurality of GAM337333 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337333 RNA, herein designated GAM RNA, and which when bound by GAM337333 RNA causes inhibition of translation of the GAM337333 target mRNA into a corresponding GAM337333 target protein.

The mechanism of the translational inhibition exerted by GAM337333 RNA, herein designated GAM RNA, on one or more GAM337333 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337333 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337333 RNA, herein designated GAM RNA, of GAM337333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337333 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337333 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337333 RNA correlate with, and may be deduced from, the identity of the GAM337333 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337334 6909 GTGGACTTAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGTAGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGCTTTGGG Messenger 337334 (GAM337334) oligonucleotides modulates expression of respective target
TGTAGGCCAG genes whose function and utility is known in the art.

GTAAGTTTCT GAM337334 is a novel bioinformatically detectable regulatory, non protein
GGTCTGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337334 was detected
CATTAGGCAC is described with additional reference to Figs. 9-15.

TTGGTAGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTAGCTAT encoded by the human genome.

GAM337334 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337334 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337334 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337334 precursor RNA is designated SEQ ID:6909, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6909 is located from position 100644251 to position 100644338 relative to chromosome 14 on the `+` strand.

GAM337334 precursor RNA folds onto itself, forming GAM337334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337334 precursor RNA, designated SEQ ID NO: 6909, and a schematic representation of a predicted secondary folding of GAM337334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337334 folded precursor RNA yielding a GAM337334 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337334 RNA, hereby incorporated herein.

GAM337334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337334 target RNA, herein designated GAM TARGET RNA.

GAM337334 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337334 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337334 RNA, herein designated GAM RNA, to target binding sites on GAM337334 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337334 target RNA into GAM337334 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337334 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337334 target genes. The mRNA of each one of this plurality of GAM337334 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337334 RNA, herein designated GAM RNA, and which when bound by GAM337334 RNA causes inhibition of translation of the GAM337334 target mRNA into a corresponding GAM337334 target protein.

The mechanism of the translational inhibition exerted by GAM337334 RNA, herein designated GAM RNA, on one or more GAM337334 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337334 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337334 RNA, herein designated GAM RNA, of GAM337334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337334 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337334 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337334 RNA correlate with, and may be deduced from, the identity of the GAM337334 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337336 5912 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337336 (GAM337336) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337336 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337336 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337336 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337336 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337336 precursor RNA is designated SEQ ID:5912, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5912 is located from position 100912899 to position 100912980 relative to chromosome 10 on the `+` strand.

GAM337336 precursor RNA folds onto itself, forming GAM337336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337336 precursor RNA, designated SEQ ID NO: 5912, and a schematic representation of a predicted secondary folding of GAM337336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337336 folded precursor RNA yielding a GAM337336 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337336 RNA, hereby incorporated herein.

GAM337336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337336 target RNA, herein designated GAM TARGET RNA.

GAM337336 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337336 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337336 RNA, herein designated GAM RNA, to target binding sites on GAM337336 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337336 target RNA into GAM337336 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337336 target genes. The mRNA of each one of this plurality of GAM337336 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337336 RNA, herein designated GAM RNA, and which when bound by GAM337336 RNA causes inhibition of translation of the GAM337336 target mRNA into a corresponding GAM337336 target protein.

The mechanism of the translational inhibition exerted by GAM337336 RNA, herein designated GAM RNA, on one or more GAM337336 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337336 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337336 RNA, herein designated GAM RNA, of GAM337336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337336 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337336 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337336 RNA correlate with, and may be deduced from, the identity of the GAM337336 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337337 6432 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCGGGAGG Messenger 337337 (GAM337337) oligonucleotides modulates expression of respective target

CAGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337337 is a novel bioinformatically detectable regulatory, non protein

GATTGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337337 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGTGAGA encoded by the human genome.

CTCTGTCTC GAM337337 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337337 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337337 precursor RNA is designated SEQ

ID:6432, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6432 is located from position 100953716 to position 100953814 relative to chromosome 12 on the `+` strand.

GAM337337 precursor RNA folds onto itself, forming GAM337337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337337 precursor RNA, designated SEQ ID NO: 6432, and a schematic representation of a predicted secondary folding of GAM337337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337337 folded precursor RNA yielding a GAM337337 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337337 RNA, hereby incorporated herein. Expression of GAM337337 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337337 target RNA, herein designated GAM TARGET RNA.

GAM337337 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337337 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337337 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337337 RNA, herein designated GAM RNA, to target binding sites on GAM337337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337337 target RNA

into GAM337337 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337337 target genes. The mRNA of each one of this plurality of GAM337337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337337 RNA, herein designated GAM RNA, and which when bound by GAM337337 RNA causes inhibition of translation of the GAM337337 target mRNA into a corresponding GAM337337 target protein.

The mechanism of the translational inhibition exerted by GAM337337 RNA, herein designated GAM RNA, on one or more GAM337337 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337337 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337337 RNA, herein designated GAM RNA, of GAM337337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337337 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337337 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337337 RNA correlate with, and may be deduced from, the identity of the GAM337337 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337341 6895 GTGACTCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATATGAAATC detected oligonucleotides of the present invention, referred to here as Genomic Address

CATTGCCAAG Messenger 337341 (GAM337341) oligonucleotides modulates expression of respective target

GCTGACCTTA genes whose function and utility is known in the art.

TCGTCACTAC GAM337341 is a novel bioinformatically detectable regulatory, non protein

GCCAGAGAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337341 was detected

TGGGATGGAG is described with additional reference to Figs. 9-15.

TCAGCAGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGGCAAAAT encoded by the human genome.

AGGAACTATG GAM337341 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTCAGCAAGT GAM337341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

CAC GAM337341 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337341 precursor RNA is designated SEQ ID:6895, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6895 is located from position 101077081 to position 101077193 relative to chromosome 6 on the `-` strand.

GAM337341 precursor RNA folds onto itself, forming GAM337341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337341 precursor RNA, designated SEQ ID NO: 6895, and a schematic representation of a predicted secondary folding of GAM337341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337341 folded precursor RNA yielding a GAM337341 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337341 RNA, hereby incorporated herein. Expression of GAM337341 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337341 target RNA, herein designated GAM TARGET RNA.

GAM337341 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337341 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337341 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337341 RNA, herein designated GAM RNA, to target binding sites on GAM337341 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337341 target RNA into GAM337341 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337341 target genes. The mRNA of each one of this plurality of GAM337341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337341 RNA, herein designated GAM RNA, and which when bound by GAM337341 RNA causes inhibition of translation of the GAM337341 target mRNA into a corresponding GAM337341 target protein.

The mechanism of the translational inhibition exerted by GAM337341 RNA, herein designated GAM RNA, on one or more GAM337341 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337341 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337341 RNA, herein designated GAM RNA, of GAM337341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337341 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337341 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337341 RNA correlate with, and may be deduced from, the identity of the GAM337341 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337343 5651 AAAGGGGGGT Fig. 8 further provides a conceptual description of another novel bioinformatically

GTAGTTATAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAGGGTCAT Messenger 337343 (GAM337343) oligonucleotides modulates expression of respective target
CTTTGATCTC genes whose function and utility is known in the art.

ATTTGGAAAA GAM337343 is a novel bioinformatically detectable regulatory, non protein
CTTCATTTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337343 was detected
AGATGGAGTT is described with additional reference to Figs. 9-15.

GCAGGTGGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTGGGGACT encoded by the human genome.

GATTCTGCAA GAM337343 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCCCCTTT GAM337343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337343 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337343 precursor RNA is designated SEQ ID:5651, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5651 is located from position 101399275 to position 101399382 relative to chromosome 7 on the `+` strand.

GAM337343 precursor RNA folds onto itself, forming GAM337343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337343 precursor RNA, designated SEQ ID NO: 5651, and a schematic representation of a predicted secondary folding of GAM337343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337343 folded precursor RNA yielding a GAM337343 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337343 RNA, hereby incorporated herein.

GAM337343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337343 target RNA, herein designated GAM TARGET RNA.

GAM337343 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337343 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337343 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337343 RNA, herein designated GAM RNA, to target binding sites on GAM337343 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337343 target RNA into GAM337343 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337343 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337343 target genes. The mRNA of each one of this plurality of GAM337343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337343 RNA, herein designated GAM RNA, and which when bound by GAM337343 RNA causes inhibition of translation of the GAM337343 target mRNA into a corresponding GAM337343 target protein.

The mechanism of the translational inhibition exerted by GAM337343 RNA, herein designated GAM RNA, on one or more GAM337343 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337343 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337343 RNA, herein designated GAM RNA, of GAM337343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337343 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337343 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337343 RNA correlate with, and may be deduced from, the identity of the GAM337343 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337344 5913 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337344 (GAM337344) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337344 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337344 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337344 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337344 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337344 precursor RNA is designated SEQ ID:5913, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5913 is located from position 101536725 to position 101536806 relative to chromosome 13 on the `-` strand.

GAM337344 precursor RNA folds onto itself, forming GAM337344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337344 precursor RNA, designated SEQ ID NO: 5913, and a schematic representation of a predicted secondary folding of GAM337344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337344 folded precursor RNA yielding a GAM337344 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337344 RNA, hereby incorporated herein.

GAM337344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337344 target RNA, herein designated GAM TARGET RNA.

GAM337344 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337344 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337344 RNA, herein designated GAM RNA, to target binding sites on GAM337344 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337344 target RNA into GAM337344 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337344 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337344 target genes. The mRNA of each one of this plurality of GAM337344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337344 RNA, herein designated GAM RNA, and which when bound by GAM337344 RNA causes inhibition of translation of the GAM337344 target mRNA into a corresponding GAM337344 target protein.

The mechanism of the translational inhibition exerted by GAM337344 RNA, herein designated GAM RNA, on one or more GAM337344 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337344 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337344 RNA, herein designated GAM RNA, of GAM337344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337344 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337344 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337344 RNA correlate with, and may be deduced from, the identity of the GAM337344 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337345 6442 GAGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGAAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGCCC Messenger 337345 (GAM337345) oligonucleotides modulates expression of respective target
AGGAATTAGA genes whose function and utility is known in the art.

GGCTGCAATG GAM337345 is a novel bioinformatically detectable regulatory, non protein
AGCTATGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337345 was detected
ATGCCACTGC is described with additional reference to Figs. 9-15.

ACTCCATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGGAGCAGA encoded by the human genome.

GCTAGACTCT GAM337345 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTCTC GAM337345 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337345 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337345 precursor RNA is designated SEQ ID:6442, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6442 is located from position 101538287 to position 101538391 relative to chromosome 7 on the `+` strand.

GAM337345 precursor RNA folds onto itself, forming GAM337345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337345 precursor RNA, designated SEQ ID NO: 6442, and a schematic representation of a predicted secondary folding of GAM337345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337345 folded precursor RNA yielding a GAM337345 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337345 RNA, hereby incorporated herein.

GAM337345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337345 target RNA, herein designated GAM TARGET RNA.

GAM337345 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337345 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337345 RNA, herein designated GAM RNA, to target binding sites on GAM337345 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337345 target RNA into GAM337345 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337345 target genes. The mRNA of each one of this plurality of GAM337345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337345 RNA, herein designated GAM RNA, and which when bound by GAM337345 RNA causes inhibition of translation of the GAM337345 target mRNA into a corresponding GAM337345 target protein.

The mechanism of the translational inhibition exerted by GAM337345 RNA, herein designated GAM RNA, on one or more GAM337345 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337345 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337345 RNA, herein designated GAM RNA, of GAM337345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337345 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337345 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337345 RNA correlate with, and may be deduced from, the identity of the GAM337345 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337346 6436 GAGGCGAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTGCTTGAA detected oligonucleotides of the present invention, referred to here as Genomic Address
CCCAGGAGGT Messenger 337346 (GAM337346) oligonucleotides modulates expression of respective target
GGAGGTTGCA genes whose function and utility is known in the art.

GTGAGCCAAG GAM337346 is a novel bioinformatically detectable regulatory, non protein
ATCATGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337346 was detected
TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGCAAGAC encoded by the human genome.

TCTGTCTC GAM337346 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337346 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337346 precursor RNA is designated SEQ ID:6436, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6436 is located from position 101601185 to position 101601282 relative to chromosome 9 on the `+` strand.

GAM337346 precursor RNA folds onto itself, forming GAM337346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337346 precursor RNA, designated SEQ ID NO: 6436, and a schematic representation of a predicted secondary folding of GAM337346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337346 folded precursor RNA yielding a GAM337346 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337346 RNA, hereby incorporated herein. Expression of GAM337346 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337346 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337346 target RNA, herein designated GAM TARGET RNA.

GAM337346 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337346 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337346 RNA, herein designated GAM RNA, to target binding sites on GAM337346 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337346 target RNA into GAM337346 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337346 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337346 target genes. The mRNA of each one of this plurality of GAM337346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337346 RNA,

herein designated GAM RNA, and which when bound by GAM337346 RNA causes inhibition of translation of the GAM337346 target mRNA into a corresponding GAM337346 target protein.

The mechanism of the translational inhibition exerted by GAM337346 RNA, herein designated GAM RNA, on one or more GAM337346 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337346 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337346 RNA, herein designated GAM RNA, of GAM337346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337346 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337346 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337346 RNA correlate with, and may be deduced from, the identity of the GAM337346 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337350 6794 GGGAGGCTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGGGAGGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
CACTTGAGCC Messenger 337350 (GAM337350) oligonucleotides modulates expression of respective target
CAGGAGTTCA genes whose function and utility is known in the art.

AGGCTGCAGT GAM337350 is a novel bioinformatically detectable regulatory, non protein
GAGCCATGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337350 was detected
TGCGCCACTG is described with additional reference to Figs. 9-15.

CACTCCAGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGGGCAACAG encoded by the human genome.

AGCAAGACCC GAM337350 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TGCCCCGCCG GAM337350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

CCT GAM337350 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337350 precursor RNA is designated SEQ ID:6794, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6794 is located from position 101642187 to position 101642299 relative to chromosome 7 on the `+` strand.

GAM337350 precursor RNA folds onto itself, forming GAM337350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337350 precursor RNA, designated SEQ ID NO: 6794, and a schematic representation of a predicted secondary folding of GAM337350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337350 folded precursor RNA yielding a GAM337350 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337350 RNA, hereby incorporated herein. Expression of GAM337350 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337350 target RNA, herein designated GAM TARGET RNA.

GAM337350 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337350 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337350 RNA, herein designated GAM RNA, to target binding sites on GAM337350 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337350 target RNA into GAM337350 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337350 target genes. The mRNA of each one of this plurality of GAM337350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337350 RNA, herein designated GAM RNA, and which when bound by GAM337350 RNA causes inhibition of translation of the GAM337350 target mRNA into a corresponding GAM337350 target protein.

The mechanism of the translational inhibition exerted by GAM337350 RNA, herein designated GAM RNA, on one or more GAM337350 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337350 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337350 RNA, herein designated GAM RNA, of GAM337350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337350 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337350 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337350 RNA correlate with, and may be deduced from, the identity of the GAM337350 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337351 6762 GGCTGAGGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAGGATCACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGAGCCCAGG Messenger 337351 (GAM337351) oligonucleotides modulates expression of respective target
AGTTCAAGGC genes whose function and utility is known in the art.

TGCAGTGAGC GAM337351 is a novel bioinformatically detectable regulatory, non protein
CATGATTGCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337351 was detected
CCACTGCACT is described with additional reference to Figs. 9-15.

CCAGCCTGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAACAGAGCA encoded by the human genome.

AGACCCTGCC GAM337351 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CCGCCGCC GAM337351 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337351 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337351 precursor RNA is designated SEQ ID:6762, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6762 is located from position 101642191 to position 101642298 relative to chromosome 7 on the `+` strand.

GAM337351 precursor RNA folds onto itself, forming GAM337351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337351 precursor RNA, designated SEQ ID NO: 6762, and a schematic representation of a predicted secondary folding of GAM337351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337351 folded precursor RNA yielding a GAM337351 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337351 RNA, hereby incorporated herein. Expression of GAM337351 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337351 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337351 target RNA, herein designated GAM TARGET RNA.

GAM337351 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337351 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337351 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337351 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337351 RNA, herein designated GAM RNA, to target binding sites on GAM337351 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337351 target RNA into GAM337351 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337351 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337351 target genes. The mRNA of each one of this plurality of GAM337351 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337351 RNA, herein designated GAM RNA, and which when bound by GAM337351 RNA causes inhibition of translation of the GAM337351 target mRNA into a corresponding GAM337351 target protein.

The mechanism of the translational inhibition exerted by GAM337351 RNA, herein designated GAM RNA, on one or more GAM337351 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337351 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337351 RNA, herein designated GAM RNA, of GAM337351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337351 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337351 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337351 RNA correlate with, and may be deduced from, the identity of the GAM337351 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337352 6816 GGGGGAGGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CACTTGAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGAGTTCA Messenger 337352 (GAM337352) oligonucleotides modulates expression of respective target
AGGCTGCAGT genes whose function and utility is known in the art.

GAGCCATGAT GAM337352 is a novel bioinformatically detectable regulatory, non protein
TGCGCCACTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337352 was detected
CACTCCAGCC is described with additional reference to Figs. 9-15.

TGGGCAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCAAGACCC encoded by the human genome.

TGCCCC GAM337352 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337352 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337352 precursor RNA is designated SEQ ID:6816, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6816 is located from position 101642197 to position 101642292 relative to chromosome 7 on the `+` strand.

GAM337352 precursor RNA folds onto itself, forming GAM337352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337352 precursor RNA, designated SEQ ID NO: 6816, and a schematic representation of a predicted secondary folding of GAM337352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337352 folded precursor RNA yielding a GAM337352 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337352 RNA, hereby incorporated herein. Expression of GAM337352 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337352 target RNA, herein designated GAM TARGET RNA.

GAM337352 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337352 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337352 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337352 RNA, herein designated GAM RNA, to target binding sites on GAM337352 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337352 target RNA into GAM337352 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337352 target genes. The mRNA of each one of this plurality of GAM337352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337352 RNA, herein designated GAM RNA, and which when bound by GAM337352 RNA causes inhibition of translation of the GAM337352 target mRNA into a corresponding GAM337352 target protein.

The mechanism of the translational inhibition exerted by GAM337352 RNA, herein designated GAM RNA, on one or more GAM337352 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337352 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337352 RNA, herein designated GAM RNA, of GAM337352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337352 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337352 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337352 RNA correlate with, and may be deduced from, the identity of the GAM337352 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337353 6509 GCCCTTCAGT CTCAGTAGCC ACATTTCAAG TGCTCAATAG TTACATGTGC CCAGTGGCTG CTGGACTGGG TGGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337353 (GAM337353) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337353 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337353 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337353 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337353 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337353 precursor RNA is designated SEQ ID:6509, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6509 is located from position 101658818 to position 101658891 relative to chromosome 13 on the `-` strand.

GAM337353 precursor RNA folds onto itself, forming GAM337353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337353 precursor RNA, designated SEQ ID NO: 6509, and a schematic representation of a predicted secondary folding of GAM337353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337353 folded precursor RNA yielding a GAM337353 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337353 RNA, hereby incorporated herein.

GAM337353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337353 target RNA, herein designated GAM TARGET RNA.

GAM337353 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337353 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337353 RNA, herein designated GAM RNA, to target binding sites on GAM337353 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337353 target RNA into GAM337353 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337353 target genes. The mRNA of each one of this plurality of GAM337353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337353 RNA, herein designated GAM RNA, and which when bound by GAM337353 RNA causes inhibition of translation of the GAM337353 target mRNA into a corresponding GAM337353 target protein.

The mechanism of the translational inhibition exerted by GAM337353 RNA, herein designated GAM RNA, on one or more GAM337353 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337353 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337353 RNA, herein designated GAM RNA, of GAM337353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337353 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337353 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337353 RNA correlate with, and may be deduced from, the identity of the GAM337353 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337354 6094 CCCTTCAGTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCAGTAGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CATTTCAAGT Messenger 337354 (GAM337354) oligonucleotides modulates expression of respective target
GCTCAATAGT genes whose function and utility is known in the art.

TACATGTGCC GAM337354 is a novel bioinformatically detectable regulatory, non protein
CAGTGGCTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337354 was detected
TGGACTGGGT is described with additional reference to Figs. 9-15.

GG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337354 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337354 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337354 precursor RNA is designated SEQ ID:6094, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6094 is located from position 101658819 to position 101658890 relative to chromosome 13 on the `-` strand.

GAM337354 precursor RNA folds onto itself, forming GAM337354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337354 precursor RNA, designated SEQ ID NO: 6094, and a schematic representation of a predicted secondary folding of GAM337354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337354 folded precursor RNA yielding a GAM337354 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337354 RNA, hereby incorporated herein.

GAM337354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337354 target RNA, herein designated GAM TARGET RNA.

GAM337354 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337354 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337354 RNA, herein designated GAM RNA, to target binding sites on GAM337354 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337354 target RNA into GAM337354 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337354 target genes. The mRNA of each one of this plurality of GAM337354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337354 RNA, herein designated GAM RNA, and which when bound by GAM337354 RNA causes inhibition of translation of the GAM337354 target mRNA into a corresponding GAM337354 target protein.

The mechanism of the translational inhibition exerted by GAM337354 RNA, herein designated GAM RNA, on one or more GAM337354 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337354 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337354 RNA, herein designated GAM RNA, of GAM337354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337354 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337354 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337354 RNA correlate with, and may be deduced from, the identity of the GAM337354 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337355 6443 GAGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGAAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGCCC Messenger 337355 (GAM337355) oligonucleotides modulates expression of respective target
AGGAATTAGA genes whose function and utility is known in the art.

GGCTGCAATG GAM337355 is a novel bioinformatically detectable regulatory, non protein
AGCTATGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337355 was detected
ATGCCACTGC is described with additional reference to Figs. 9-15.

ACTCCATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGGGAGCAGA encoded by the human genome.

GCTAGACTCT GAM337355 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GTCTC GAM337355 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337355 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337355 precursor RNA is designated SEQ ID:6443, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6443 is located from position 101744915 to position 101745019 relative to chromosome 7 on the `-` strand.

GAM337355 precursor RNA folds onto itself, forming GAM337355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337355 precursor RNA, designated SEQ ID NO: 6443, and a schematic representation of a predicted secondary folding of GAM337355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337355 folded precursor RNA yielding a GAM337355 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337355 RNA, hereby incorporated herein.

GAM337355 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337355 target RNA, herein designated GAM TARGET RNA.

GAM337355 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337355 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337355 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337355 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337355 RNA, herein designated GAM RNA, to target binding sites on GAM337355 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337355 target RNA into GAM337355 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337355 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337355 target genes. The mRNA of each one of this plurality of GAM337355 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337355 RNA, herein designated GAM RNA, and which when bound by GAM337355 RNA causes inhibition of translation of the GAM337355 target mRNA into a corresponding GAM337355 target protein.

The mechanism of the translational inhibition exerted by GAM337355 RNA, herein designated GAM RNA, on one or more GAM337355 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337355 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337355 RNA, herein designated GAM RNA, of GAM337355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337355 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337355 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337355 RNA correlate with, and may be deduced from, the identity of the GAM337355 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337356 7012 TCAGTTCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTATCTGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCTCCTACCC Messenger 337356 (GAM337356) oligonucleotides modulates expression of respective target

AGAGATTCTA genes whose function and utility is known in the art.

CCCAGTGAAA GAM337356 is a novel bioinformatically detectable regulatory, non protein

CTCCCACAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337356 was detected

AGCGCAGGTA is described with additional reference to Figs. 9-15.

GATGGGGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

A encoded by the human genome.

GAM337356 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337356 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337356 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337356 precursor RNA is designated SEQ

ID:7012, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7012 is located from position 101746098 to position 101746178 relative to chromosome 9 on the `+` strand.

GAM337356 precursor RNA folds onto itself, forming GAM337356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337356 precursor RNA, designated SEQ ID NO: 7012, and a schematic representation of a predicted secondary folding of GAM337356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337356 folded precursor RNA yielding a GAM337356 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337356 RNA, hereby incorporated herein.

GAM337356 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337356 target RNA, herein designated GAM TARGET RNA.

GAM337356 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337356 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337356 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337356 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337356 RNA, herein designated GAM RNA, to target binding sites on GAM337356 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337356 target RNA into GAM337356 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337356 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337356 target genes. The mRNA of each one of this plurality of GAM337356 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337356 RNA, herein designated GAM RNA, and which when bound by GAM337356 RNA causes inhibition of translation of the GAM337356 target mRNA into a corresponding GAM337356 target protein.

The mechanism of the translational inhibition exerted by GAM337356 RNA, herein designated GAM RNA, on one or more GAM337356 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337356 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337356 RNA, herein designated GAM RNA, of GAM337356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337356 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337356 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337356 RNA correlate with, and may be deduced from, the identity of the GAM337356 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337357 6444 GAGGCTGAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AAAGAAGATT detected oligonucleotides of the present invention, referred to here as Genomic Address
GCTTGAGCCC Messenger 337357 (GAM337357) oligonucleotides modulates expression of respective target
AGGAATTAGA genes whose function and utility is known in the art.

GGCTGCAATG GAM337357 is a novel bioinformatically detectable regulatory, non protein
AGCTATGATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337357 was detected
ATGCCACTGC is described with additional reference to Figs. 9-15.

ACTCCATCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGGGAGCAGA encoded by the human genome.

GCTAGACTCT GAM337357 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GTCTC GAM337357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337357 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337357 precursor RNA is designated SEQ ID:6444, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6444 is located from position 101843971 to position 101844075 relative to chromosome 7 on the `-` strand.

GAM337357 precursor RNA folds onto itself, forming GAM337357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337357 precursor RNA, designated SEQ ID NO: 6444, and a schematic representation of a predicted secondary folding of GAM337357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337357 folded precursor RNA yielding a GAM337357 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337357 RNA, hereby incorporated herein.

GAM337357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337357 target RNA, herein designated GAM TARGET RNA.

GAM337357 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337357 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337357 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337357 RNA, herein designated GAM RNA, to target binding sites on GAM337357 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337357 target RNA into GAM337357 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337357 target genes. The mRNA of each one of this plurality of GAM337357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337357 RNA, herein designated GAM RNA, and which when bound by GAM337357 RNA causes inhibition of translation of the GAM337357 target mRNA into a corresponding GAM337357 target protein.

The mechanism of the translational inhibition exerted by GAM337357 RNA, herein designated GAM RNA, on one or more GAM337357 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337357 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337357 RNA, herein designated GAM RNA, of GAM337357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337357 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337357 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337357 RNA correlate with, and may be deduced from, the identity of the GAM337357 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337358 5646 AAAATAAAAT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAAATCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGTCTAGG Messenger 337358 (GAM337358) oligonucleotides modulates expression of respective target

CTTTTGGAGA genes whose function and utility is known in the art.

AGCATATGCT GAM337358 is a novel bioinformatically detectable regulatory, non protein
GTGAAAATGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337358 was detected
TCACGGCTGT is described with additional reference to Figs. 9-15.

GCTCCTAAAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCCAGTCATG encoded by the human genome.

TTTCTGTAAC GAM337358 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AGTTTT GAM337358 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337358 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337358 precursor RNA is designated SEQ ID:5646, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5646 is located from position 101964516 to position 101964621 relative to chromosome 14 on the `-` strand.

GAM337358 precursor RNA folds onto itself, forming GAM337358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337358 precursor RNA, designated SEQ ID NO: 5646, and a schematic representation of a predicted secondary folding of GAM337358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337358 folded precursor RNA yielding a GAM337358 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337358 RNA, hereby incorporated herein.

GAM337358 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337358 target RNA, herein designated GAM TARGET RNA.

GAM337358 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337358 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337358 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337358 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337358 RNA, herein designated GAM RNA, to target binding sites on GAM337358 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337358 target RNA into GAM337358 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337358 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337358 target genes. The mRNA of each one of this plurality of GAM337358 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337358 RNA, herein designated GAM RNA, and which when bound by GAM337358 RNA causes inhibition of translation of the GAM337358 target mRNA into a corresponding GAM337358 target protein.

The mechanism of the translational inhibition exerted by GAM337358 RNA, herein designated GAM RNA, on one or more GAM337358 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337358 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337358 RNA, herein designated GAM RNA, of GAM337358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337358 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337358 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337358 RNA correlate with, and may be deduced from, the identity of the GAM337358 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337359 5951 ATAGAAATCA Fig. 8 further provides a conceptual description of another novel bioinformatically
TTATTGTCTA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTTTTGGA Messenger 337359 (GAM337359) oligonucleotides modulates expression of respective target
GAAGCATATG genes whose function and utility is known in the art.

CTGTGAAAAT GAM337359 is a novel bioinformatically detectable regulatory, non protein
GATCACGGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337359 was detected
GTGCTCCTAA is described with additional reference to Figs. 9-15.

AAGCCAGTCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGTTTCTGT encoded by the human genome.

GAM337359 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337359 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337359 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337359 precursor RNA is designated SEQ ID:5951, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5951 is located from position 101964525 to position 101964613 relative to chromosome 14 on the `-` strand.

GAM337359 precursor RNA folds onto itself, forming GAM337359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337359 precursor RNA, designated SEQ ID NO: 5951, and a schematic representation of a predicted secondary folding of GAM337359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337359 folded precursor RNA yielding a GAM337359 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337359 RNA, hereby incorporated herein.

GAM337359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337359 target RNA, herein designated GAM TARGET RNA.

GAM337359 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337359 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337359 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337359 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337359 RNA, herein designated GAM RNA, to target binding sites on GAM337359 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337359 target RNA into GAM337359 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337359 target genes. The mRNA of each one of this plurality of GAM337359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337359 RNA, herein designated GAM RNA, and which when bound by GAM337359 RNA causes inhibition of translation of the GAM337359 target mRNA into a corresponding GAM337359 target protein.

The mechanism of the translational inhibition exerted by GAM337359 RNA, herein designated GAM RNA, on one or more GAM337359 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337359 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337359 RNA, herein designated GAM RNA, of GAM337359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337359 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337359 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337359 RNA correlate with, and may be deduced from, the identity of the GAM337359 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337361 6243 CTGTGATGGT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGTTCTAT detected oligonucleotides of the present invention, referred to here as Genomic Address
TATAAAGTGG Messenger 337361 (GAM337361) oligonucleotides modulates expression of respective target
CACCATTGGA genes whose function and utility is known in the art.

GTCTAAGGGT GAM337361 is a novel bioinformatically detectable regulatory, non protein
GCTTGTTTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337361 was detected
CCTTACACTA is described with additional reference to Figs. 9-15.

AATGGTCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTGTTTATG encoded by the human genome.

TGGTTCTGAC GAM337361 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ACTGCCGTCC GAM337361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
AG GAM337361 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337361 precursor RNA is designated SEQ ID:6243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6243 is located from position 103489943 to position 103490054 relative to chromosome 10 on the `+` strand.

GAM337361 precursor RNA folds onto itself, forming GAM337361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337361 precursor RNA, designated SEQ ID NO: 6243, and a schematic representation of a predicted secondary folding of GAM337361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337361 folded precursor RNA yielding a GAM337361 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337361 RNA, hereby incorporated herein.

GAM337361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337361 target RNA, herein designated GAM TARGET RNA.

GAM337361 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337361 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337361 RNA, herein designated GAM RNA, to target binding sites on GAM337361 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337361 target RNA into GAM337361 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337361 target genes. The mRNA of each one of this plurality of GAM337361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337361 RNA, herein designated GAM RNA, and which when bound by GAM337361 RNA causes inhibition of translation of the GAM337361 target mRNA into a corresponding GAM337361 target protein.

The mechanism of the translational inhibition exerted by GAM337361 RNA, herein designated GAM RNA, on one or more GAM337361 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337361 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337361 RNA, herein designated GAM RNA, of

GAM337361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337361 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337361 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337361 RNA correlate with, and may be deduced from, the identity of the GAM337361 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337363 5914 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337363 (GAM337363) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337363 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337363 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337363 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337363 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337363 precursor RNA is designated SEQ ID:5914, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5914 is located from position 103632887 to position 103632968 relative to chromosome 3 on the `+` strand.

GAM337363 precursor RNA folds onto itself, forming GAM337363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337363 precursor RNA, designated SEQ ID NO: 5914, and

a schematic representation of a predicted secondary folding of GAM337363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337363 folded precursor RNA yielding a GAM337363 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337363 RNA, hereby incorporated herein.

GAM337363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337363 target RNA, herein designated GAM TARGET RNA.

GAM337363 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337363 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337363 RNA, herein designated GAM RNA, to target binding sites on GAM337363 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337363 target RNA into GAM337363 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337363 target genes. The mRNA of each one of this plurality of GAM337363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337363 RNA, herein designated GAM RNA, and which when bound by GAM337363 RNA causes inhibition of translation of the GAM337363 target mRNA into a corresponding GAM337363 target protein.

The mechanism of the translational inhibition exerted by GAM337363 RNA, herein designated GAM RNA, on one or more GAM337363 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337363 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337363 RNA, herein designated GAM RNA, of GAM337363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337363 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337363 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337363 RNA correlate with, and may be deduced from, the identity of the GAM337363 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337364 6154 CTAGGGTGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGTTTTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAGGCTCGC Messenger 337364 (GAM337364) oligonucleotides modulates expression of respective target

TCTCTCAGGG genes whose function and utility is known in the art.

GGACCATCCC GAM337364 is a novel bioinformatically detectable regulatory, non protein

GCACTTGCAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337364 was detected

GCCCTTGAGA is described with additional reference to Figs. 9-15.

ATGAGGTCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTTAAATAT encoded by the human genome.

TCACTCTGG GAM337364 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337364 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337364 precursor RNA is designated SEQ ID:6154, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6154 is located from position 103784499 to position 103784597 relative to chromosome 9 on the `+` strand.

GAM337364 precursor RNA folds onto itself, forming GAM337364 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337364 precursor RNA, designated SEQ ID NO: 6154, and a schematic representation of a predicted secondary folding of GAM337364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337364 folded precursor RNA yielding a GAM337364 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337364 RNA, hereby incorporated herein.

GAM337364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337364 target RNA, herein designated GAM TARGET RNA.

GAM337364 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337364 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337364 RNA, herein designated GAM RNA, to target binding sites on GAM337364 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337364 target RNA into GAM337364 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337364 target genes. The mRNA of each one of this plurality of GAM337364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337364 RNA,

herein designated GAM RNA, and which when bound by GAM337364 RNA causes inhibition of translation of the GAM337364 target mRNA into a corresponding GAM337364 target protein.

The mechanism of the translational inhibition exerted by GAM337364 RNA, herein designated GAM RNA, on one or more GAM337364 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337364 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337364 RNA, herein designated GAM RNA, of GAM337364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337364 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337364 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337364 RNA correlate with, and may be deduced from, the identity of the GAM337364 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337366 6502 GCATTGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCAAGGCTG Messenger 337366 (GAM337366) oligonucleotides modulates expression of respective target

CAGTGAGTCA genes whose function and utility is known in the art.

AGGTCATGCC GAM337366 is a novel bioinformatically detectable regulatory, non protein

ACTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337366 was detected

ATCCTGGGAC is described with additional reference to Figs. 9-15.

AGAGCAAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337366 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337366 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337366 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337366 precursor RNA is designated SEQ ID:6502, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6502 is located from position 104305997 to position 104306075 relative to chromosome 7 on the `+` strand.

GAM337366 precursor RNA folds onto itself, forming GAM337366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337366 precursor RNA, designated SEQ ID NO: 6502, and a schematic representation of a predicted secondary folding of GAM337366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337366 folded precursor RNA yielding a GAM337366 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337366 RNA, hereby incorporated herein.

GAM337366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337366 target RNA, herein designated GAM TARGET RNA.

GAM337366 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337366 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337366 RNA, herein designated GAM RNA, to target binding sites on GAM337366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337366 target RNA

into GAM337366 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337366 target genes. The mRNA of each one of this plurality of GAM337366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337366 RNA, herein designated GAM RNA, and which when bound by GAM337366 RNA causes inhibition of translation of the GAM337366 target mRNA into a corresponding GAM337366 target protein.

The mechanism of the translational inhibition exerted by GAM337366 RNA, herein designated GAM RNA, on one or more GAM337366 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337366 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337366 RNA, herein designated GAM RNA, of GAM337366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337366 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337366 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337366 RNA correlate with, and may be deduced from, the identity of the GAM337366 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337367 6054 CCAGGCCTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CGGTAGGTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

AGAATGAGGT Messenger 337367 (GAM337367) oligonucleotides modulates expression of respective target

CTGTGTCACT genes whose function and utility is known in the art.

GTGGTATTAC GAM337367 is a novel bioinformatically detectable regulatory, non protein

GATATTTTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337367 was detected

CTGGTTATTA is described with additional reference to Figs. 9-15.

TAACCACAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTCACAGAGT encoded by the human genome.

CCATCAAAAA GAM337367 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CCCATGCCTG GAM337367 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

G GAM337367 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337367 precursor RNA is designated SEQ ID:6054, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6054 is located from position 104342178 to position 104342288 relative to chromosome 14 on the `-` strand.

GAM337367 precursor RNA folds onto itself, forming GAM337367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337367 precursor RNA, designated SEQ ID NO: 6054, and a schematic representation of a predicted secondary folding of GAM337367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337367 folded precursor RNA yielding a GAM337367 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337367 RNA, hereby incorporated herein.

GAM337367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337367 target RNA, herein designated GAM TARGET RNA.

GAM337367 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337367 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337367 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337367 RNA, herein designated GAM RNA, to target binding sites on GAM337367 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337367 target RNA into GAM337367 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337367 target genes. The mRNA of each one of this plurality of GAM337367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337367 RNA, herein designated GAM RNA, and which when bound by GAM337367 RNA causes inhibition of translation of the GAM337367 target mRNA into a corresponding GAM337367 target protein.

The mechanism of the translational inhibition exerted by GAM337367 RNA, herein designated GAM RNA, on one or more GAM337367 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337367 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337367 RNA, herein designated GAM RNA, of GAM337367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337367 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337367 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337367 RNA correlate with, and may be deduced from, the identity of the GAM337367 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337368 6831 GGTAGGTTTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGAGGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTGTCACTG Messenger 337368 (GAM337368) oligonucleotides modulates expression of respective target

TGGTATTACG genes whose function and utility is known in the art.

ATATTTTGAC GAM337368 is a novel bioinformatically detectable regulatory, non protein
TGGTTATTAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337368 was detected
AACCACAGTG is described with additional reference to Figs. 9-15.

TCACAGAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CATCAAAAAC encoded by the human genome.

CCATGCC GAM337368 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337368 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337368 precursor RNA is designated SEQ ID:6831, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6831 is located from position 104342181 to position 104342277 relative to chromosome 14 on the `-` strand.

GAM337368 precursor RNA folds onto itself, forming GAM337368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337368 precursor RNA, designated SEQ ID NO: 6831, and a schematic representation of a predicted secondary folding of GAM337368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337368 folded precursor RNA yielding a GAM337368 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337368 RNA, hereby incorporated herein.

GAM337368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337368 target RNA, herein designated GAM TARGET RNA.

GAM337368 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337368 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337368 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337368 RNA, herein designated GAM RNA, to target binding sites on GAM337368 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337368 target RNA into GAM337368 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337368 target genes. The mRNA of each one of this plurality of GAM337368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337368 RNA, herein designated GAM RNA, and which when bound by GAM337368 RNA causes inhibition of translation of the GAM337368 target mRNA into a corresponding GAM337368 target protein.

The mechanism of the translational inhibition exerted by GAM337368 RNA, herein designated GAM RNA, on one or more GAM337368 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337368 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337368 RNA, herein designated GAM RNA, of GAM337368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337368 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337368 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337368 RNA correlate with, and may be deduced from, the identity of the GAM337368 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337370 6778 GGGACAGCAT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTTTTTTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
CATTTGTTTG Messenger 337370 (GAM337370) oligonucleotides modulates expression of respective target
TTGCGGGTGG genes whose function and utility is known in the art.

GGAGAGGATT GAM337370 is a novel bioinformatically detectable regulatory, non protein
GAACCCTTAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337370 was detected
CCTCACCTCG is described with additional reference to Figs. 9-15.

CTCGCAAGTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAAGAAAGG encoded by the human genome.

GAACCTGACC GAM337370 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
C GAM337370 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337370 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337370 precursor RNA is designated SEQ ID:6778, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6778 is located from position 104509126 to position 104509226 relative to chromosome 10 on the `+` strand.

GAM337370 precursor RNA folds onto itself, forming GAM337370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337370 precursor RNA, designated SEQ ID NO: 6778, and a schematic representation of a predicted secondary folding of GAM337370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337370 folded precursor RNA yielding a GAM337370 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337370 RNA, hereby incorporated herein.

GAM337370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337370 target RNA, herein designated GAM TARGET RNA.

GAM337370 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337370 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337370 RNA, herein designated GAM RNA, to target binding sites on GAM337370 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337370 target RNA into GAM337370 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337370 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337370 target genes. The mRNA of each one of this plurality of GAM337370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337370 RNA, herein designated GAM RNA, and which when bound by GAM337370 RNA causes inhibition of translation of the GAM337370 target mRNA into a corresponding GAM337370 target protein.

The mechanism of the translational inhibition exerted by GAM337370 RNA, herein designated GAM RNA, on one or more GAM337370 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337370 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337370 RNA, herein designated GAM RNA, of GAM337370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337370 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337370 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337370 RNA correlate with, and may be deduced from, the identity of the GAM337370 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337371 7027 TCCCCTTCCT Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTTCCCTCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTTGTAAA Messenger 337371 (GAM337371) oligonucleotides modulates expression of respective target

TAACATTTTT genes whose function and utility is known in the art.

TAGCAGCAAT GAM337371 is a novel bioinformatically detectable regulatory, non protein

GTAATCTGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337371 was detected

AAATGTTAGT is described with additional reference to Figs. 9-15.

TGTTTAGGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTCCTGAGA encoded by the human genome.

AAAGGGGA GAM337371 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337371 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337371 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337371 precursor RNA is designated SEQ ID:7027, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7027 is located from position 104616032 to position 104616129 relative to chromosome 12 on the `+` strand.

GAM337371 precursor RNA folds onto itself, forming GAM337371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337371 precursor RNA, designated SEQ ID NO: 7027, and a schematic representation of a predicted secondary folding of GAM337371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337371 folded precursor RNA yielding a GAM337371 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337371 RNA, hereby incorporated herein.

GAM337371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337371 target RNA, herein designated GAM TARGET RNA.

GAM337371 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337371 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337371 RNA, herein designated GAM RNA, to target binding sites on GAM337371 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337371 target RNA into GAM337371 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337371 target genes. The mRNA of each one of this plurality of GAM337371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337371 RNA, herein designated GAM RNA, and which when bound by GAM337371 RNA causes inhibition of translation of the GAM337371 target mRNA into a corresponding GAM337371 target protein.

The mechanism of the translational inhibition exerted by GAM337371 RNA, herein designated GAM RNA, on one or more GAM337371 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337371 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337371 RNA, herein designated GAM RNA, of GAM337371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337371 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337371 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337371 RNA correlate with, and may be deduced from, the identity of the GAM337371 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337372 6088 CCCTGGAGGC AGGTGCAGAT GGAGGCTGTT TCCTGTCAGG ATGTGGGACT TTGTCTTCTT CTGACAGTTC CCCAGGG

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337372 (GAM337372) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337372 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337372 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337372 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337372 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337372 precursor RNA is designated SEQ ID:6088, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6088 is located from position 104762497 to position 104762573 relative to chromosome 14 on the `-` strand.

GAM337372 precursor RNA folds onto itself, forming GAM337372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337372 precursor RNA, designated SEQ ID NO: 6088, and a schematic representation of a predicted secondary folding of GAM337372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337372 folded precursor RNA yielding a GAM337372 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337372 RNA, hereby incorporated herein.

GAM337372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337372 target RNA, herein designated GAM TARGET RNA.

GAM337372 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337372 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337372 RNA, herein designated GAM RNA, to target binding sites on GAM337372 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337372 target RNA into GAM337372 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337372 target genes. The mRNA of each one of this plurality of GAM337372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337372 RNA, herein designated GAM RNA, and which when bound by GAM337372 RNA causes inhibition of translation of the GAM337372 target mRNA into a corresponding GAM337372 target protein.

The mechanism of the translational inhibition exerted by GAM337372 RNA, herein designated GAM RNA, on one or more GAM337372 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337372 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337372 RNA, herein designated GAM RNA, of GAM337372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337372 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337372 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337372 RNA correlate with, and may be deduced from, the identity of the GAM337372 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337373 6089 CCCTGGAGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGTGCAGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGCTGTT Messenger 337373 (GAM337373) oligonucleotides modulates expression of respective target
TCCTGTCAGG genes whose function and utility is known in the art.

ATGTGGGACT GAM337373 is a novel bioinformatically detectable regulatory, non protein
TTGTCTTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337373 was detected
CTGACAGTTC is described with additional reference to Figs. 9-15.

CCCAGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337373 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337373 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337373 precursor RNA is designated SEQ ID:6089, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6089 is located from position 104787214 to position 104787290 relative to chromosome 14 on the `-` strand.

GAM337373 precursor RNA folds onto itself, forming GAM337373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337373 precursor RNA, designated SEQ ID NO: 6089, and a schematic representation of a predicted secondary folding of GAM337373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337373 folded precursor RNA yielding a GAM337373 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337373 RNA, hereby incorporated herein.

GAM337373 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337373 target RNA, herein designated GAM TARGET RNA.

GAM337373 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337373 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337373 RNA, herein designated GAM RNA, to target binding sites on GAM337373 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337373 target RNA into GAM337373 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337373 target genes. The mRNA of each one of this

plurality of GAM337373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337373 RNA, herein designated GAM RNA, and which when bound by GAM337373 RNA causes inhibition of translation of the GAM337373 target mRNA into a corresponding GAM337373 target protein.

The mechanism of the translational inhibition exerted by GAM337373 RNA, herein designated GAM RNA, on one or more GAM337373 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337373 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337373 RNA, herein designated GAM RNA, of GAM337373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337373 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337373 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337373 RNA correlate with, and may be deduced from, the identity of the GAM337373 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337374 6797 GGGATGCCAA Fig. 8 further provides a conceptual description of another novel bioinformatically

ACCCTCTCCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TGTGTTACAT Messenger 337374 (GAM337374) oligonucleotides modulates expression of respective target

TAGTGCTATG genes whose function and utility is known in the art.

ACTGAACATA GAM337374 is a novel bioinformatically detectable regulatory, non protein

AACACTGCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337374 was detected

TAATGGACGG is described with additional reference to Figs. 9-15.

TGAGATCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGTCATCCT encoded by the human genome.

GAM337374 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337374 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337374 precursor RNA is designated SEQ ID:6797, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6797 is located from position 104818818 to position 104818907 relative to chromosome 10 on the `+` strand.

GAM337374 precursor RNA folds onto itself, forming GAM337374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337374 precursor RNA, designated SEQ ID NO: 6797, and a schematic representation of a predicted secondary folding of GAM337374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337374 folded precursor RNA yielding a GAM337374 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337374 RNA, hereby incorporated herein.

GAM337374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337374 target RNA, herein designated GAM TARGET RNA.

GAM337374 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337374 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337374 RNA, herein designated GAM RNA, to target binding sites on GAM337374 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337374 target RNA into GAM337374 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337374 target genes. The mRNA of each one of this plurality of GAM337374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337374 RNA, herein designated GAM RNA, and which when bound by GAM337374 RNA causes inhibition of translation of the GAM337374 target mRNA into a corresponding GAM337374 target protein.

The mechanism of the translational inhibition exerted by GAM337374 RNA, herein designated GAM RNA, on one or more GAM337374 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337374 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337374 RNA, herein designated GAM RNA, of GAM337374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337374 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337374 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337374 RNA correlate with, and may be deduced from, the identity of the GAM337374 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337375 6183 CTCTTGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGAGGTGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGTTGGGGT Messenger 337375 (GAM337375) oligonucleotides modulates expression of respective target
GAGCTGAGAT genes whose function and utility is known in the art.

CACTCCATTG GAM337375 is a novel bioinformatically detectable regulatory, non protein
CACTCCAGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337375 was detected
TGGGCAACGA is described with additional reference to Figs. 9-15.

GAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337375 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337375 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337375 precursor RNA is designated SEQ ID:6183, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6183 is located from position 104911214 to position 104911286 relative to chromosome 8 on the `+` strand.

GAM337375 precursor RNA folds onto itself, forming GAM337375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337375 precursor RNA, designated SEQ ID NO: 6183, and a schematic representation of a predicted secondary folding of GAM337375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337375 folded precursor RNA yielding a GAM337375 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337375 RNA, hereby incorporated herein.

GAM337375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337375 target RNA, herein designated GAM TARGET RNA.

GAM337375 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337375 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337375 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337375 RNA, herein designated GAM RNA, to target binding sites on GAM337375 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337375 target RNA into GAM337375 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337375 target genes. The mRNA of each one of this plurality of GAM337375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337375 RNA, herein designated GAM RNA, and which when bound by GAM337375 RNA causes inhibition of translation of the GAM337375 target mRNA into a corresponding GAM337375 target protein.

The mechanism of the translational inhibition exerted by GAM337375 RNA, herein designated GAM RNA, on one or more GAM337375 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337375 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337375 RNA, herein designated GAM RNA, of GAM337375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337375 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337375 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337375 RNA correlate with, and may be deduced from, the identity of the GAM337375 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337376 6363 GAGCTGCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

CATGGCTAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGAAGCAGG Messenger 337376 (GAM337376) oligonucleotides modulates expression of respective target

TAGGAGAAAT genes whose function and utility is known in the art.

TGGAGAGACT GAM337376 is a novel bioinformatically detectable regulatory, non protein
AGACTTGTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337376 was detected
AGTCTTCCAG is described with additional reference to Figs. 9-15.

CCTCCATCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTCCCATGC encoded by the human genome.

TGGATGCTT GAM337376 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337376 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337376 precursor RNA is designated SEQ ID:6363, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6363 is located from position 104932380 to position 104932478 relative to chromosome 14 on the `+` strand.

GAM337376 precursor RNA folds onto itself, forming GAM337376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337376 precursor RNA, designated SEQ ID NO: 6363, and a schematic representation of a predicted secondary folding of GAM337376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337376 folded precursor RNA yielding a GAM337376 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337376 RNA, hereby incorporated herein.

GAM337376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337376 target RNA, herein designated GAM TARGET RNA.

GAM337376 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337376 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337376 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337376 RNA, herein designated GAM RNA, to target binding sites on GAM337376 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337376 target RNA into GAM337376 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337376 target genes. The mRNA of each one of this plurality of GAM337376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337376 RNA, herein designated GAM RNA, and which when bound by GAM337376 RNA causes inhibition of translation of the GAM337376 target mRNA into a corresponding GAM337376 target protein.

The mechanism of the translational inhibition exerted by GAM337376 RNA, herein designated GAM RNA, on one or more GAM337376 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337376 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337376 RNA, herein designated GAM RNA, of GAM337376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337376 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337376 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337376 RNA correlate with, and may be deduced from, the identity of the GAM337376 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337377 6584 GGAATCTTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTGTAGCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCTGGAGT Messenger 337377 (GAM337377) oligonucleotides modulates expression of respective target
GCAGTGGTGT genes whose function and utility is known in the art.

GATCTTGGCT GAM337377 is a novel bioinformatically detectable regulatory, non protein
CACGGCAACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337377 was detected
TCTGCCTCCC is described with additional reference to Figs. 9-15.

GGGTCTAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAAGCAGTT encoded by the human genome.

CTCC GAM337377 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337377 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337377 precursor RNA is designated SEQ ID:6584, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6584 is located from position 105033873 to position 105033966 relative to chromosome 10 on the `-` strand.

GAM337377 precursor RNA folds onto itself, forming GAM337377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337377 precursor RNA, designated SEQ ID NO: 6584, and a schematic representation of a predicted secondary folding of GAM337377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337377 folded precursor RNA yielding a GAM337377 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337377 RNA, hereby incorporated herein.

GAM337377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337377 target RNA, herein designated GAM TARGET RNA.

GAM337377 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337377 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337377 RNA, herein designated GAM RNA, to target binding sites on GAM337377 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337377 target RNA into GAM337377 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337377 target genes. The mRNA of each one of this plurality of GAM337377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337377 RNA, herein designated GAM RNA, and which when bound by GAM337377 RNA causes inhibition of translation of the GAM337377 target mRNA into a corresponding GAM337377 target protein.

The mechanism of the translational inhibition exerted by GAM337377 RNA, herein designated GAM RNA, on one or more GAM337377 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337377 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337377 RNA, herein designated GAM RNA, of GAM337377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337377 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337377 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337377 RNA correlate with, and may be deduced from, the identity of the GAM337377 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337378 6583 GGAATCTTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTTGTAGCCC detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCTGGAGT Messenger 337378 (GAM337378) oligonucleotides modulates expression of respective target
GCAGTGGTGT genes whose function and utility is known in the art.

GATCTTGGCT GAM337378 is a novel bioinformatically detectable regulatory, non protein
CACGGCAACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337378 was detected
TCTGCCTCCC is described with additional reference to Figs. 9-15.

GGGTCTAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCAAGCAGTT encoded by the human genome.

CT GAM337378 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337378 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337378 precursor RNA is designated SEQ ID:6583, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6583 is located from position 105033875 to position 105033966 relative to chromosome 10 on the `-` strand.

GAM337378 precursor RNA folds onto itself, forming GAM337378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337378 precursor RNA, designated SEQ ID NO: 6583, and a schematic representation of a predicted secondary folding of GAM337378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337378 folded precursor

RNA yielding a GAM337378 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337378 RNA, hereby incorporated herein.

GAM337378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337378 target RNA, herein designated GAM TARGET RNA.

GAM337378 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337378 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337378 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337378 RNA, herein designated GAM RNA, to target binding sites on GAM337378 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337378 target RNA into GAM337378 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337378 target genes. The mRNA of each one of this plurality of GAM337378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337378 RNA, herein designated GAM RNA, and which when bound by GAM337378 RNA causes inhibition of translation of the GAM337378 target mRNA into a corresponding GAM337378 target protein.

The mechanism of the translational inhibition exerted by GAM337378 RNA, herein designated GAM RNA, on one or more GAM337378 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337378 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337378 RNA, herein designated GAM RNA, of GAM337378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337378 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337378 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337378 RNA correlate with, and may be deduced from, the identity of the GAM337378 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337379 7040 TCCTCTCCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTTTACTTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TAGGTAACTG Messenger 337379 (GAM337379) oligonucleotides modulates expression of respective target

CTTTTGTTGT genes whose function and utility is known in the art.

GCAGGGACTG GAM337379 is a novel bioinformatically detectable regulatory, non protein

GTGTACCACA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337379 was detected

GCACACCTCC is described with additional reference to Figs. 9-15.

TCCCGCCTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGTAAAGCAG encoded by the human genome.

CTGACCGCGT GAM337379 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAAGGGGA GAM337379 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337379 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337379 precursor RNA is designated SEQ ID:7040, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7040 is located from position 105338344 to position 105338451 relative to chromosome 9 on the `-` strand.

GAM337379 precursor RNA folds onto itself, forming GAM337379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337379 precursor RNA, designated SEQ ID NO: 7040, and a schematic representation of a predicted secondary folding of GAM337379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337379 folded precursor RNA yielding a GAM337379 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337379 RNA, hereby incorporated herein.

GAM337379 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337379 target RNA, herein designated GAM TARGET RNA.

GAM337379 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337379 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337379 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337379 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337379 RNA, herein designated GAM RNA, to target binding sites on GAM337379 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337379 target RNA into GAM337379 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337379 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337379 target genes. The mRNA of each one of this plurality of GAM337379 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337379 RNA, herein designated GAM RNA, and which when bound by GAM337379 RNA causes inhibition of translation of the GAM337379 target mRNA into a corresponding GAM337379 target protein.

The mechanism of the translational inhibition exerted by GAM337379 RNA, herein designated GAM RNA, on one or more GAM337379 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337379 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337379 RNA, herein designated GAM RNA, of GAM337379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337379 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337379 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337379 RNA correlate with, and may be deduced from, the identity of the GAM337379 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337380 6654 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 337380 (GAM337380) oligonucleotides modulates expression of respective target

TTGCGGGGAG genes whose function and utility is known in the art.

CCAAGATCGC GAM337380 is a novel bioinformatically detectable regulatory, non protein

ACCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337380 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CGAAACTCC encoded by the human genome.

GAM337380 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337380 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337380 precursor RNA is designated SEQ ID:6654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6654 is located from position 105566898 to position 105566986 relative to chromosome 2 on the `+` strand.

GAM337380 precursor RNA folds onto itself, forming GAM337380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337380 precursor RNA, designated SEQ ID NO: 6654, and a schematic representation of a predicted secondary folding of GAM337380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337380 folded precursor RNA yielding a GAM337380 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337380 RNA, hereby incorporated herein. Expression of GAM337380 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337380 target RNA, herein designated GAM TARGET RNA.

GAM337380 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337380 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337380 RNA, herein designated GAM RNA, to target binding sites on GAM337380 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337380 target RNA into GAM337380 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337380 target genes. The mRNA of each one of this plurality of GAM337380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337380 RNA, herein designated GAM RNA, and which when bound by GAM337380 RNA causes inhibition of translation of the GAM337380 target mRNA into a corresponding GAM337380 target protein.

The mechanism of the translational inhibition exerted by GAM337380 RNA, herein designated GAM RNA, on one or more GAM337380 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337380 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337380 RNA, herein designated GAM RNA, of GAM337380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337380 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337380 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337380 RNA correlate with, and may be deduced from, the identity of the GAM337380 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337383 7036 TCCTACAACT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGAGTCTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATACTGGTGT Messenger 337383 (GAM337383) oligonucleotides modulates expression of respective target
CACTTTCAGG genes whose function and utility is known in the art.

AGCTCTAAGA GAM337383 is a novel bioinformatically detectable regulatory, non protein
ATACGTCAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337383 was detected
TCTCGCTTCT is described with additional reference to Figs. 9-15.

GAGTTGGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCCCTCAACC encoded by the human genome.

AAGAAAGGA GAM337383 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337383 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337383 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337383 precursor RNA is designated SEQ ID:7036, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7036 is located from position 106366445 to position 106366543 relative to chromosome 10 on the `-` strand.

GAM337383 precursor RNA folds onto itself, forming GAM337383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337383 precursor RNA, designated SEQ ID NO: 7036, and a schematic representation of a predicted secondary folding of GAM337383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337383 folded precursor RNA yielding a GAM337383 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337383 RNA, hereby incorporated herein.

GAM337383 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337383 target RNA, herein designated GAM TARGET RNA.

GAM337383 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337383 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337383 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337383 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337383 RNA, herein designated GAM RNA, to target binding sites on GAM337383 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337383 target RNA into GAM337383 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337383 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337383 target genes. The mRNA of each one of this plurality of GAM337383 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337383 RNA, herein designated GAM RNA, and which when bound by GAM337383 RNA causes inhibition of translation of the GAM337383 target mRNA into a corresponding GAM337383 target protein.

The mechanism of the translational inhibition exerted by GAM337383 RNA, herein designated GAM RNA, on one or more GAM337383 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337383 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337383 RNA, herein designated GAM RNA, of GAM337383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337383 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337383 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337383 RNA correlate with, and may be deduced from, the identity of the GAM337383 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337384 6786 GGGAGCAAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAGGGGTCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTAGTGCTC Messenger 337384 (GAM337384) oligonucleotides modulates expression of respective target

CTCTTTTCCC genes whose function and utility is known in the art.

CTGAAATCAC GAM337384 is a novel bioinformatically detectable regulatory, non protein
ACAAGAATGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337384 was detected
GGAGGGCTTT is described with additional reference to Figs. 9-15.

CCCTGACTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAAAGACTC encoded by the human genome.

CCTCCC GAM337384 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337384 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337384 precursor RNA is designated SEQ ID:6786, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6786 is located from position 106504624 to position 106504719 relative to chromosome 12 on the `+` strand.

GAM337384 precursor RNA folds onto itself, forming GAM337384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337384 precursor RNA, designated SEQ ID NO: 6786, and a schematic representation of a predicted secondary folding of GAM337384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337384 folded precursor RNA yielding a GAM337384 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337384 RNA, hereby incorporated herein.

GAM337384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337384 target RNA, herein designated GAM TARGET RNA.

GAM337384 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337384 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337384 RNA, herein designated GAM RNA, to target binding sites on GAM337384 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337384 target RNA into GAM337384 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337384 target genes. The mRNA of each one of this plurality of GAM337384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337384 RNA, herein designated GAM RNA, and which when bound by GAM337384 RNA causes inhibition of translation of the GAM337384 target mRNA into a corresponding GAM337384 target protein.

The mechanism of the translational inhibition exerted by GAM337384 RNA, herein designated GAM RNA, on one or more GAM337384 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337384 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337384 RNA, herein designated GAM RNA, of GAM337384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337384 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337384 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337384 RNA correlate with, and may be deduced from, the identity of the GAM337384 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337385 7180 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCGGGAG Messenger 337385 (GAM337385) oligonucleotides modulates expression of respective target
GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337385 is a novel bioinformatically detectable regulatory, non protein
GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337385 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337385 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCA GAM337385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337385 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337385 precursor RNA is designated SEQ ID:7180, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7180 is located from position 106622467 to position 106622569 relative to chromosome 2 on the `-` strand.

GAM337385 precursor RNA folds onto itself, forming GAM337385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337385 precursor RNA, designated SEQ ID NO: 7180, and a schematic representation of a predicted secondary folding of GAM337385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337385 folded precursor RNA yielding a GAM337385 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337385 RNA, hereby incorporated herein. Expression of GAM337385 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337385 target RNA, herein designated GAM TARGET RNA.

GAM337385 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337385 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337385 RNA, herein designated GAM RNA, to target binding sites on GAM337385 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337385 target RNA into GAM337385 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337385 target genes. The mRNA of each one of this plurality of GAM337385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337385 RNA, herein designated GAM RNA, and which when bound by GAM337385 RNA causes inhibition of translation of the GAM337385 target mRNA into a corresponding GAM337385 target protein.

The mechanism of the translational inhibition exerted by GAM337385 RNA, herein designated GAM RNA, on one or more GAM337385 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337385 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337385 RNA, herein designated GAM RNA, of GAM337385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337385 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337385 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337385 RNA correlate with, and may be deduced from, the identity of the GAM337385 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337386 6658 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGGGAGGC Messenger 337386 (GAM337386) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337386 is a novel bioinformatically detectable regulatory, non protein
CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337386 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACC encoded by the human genome.

GAM337386 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337386 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337386 precursor RNA is designated SEQ ID:6658, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6658 is located from position 106622476 to position 106622562 relative to chromosome 2 on the `-` strand.

GAM337386 precursor RNA folds onto itself, forming GAM337386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337386 precursor RNA, designated SEQ ID NO: 6658, and a schematic representation of a predicted secondary folding of GAM337386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337386 folded precursor

RNA yielding a GAM337386 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337386 RNA, hereby incorporated herein. Expression of GAM337386 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337386 target RNA, herein designated GAM TARGET RNA.

GAM337386 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337386 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337386 RNA, herein designated GAM RNA, to target binding sites on GAM337386 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337386 target RNA into GAM337386 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337386 target genes. The mRNA of each one of this plurality of GAM337386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337386 RNA, herein designated GAM RNA, and which when bound by GAM337386 RNA causes inhibition of translation of the GAM337386 target mRNA into a corresponding GAM337386 target protein.

The mechanism of the translational inhibition exerted by GAM337386 RNA, herein designated GAM RNA, on one or more GAM337386 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337386 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337386 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337386 RNA, herein designated GAM RNA, of GAM337386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337386 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337386 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337386 RNA correlate with, and may be deduced from, the identity of the GAM337386 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337387 7054 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337387 (GAM337387) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337387 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337387 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337387 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337387 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337387 precursor RNA is designated SEQ ID:7054, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7054 is located from position 106622480 to position 106622556 relative to chromosome 2 on the `-` strand.

GAM337387 precursor RNA folds onto itself, forming GAM337387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337387 precursor RNA, designated SEQ ID NO: 7054, and a schematic representation of a predicted secondary folding of GAM337387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337387 folded precursor RNA yielding a GAM337387 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337387 RNA, hereby incorporated herein. Expression of GAM337387 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337387 target RNA, herein designated GAM TARGET RNA.

GAM337387 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337387 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337387 RNA, herein designated GAM RNA, to target binding sites on GAM337387 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337387 target RNA into GAM337387 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337387 target genes. The mRNA of each one of this plurality of GAM337387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337387 RNA, herein designated GAM RNA, and which when bound by GAM337387 RNA causes inhibition of translation of the GAM337387 target mRNA into a corresponding GAM337387 target protein.

The mechanism of the translational inhibition exerted by GAM337387 RNA, herein designated GAM RNA, on one or more GAM337387 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337387 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337387 RNA, herein designated GAM RNA, of GAM337387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337387 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337387 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337387 RNA correlate with, and may be deduced from, the identity of the GAM337387 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337388 6033 CATAATGAGT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCACAGCCTC detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGGACGAT Messenger 337388 (GAM337388) oligonucleotides modulates expression of respective target

TGTTCCTGTT genes whose function and utility is known in the art.

TCTGTAGAAT GAM337388 is a novel bioinformatically detectable regulatory, non protein

TGATTTGAAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337388 was detected

CTTGAATAAT is described with additional reference to Figs. 9-15.

GTCCCACTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGGCAAGGT encoded by the human genome.

GATCATAAAT GAM337388 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

G GAM337388 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337388 precursor RNA does not encode a protein. A nucleotide sequence identical or

highly similar to the nucleotide sequence of GAM337388 precursor RNA is designated SEQ ID:6033, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6033 is located from position 106717983 to position 106718083 relative to chromosome 8 on the `-` strand.

GAM337388 precursor RNA folds onto itself, forming GAM337388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337388 precursor RNA, designated SEQ ID NO: 6033, and a schematic representation of a predicted secondary folding of GAM337388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337388 folded precursor RNA yielding a GAM337388 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337388 RNA, hereby incorporated herein.

GAM337388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337388 target RNA, herein designated GAM TARGET RNA.

GAM337388 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337388 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337388 RNA, herein designated GAM RNA, to target binding sites on GAM337388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337388 target RNA into GAM337388 target protein, herein designated GAM TARGET PROTEIN,, which is shown

surrounded by a broken line.

It is appreciated that GAM337388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337388 target genes. The mRNA of each one of this plurality of GAM337388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337388 RNA, herein designated GAM RNA, and which when bound by GAM337388 RNA causes inhibition of translation of the GAM337388 target mRNA into a corresponding GAM337388 target protein.

The mechanism of the translational inhibition exerted by GAM337388 RNA, herein designated GAM RNA, on one or more GAM337388 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337388 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337388 RNA, herein designated GAM RNA, of GAM337388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337388 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337388 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337388 RNA correlate with, and may be deduced from, the identity of the GAM337388 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337389 5967 ATGAGTCCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGCCTCGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GACGATTGTT Messenger 337389 (GAM337389) oligonucleotides modulates expression of respective target

CCTGTTTCTG genes whose function and utility is known in the art.

TAGAATTGAT GAM337389 is a novel bioinformatically detectable regulatory, non protein

TTGAAACTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337389 was detected

AATAATGTCC is described with additional reference to Figs. 9-15.

CACTGGGAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGGTGATC encoded by the human genome.

AT GAM337389 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337389 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337389 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337389 precursor RNA is designated SEQ ID:5967, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5967 is located from position 106717988 to position 106718079 relative to chromosome 8 on the `-` strand.

GAM337389 precursor RNA folds onto itself, forming GAM337389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337389 precursor RNA, designated SEQ ID NO: 5967, and a schematic representation of a predicted secondary folding of GAM337389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337389 folded precursor RNA yielding a GAM337389 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337389 RNA, hereby incorporated herein.

GAM337389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337389 target RNA, herein designated GAM TARGET RNA.

GAM337389 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337389 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337389 RNA, herein designated GAM RNA, to target binding sites on GAM337389 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337389 target RNA into GAM337389 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337389 target genes. The mRNA of each one of this plurality of GAM337389 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337389 RNA, herein designated GAM RNA, and which when bound by GAM337389 RNA causes inhibition of translation of the GAM337389 target mRNA into a corresponding GAM337389 target protein.

The mechanism of the translational inhibition exerted by GAM337389 RNA, herein designated GAM RNA, on one or more GAM337389 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337389 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337389 RNA, herein designated GAM RNA, of GAM337389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337389 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337389 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337389 RNA correlate with, and may be deduced from, the identity of the GAM337389 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337390 6062 CCATGCTAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TAAAGGAGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTAGGTAGA Messenger 337390 (GAM337390) oligonucleotides modulates expression of respective target

CAGACTTGAC genes whose function and utility is known in the art.

CTTGGAGAGG GAM337390 is a novel bioinformatically detectable regulatory, non protein
CCAGAGAAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337390 was detected
CTTCTCTGAG is described with additional reference to Figs. 9-15.

GACAGAAAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTGTGCTGAA encoded by the human genome.

GTCTGAAGTG GAM337390 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TAAGTAGG GAM337390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337390 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337390 precursor RNA is designated SEQ ID:6062, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6062 is located from position 106800362 to position 106800469 relative to chromosome 9 on the `+` strand.

GAM337390 precursor RNA folds onto itself, forming GAM337390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337390 precursor RNA, designated SEQ ID NO: 6062, and a schematic representation of a predicted secondary folding of GAM337390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337390 folded precursor RNA yielding a GAM337390 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337390 RNA, hereby incorporated herein.

GAM337390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337390 target RNA, herein designated GAM TARGET RNA.

GAM337390 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337390 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337390 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337390 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337390 RNA, herein designated GAM RNA, to target binding sites on GAM337390 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337390 target RNA into GAM337390 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337390 target genes. The mRNA of each one of this plurality of GAM337390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337390 RNA, herein designated GAM RNA, and which when bound by GAM337390 RNA causes inhibition of translation of the GAM337390 target mRNA into a corresponding GAM337390 target protein.

The mechanism of the translational inhibition exerted by GAM337390 RNA, herein designated GAM RNA, on one or more GAM337390 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337390 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337390 RNA, herein designated GAM RNA, of GAM337390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337390 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337390 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337390 RNA correlate with, and may be deduced from, the identity of the GAM337390 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337391 5728 AGAGCTTAGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TAGACAGACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGACCTTGGA Messenger 337391 (GAM337391) oligonucleotides modulates expression of respective target
GAGGCCAGAG genes whose function and utility is known in the art.

AAGCCTTCTC GAM337391 is a novel bioinformatically detectable regulatory, non protein
TGAGGACAGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337391 was detected
AAGTTTGTGC is described with additional reference to Figs. 9-15.

TGAAGTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337391 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337391 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337391 precursor RNA is designated SEQ ID:5728, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5728 is located from position 106800378 to position 106800455 relative to chromosome 9 on the `+` strand.

GAM337391 precursor RNA folds onto itself, forming GAM337391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337391 precursor RNA, designated SEQ ID NO: 5728, and a schematic representation of a predicted secondary folding of GAM337391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337391 folded precursor RNA yielding a GAM337391 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337391 RNA, hereby incorporated herein.

GAM337391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337391 target RNA, herein designated GAM TARGET RNA.

GAM337391 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337391 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337391 RNA, herein designated GAM RNA, to target binding sites on GAM337391 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337391 target RNA into GAM337391 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337391 target genes. The mRNA of each one of this plurality of GAM337391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337391 RNA, herein designated GAM RNA, and which when bound by GAM337391 RNA causes inhibition of translation of the GAM337391 target mRNA into a corresponding GAM337391 target protein.

The mechanism of the translational inhibition exerted by GAM337391 RNA, herein designated GAM RNA, on one or more GAM337391 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337391 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337391 RNA, herein designated GAM RNA, of GAM337391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337391 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337391 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337391 RNA correlate with, and may be deduced from, the identity of the GAM337391 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337393 6682 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GACGTGGAGG Messenger 337393 (GAM337393) oligonucleotides modulates expression of respective target
TTGCCATGAG genes whose function and utility is known in the art.

CTGAGATCAC GAM337393 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337393 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGAAACTCC encoded by the human genome.

GAM337393 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337393 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337393 precursor RNA is designated SEQ ID:6682, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6682 is located from position 107416407 to position 107416495 relative to chromosome 11 on the `-` strand.

GAM337393 precursor RNA folds onto itself, forming GAM337393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337393 precursor RNA, designated SEQ ID NO: 6682, and a schematic representation of a predicted secondary folding of GAM337393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337393 folded precursor RNA yielding a GAM337393 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337393 RNA, hereby incorporated herein. Expression of GAM337393 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337393 target RNA, herein designated GAM TARGET RNA.

GAM337393 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337393 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337393 RNA, herein designated GAM RNA, to target binding sites on GAM337393 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337393 target RNA into GAM337393 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337393 target genes. The mRNA of each one of this plurality of GAM337393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337393 RNA, herein designated GAM RNA, and which when bound by GAM337393 RNA causes inhibition of translation of the GAM337393 target mRNA into a corresponding GAM337393 target protein.

The mechanism of the translational inhibition exerted by GAM337393 RNA, herein designated GAM RNA, on one or more GAM337393 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337393 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337393 RNA, herein designated GAM RNA, of GAM337393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337393 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337393 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337393 RNA correlate with, and may be deduced from, the identity of the GAM337393 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337394 6007 CACTTGAACC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGAAGGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGTTGCAGT Messenger 337394 (GAM337394) oligonucleotides modulates expression of respective target

GAGCTGAGAT genes whose function and utility is known in the art.

TGTGCCATTG GAM337394 is a novel bioinformatically detectable regulatory, non protein

CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337394 was detected

TGGGCAACAA is described with additional reference to Figs. 9-15.

GTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337394 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337394 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337394 precursor RNA is designated SEQ ID:6007, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6007 is located from position 107752512 to position 107752584 relative to chromosome 5 on the `+` strand.

GAM337394 precursor RNA folds onto itself, forming GAM337394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337394 precursor RNA, designated SEQ ID NO: 6007, and a schematic representation of a predicted secondary folding of GAM337394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337394 folded precursor RNA yielding a GAM337394 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337394 RNA, hereby incorporated herein. Expression of GAM337394 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337394 target RNA, herein designated GAM TARGET RNA.

GAM337394 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337394 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337394 RNA, herein designated GAM RNA, to target binding sites on GAM337394 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337394 target RNA into GAM337394 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337394 target genes. The mRNA of each one of this plurality of GAM337394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337394 RNA, herein designated GAM RNA, and which when bound by GAM337394 RNA causes inhibition of translation of the GAM337394 target mRNA into a corresponding GAM337394 target protein.

The mechanism of the translational inhibition exerted by GAM337394 RNA, herein designated GAM RNA, on one or more GAM337394 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337394 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337394 RNA, herein designated GAM RNA, of GAM337394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337394 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337394 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337394 RNA correlate with, and may be deduced from, the identity of the GAM337394 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337395 7181 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTCGGGAG Messenger 337395 (GAM337395) oligonucleotides modulates expression of respective target

GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337395 is a novel bioinformatically detectable regulatory, non protein

GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337395 was detected

CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337395 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCA GAM337395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337395 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337395 precursor RNA is designated SEQ ID:7181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7181 is located from position 108115430 to position 108115532

relative to chromosome 2 on the `+` strand.

GAM337395 precursor RNA folds onto itself, forming GAM337395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337395 precursor RNA, designated SEQ ID NO: 7181, and a schematic representation of a predicted secondary folding of GAM337395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337395 folded precursor RNA yielding a GAM337395 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337395 RNA, hereby incorporated herein. Expression of GAM337395 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337395 target RNA, herein designated GAM TARGET RNA.

GAM337395 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337395 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337395 RNA, herein designated GAM RNA, to target binding sites on GAM337395 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337395 target RNA into GAM337395 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337395 target genes. The mRNA of each one of this plurality of GAM337395 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337395 RNA, herein designated GAM RNA, and which when bound by GAM337395 RNA causes inhibition of translation of the GAM337395 target mRNA into a corresponding GAM337395 target protein.

The mechanism of the translational inhibition exerted by GAM337395 RNA, herein designated GAM RNA, on one or more GAM337395 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337395 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337395 RNA, herein designated GAM RNA, of GAM337395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337395 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337395 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337395 RNA correlate with, and may be deduced from, the identity of the GAM337395 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337396 6659 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGGGAGGC Messenger 337396 (GAM337396) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337396 is a novel bioinformatically detectable regulatory, non protein

CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337396 was detected

CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACC encoded by the human genome.

GAM337396 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337396 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337396 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337396 precursor RNA is designated SEQ ID:6659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6659 is located from position 108115437 to position 108115523 relative to chromosome 2 on the `+` strand.

GAM337396 precursor RNA folds onto itself, forming GAM337396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337396 precursor RNA, designated SEQ ID NO: 6659, and a schematic representation of a predicted secondary folding of GAM337396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337396 folded precursor RNA yielding a GAM337396 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337396 RNA, hereby incorporated herein. Expression of GAM337396 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337396 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337396 target RNA, herein designated GAM TARGET RNA.

GAM337396 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337396 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337396 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337396 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337396 RNA, herein designated GAM RNA, to target binding sites on GAM337396 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337396 target RNA into GAM337396 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337396 target genes. The mRNA of each one of this plurality of GAM337396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337396 RNA, herein designated GAM RNA, and which when bound by GAM337396 RNA causes inhibition of translation of the GAM337396 target mRNA into a corresponding GAM337396 target protein.

The mechanism of the translational inhibition exerted by GAM337396 RNA, herein designated GAM RNA, on one or more GAM337396 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337396 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337396 RNA, herein designated GAM RNA, of GAM337396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337396 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337396 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337396 RNA correlate with, and may be deduced from, the identity of the GAM337396 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337397 7055 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337397 (GAM337397) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337397 is a novel bioinformatically detectable regulatory, non protein
TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337397 was detected
CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337397 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337397 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337397 precursor RNA is designated SEQ ID:7055, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7055 is located from position 108115443 to position 108115519 relative to chromosome 2 on the `+` strand.

GAM337397 precursor RNA folds onto itself, forming GAM337397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337397 precursor RNA, designated SEQ ID NO: 7055, and a schematic representation of a predicted secondary folding of GAM337397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337397 folded precursor RNA yielding a GAM337397 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337397 RNA, hereby incorporated herein. Expression of GAM337397 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337397 target RNA, herein designated GAM TARGET RNA.

GAM337397 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337397 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337397 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337397 RNA, herein designated GAM RNA, to target binding sites on GAM337397 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337397 target RNA into GAM337397 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337397 target genes. The mRNA of each one of this plurality of GAM337397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337397 RNA, herein designated GAM RNA, and which when bound by GAM337397 RNA causes inhibition of translation of the GAM337397 target mRNA into a corresponding GAM337397 target protein.

The mechanism of the translational inhibition exerted by GAM337397 RNA, herein designated GAM RNA, on one or more GAM337397 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337397 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337397 RNA, herein designated GAM RNA, of GAM337397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337397 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337397 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337397 RNA correlate with, and may be deduced from, the identity of the GAM337397 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337399 7179 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCGGGAG Messenger 337399 (GAM337399) oligonucleotides modulates expression of respective target
GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337399 is a novel bioinformatically detectable regulatory, non protein
GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337399 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337399 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCA GAM337399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337399 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337399 precursor RNA is designated SEQ ID:7179, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7179 is located from position 108732269 to position 108732371 relative to chromosome 2 on the `+` strand.

GAM337399 precursor RNA folds onto itself, forming GAM337399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337399 precursor RNA, designated SEQ ID NO: 7179, and a schematic representation of a predicted secondary folding of GAM337399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337399 folded precursor RNA yielding a GAM337399 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337399 RNA, hereby incorporated herein.

Expression of GAM337399 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337399 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337399 target RNA, herein designated GAM TARGET RNA.

GAM337399 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337399 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337399 RNA, herein designated GAM RNA, to target binding sites on GAM337399 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337399 target RNA into GAM337399 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337399 target genes. The mRNA of each one of this plurality of GAM337399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337399 RNA, herein designated GAM RNA, and which when bound by GAM337399 RNA causes inhibition of translation of the GAM337399 target mRNA into a corresponding GAM337399 target protein.

The mechanism of the translational inhibition exerted by GAM337399 RNA, herein designated GAM RNA, on one or more GAM337399 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337399 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337399 RNA, herein designated GAM RNA, of GAM337399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337399 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337399 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337399 RNA correlate with, and may be deduced from, the identity of the GAM337399 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337400 6618 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGGGAGGC Messenger 337400 (GAM337400) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337400 is a novel bioinformatically detectable regulatory, non protein
CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337400 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACC encoded by the human genome.

GAM337400 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337400 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337400 precursor RNA is designated SEQ ID:6618, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6618 is located from position 108732276 to position 108732362 relative to chromosome 2 on the `+` strand.

GAM337400 precursor RNA folds onto itself, forming GAM337400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337400 precursor RNA, designated SEQ ID NO: 6618, and a schematic representation of a predicted secondary folding of GAM337400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337400 folded precursor RNA yielding a GAM337400 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337400 RNA, hereby incorporated herein. Expression of GAM337400 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337400 target RNA, herein designated GAM TARGET RNA.

GAM337400 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337400 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337400 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337400 RNA, herein designated GAM RNA, to target binding sites on GAM337400 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337400 target RNA into GAM337400 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337400 target genes. The mRNA of each one of this plurality of GAM337400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337400 RNA, herein designated GAM RNA, and which when bound by GAM337400 RNA causes inhibition of translation of the GAM337400 target mRNA into a corresponding GAM337400 target protein.

The mechanism of the translational inhibition exerted by GAM337400 RNA, herein designated GAM RNA, on one or more GAM337400 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337400 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337400 RNA, herein designated GAM RNA, of GAM337400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337400 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337400 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337400 RNA correlate with, and may be deduced from, the identity of the GAM337400 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337401 6619 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGGGAGGC Messenger 337401 (GAM337401) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337401 is a novel bioinformatically detectable regulatory, non protein
CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337401 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACCC encoded by the human genome.

GAM337401 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337401 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337401 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337401 precursor RNA is designated SEQ ID:6619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6619 is located from position 108732276 to position 108732363 relative to chromosome 2 on the `+` strand.

GAM337401 precursor RNA folds onto itself, forming GAM337401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337401 precursor RNA, designated SEQ ID NO: 6619, and a schematic representation of a predicted secondary folding of GAM337401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337401 folded precursor RNA yielding a GAM337401 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337401 RNA, hereby incorporated herein. Expression of GAM337401 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337401 target RNA, herein designated GAM TARGET RNA.

GAM337401 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337401 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337401 RNA, herein designated GAM RNA, to target binding sites on GAM337401 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337401 target RNA into GAM337401 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337401 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337401 target genes. The mRNA of each one of this plurality of GAM337401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337401 RNA,

herein designated GAM RNA, and which when bound by GAM337401 RNA causes inhibition of translation of the GAM337401 target mRNA into a corresponding GAM337401 target protein.

The mechanism of the translational inhibition exerted by GAM337401 RNA, herein designated GAM RNA, on one or more GAM337401 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337401 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337401 RNA, herein designated GAM RNA, of GAM337401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337401 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337401 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337401 RNA correlate with, and may be deduced from, the identity of the GAM337401 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337402 7004 TCACTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337402 (GAM337402) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337402 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337402 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337402 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337402 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337402 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337402 precursor RNA is designated SEQ ID:7004, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7004 is located from position 108732282 to position 108732358 relative to chromosome 2 on the `+` strand.

GAM337402 precursor RNA folds onto itself, forming GAM337402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337402 precursor RNA, designated SEQ ID NO: 7004, and a schematic representation of a predicted secondary folding of GAM337402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337402 folded precursor RNA yielding a GAM337402 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337402 RNA, hereby incorporated herein. Expression of GAM337402 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337402 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337402 target RNA, herein designated GAM TARGET RNA.

GAM337402 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337402 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337402 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337402 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337402 RNA, herein designated GAM RNA, to target binding sites on GAM337402 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337402 target RNA into GAM337402 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337402 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337402 target genes. The mRNA of each one of this plurality of GAM337402 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337402 RNA, herein designated GAM RNA, and which when bound by GAM337402 RNA causes inhibition of translation of the GAM337402 target mRNA into a corresponding GAM337402 target protein.

The mechanism of the translational inhibition exerted by GAM337402 RNA, herein designated GAM RNA, on one or more GAM337402 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337402 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337402 RNA, herein designated GAM RNA, of GAM337402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337402 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337402 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337402 RNA correlate with, and may be deduced from, the identity of the GAM337402 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337403 7011 TCAGTCCCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
TGGGTGTGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCTGTACAC Messenger 337403 (GAM337403) oligonucleotides modulates expression of respective target
ATTTTCATGT genes whose function and utility is known in the art.

TACCATTGAC GAM337403 is a novel bioinformatically detectable regulatory, non protein
ATCTTCAGTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337403 was detected
TTTCAATGTG is described with additional reference to Figs. 9-15.

ATGTGTAATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CATATAAGCA encoded by the human genome.

GCATATGTAG GAM337403 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGGTTGA GAM337403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337403 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337403 precursor RNA is designated SEQ ID:7011, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7011 is located from position 109155677 to position 109155783 relative to chromosome 8 on the `+` strand.

GAM337403 precursor RNA folds onto itself, forming GAM337403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337403 precursor RNA, designated SEQ ID NO: 7011, and a schematic representation of a predicted secondary folding of GAM337403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337403 folded precursor RNA yielding a GAM337403 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337403 RNA, hereby incorporated herein.

GAM337403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337403 target RNA, herein designated GAM TARGET RNA.

GAM337403 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337403 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337403 RNA, herein designated GAM RNA, to target binding sites on GAM337403 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337403 target RNA into GAM337403 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337403 target genes. The mRNA of each one of this plurality of GAM337403 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337403 RNA, herein designated GAM RNA, and which when bound by GAM337403 RNA causes inhibition of translation of the GAM337403 target mRNA into a corresponding GAM337403 target protein.

The mechanism of the translational inhibition exerted by GAM337403 RNA, herein designated GAM RNA, on one or more GAM337403 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337403 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337403 RNA, herein designated GAM RNA, of GAM337403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337403 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337403 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337403 RNA correlate with, and may be deduced from, the identity of the GAM337403 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337405 6206 CTGAGGCAGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAATTGCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTACCCGGGA Messenger 337405 (GAM337405) oligonucleotides modulates expression of respective target
GGTGAAGGTT genes whose function and utility is known in the art.

GCAGTGAGCC GAM337405 is a novel bioinformatically detectable regulatory, non protein
GAGATGGTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337405 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAGAGCAA encoded by the human genome.

GGCCCTGTTT GAM337405 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CAG GAM337405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337405 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337405 precursor RNA is designated SEQ ID:6206, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6206 is located from position 109967299 to position 109967401 relative to chromosome 4 on the `+` strand.

GAM337405 precursor RNA folds onto itself, forming GAM337405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337405 precursor RNA, designated SEQ ID NO: 6206, and a schematic representation of a predicted secondary folding of GAM337405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337405 folded precursor RNA yielding a GAM337405 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337405 RNA, hereby incorporated herein. Expression of GAM337405 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337405 target RNA, herein designated GAM TARGET RNA.

GAM337405 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337405 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337405 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337405 RNA, herein designated GAM RNA, to target binding sites on GAM337405 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337405 target RNA into GAM337405 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337405 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337405 target genes. The mRNA of each one of this plurality of GAM337405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337405 RNA, herein designated GAM RNA, and which when bound by GAM337405 RNA causes inhibition of translation of the GAM337405 target mRNA into a corresponding GAM337405 target protein.

The mechanism of the translational inhibition exerted by GAM337405 RNA, herein designated GAM RNA, on one or more GAM337405 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337405 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337405 RNA, herein designated GAM RNA, of GAM337405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337405 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337405 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337405 RNA correlate with, and may be deduced from, the identity of the GAM337405 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337407 5915 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337407 (GAM337407) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337407 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337407 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337407 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337407 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337407 precursor RNA is designated SEQ ID:5915, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5915 is located from position 110039924 to position 110040005 relative to chromosome 5 on the `-` strand.

GAM337407 precursor RNA folds onto itself, forming GAM337407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337407 precursor RNA, designated SEQ ID NO: 5915, and a schematic representation of a predicted secondary folding of GAM337407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337407 folded precursor RNA yielding a GAM337407 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337407 RNA, hereby incorporated herein.

GAM337407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337407 target RNA, herein designated GAM TARGET RNA.

GAM337407 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337407 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337407 RNA, herein designated GAM RNA, to target binding sites on GAM337407 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337407 target RNA into GAM337407 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337407 target genes. The mRNA of each one of this plurality of GAM337407 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337407 RNA, herein designated GAM RNA, and which when bound by GAM337407 RNA causes inhibition of translation of the GAM337407 target mRNA into a corresponding GAM337407 target protein.

The mechanism of the translational inhibition exerted by GAM337407 RNA, herein designated GAM RNA, on one or more GAM337407 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337407 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337407 RNA, herein designated GAM RNA, of GAM337407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337407 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337407 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337407 RNA correlate with, and may be deduced from, the identity of the GAM337407 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337408 7287 TTAGGAAAGT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTTTAATC detected oligonucleotides of the present invention, referred to here as Genomic Address
TCATAGGCCC Messenger 337408 (GAM337408) oligonucleotides modulates expression of respective target
CCAGTGGGGA genes whose function and utility is known in the art.

TCCCCTGGGA GAM337408 is a novel bioinformatically detectable regulatory, non protein
TCCTCTGGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337408 was detected
ATGCTGTGAG is described with additional reference to Figs. 9-15.

AACTGCTAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTAG encoded by the human genome.

GAM337408 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337408 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337408 precursor RNA is designated SEQ ID:7287, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7287 is located from position 110149400 to position 110149483 relative to chromosome 7 on the `+` strand.

GAM337408 precursor RNA folds onto itself, forming GAM337408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337408 precursor RNA, designated SEQ ID NO: 7287, and a schematic representation of a predicted secondary folding of GAM337408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337408 folded precursor RNA yielding a GAM337408 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337408 RNA, hereby incorporated herein.

GAM337408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337408 target RNA, herein designated GAM TARGET RNA.

GAM337408 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337408 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337408 RNA, herein designated GAM RNA, to target binding sites on GAM337408 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337408 target RNA into GAM337408 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337408 target genes. The mRNA of each one of this plurality of GAM337408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337408 RNA, herein designated GAM RNA, and which when bound by GAM337408 RNA causes inhibition of translation of the GAM337408 target mRNA into a corresponding GAM337408 target protein.

The mechanism of the translational inhibition exerted by GAM337408 RNA, herein designated GAM RNA, on one or more GAM337408 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337408 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337408 RNA, herein designated GAM RNA, of GAM337408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337408 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337408 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337408 RNA correlate with, and may be deduced from, the identity of the GAM337408 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337409 7182 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTCGGGAG Messenger 337409 (GAM337409) oligonucleotides modulates expression of respective target

GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337409 is a novel bioinformatically detectable regulatory, non protein

GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337409 was detected

CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337409 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCA GAM337409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337409 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337409 precursor RNA is designated SEQ ID:7182, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7182 is located from position 110164979 to position 110165081 relative to chromosome 2 on the `+` strand.

GAM337409 precursor RNA folds onto itself, forming GAM337409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337409 precursor RNA, designated SEQ ID NO: 7182, and a schematic representation of a predicted secondary folding of GAM337409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337409 folded precursor RNA yielding a GAM337409 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337409 RNA, hereby incorporated herein. Expression of GAM337409 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337409 target RNA, herein designated GAM TARGET RNA.

GAM337409 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337409 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337409 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337409 RNA, herein designated GAM RNA, to target binding sites on GAM337409 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337409 target RNA into GAM337409 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337409 target genes. The mRNA of each one of this plurality of GAM337409 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337409 RNA,

herein designated GAM RNA, and which when bound by GAM337409 RNA causes inhibition of translation of the GAM337409 target mRNA into a corresponding GAM337409 target protein.

The mechanism of the translational inhibition exerted by GAM337409 RNA, herein designated GAM RNA, on one or more GAM337409 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337409 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337409 RNA, herein designated GAM RNA, of GAM337409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337409 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337409 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337409 RNA correlate with, and may be deduced from, the identity of the GAM337409 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337410 6660 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGGGAGGC Messenger 337410 (GAM337410) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337410 is a novel bioinformatically detectable regulatory, non protein

CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337410 was detected

CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACC encoded by the human genome.

GAM337410 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337410 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337410 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337410 precursor RNA is designated SEQ ID:6660, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6660 is located from position 110164986 to position 110165072 relative to chromosome 2 on the `+` strand.

GAM337410 precursor RNA folds onto itself, forming GAM337410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337410 precursor RNA, designated SEQ ID NO: 6660, and a schematic representation of a predicted secondary folding of GAM337410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337410 folded precursor RNA yielding a GAM337410 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337410 RNA, hereby incorporated herein. Expression of GAM337410 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337410 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337410 target RNA, herein designated GAM TARGET RNA.

GAM337410 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337410 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337410 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337410 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337410 RNA, herein designated GAM RNA, to target binding sites on GAM337410 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337410 target RNA into GAM337410 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337410 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337410 target genes. The mRNA of each one of this plurality of GAM337410 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337410 RNA, herein designated GAM RNA, and which when bound by GAM337410 RNA causes inhibition of translation of the GAM337410 target mRNA into a corresponding GAM337410 target protein.

The mechanism of the translational inhibition exerted by GAM337410 RNA, herein designated GAM RNA, on one or more GAM337410 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337410 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337410 RNA, herein designated GAM RNA, of GAM337410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337410 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337410 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337410 RNA correlate with, and may be deduced from, the identity of the GAM337410 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337411 7056 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337411 (GAM337411) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337411 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337411 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337411 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337411 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337411 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337411 precursor RNA is designated SEQ ID:7056, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7056 is located from position 110164992 to position 110165068 relative to chromosome 2 on the `+` strand.

GAM337411 precursor RNA folds onto itself, forming GAM337411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337411 precursor RNA, designated SEQ ID NO: 7056, and a schematic representation of a predicted secondary folding of GAM337411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337411 folded precursor RNA yielding a GAM337411 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337411 RNA, hereby incorporated herein. Expression of GAM337411 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337411 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337411 target RNA, herein designated GAM TARGET RNA.

GAM337411 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337411 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337411 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337411 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337411 RNA, herein designated GAM RNA, to target binding sites on GAM337411 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337411 target RNA into GAM337411 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337411 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337411 target genes. The mRNA of each one of this plurality of GAM337411 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337411 RNA, herein designated GAM RNA, and which when bound by GAM337411 RNA causes inhibition of translation of the GAM337411 target mRNA into a corresponding GAM337411 target protein.

The mechanism of the translational inhibition exerted by GAM337411 RNA, herein designated GAM RNA, on one or more GAM337411 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337411 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337411 RNA, herein designated GAM RNA, of GAM337411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337411 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337411 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337411 RNA correlate with, and may be deduced from, the identity of the GAM337411 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337413 7111 TGAGGCACGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337413 (GAM337413) oligonucleotides modulates expression of respective target
GCGGAGGCTG genes whose function and utility is known in the art.

CAGTGAGCAG GAM337413 is a novel bioinformatically detectable regulatory, non protein
AGATCACGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337413 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGGGAG encoded by the human genome.

ACTCTGTCTC GAM337413 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337413 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337413 precursor RNA is designated SEQ ID:7111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7111 is located from position 110356261 to position 110356361 relative to chromosome 12 on the `+` strand.

GAM337413 precursor RNA folds onto itself, forming GAM337413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337413 precursor RNA, designated SEQ ID NO: 7111, and a schematic representation of a predicted secondary folding of GAM337413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337413 folded precursor RNA yielding a GAM337413 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337413 RNA, hereby incorporated herein. Expression of GAM337413 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337413 target RNA, herein designated GAM TARGET RNA.

GAM337413 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337413 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337413 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337413 RNA, herein designated GAM RNA, to target binding sites on GAM337413 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337413 target RNA into GAM337413 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337413 target genes. The mRNA of each one of this plurality of GAM337413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337413 RNA, herein designated GAM RNA, and which when bound by GAM337413 RNA causes inhibition of translation of the GAM337413 target mRNA into a corresponding GAM337413 target protein.

The mechanism of the translational inhibition exerted by GAM337413 RNA, herein designated GAM RNA, on one or more GAM337413 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337413 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337413 RNA, herein designated GAM RNA, of GAM337413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337413 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337413 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337413 RNA correlate with, and may be deduced from, the identity of the GAM337413 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337414 6041 CATGTTGGCC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGACTGGTCT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTAACTCCAG Messenger 337414 (GAM337414) oligonucleotides modulates expression of respective target
ACTTCAGGTG genes whose function and utility is known in the art.

ATCTGCCCAC GAM337414 is a novel bioinformatically detectable regulatory, non protein
CTTGGCCTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337414 was detected
CAAAGTGCTG is described with additional reference to Figs. 9-15.

GGATTACAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCTGAGCCAC encoded by the human genome.

CATG GAM337414 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337414 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337414 precursor RNA is designated SEQ ID:6041, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6041 is located from position 110439070 to position 110439163 relative to chromosome 10 on the `-` strand.

GAM337414 precursor RNA folds onto itself, forming GAM337414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337414 precursor RNA, designated SEQ ID NO: 6041, and a schematic representation of a predicted secondary folding of GAM337414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337414 folded precursor RNA yielding a GAM337414 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337414 RNA, hereby incorporated herein.

GAM337414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337414 target RNA, herein designated GAM TARGET RNA.

GAM337414 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337414 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337414 RNA, herein designated GAM RNA, to target binding sites on GAM337414 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337414 target RNA into GAM337414 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337414 target genes. The mRNA of each one of this plurality of GAM337414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337414 RNA, herein designated GAM RNA, and which when bound by GAM337414 RNA causes inhibition of translation of the GAM337414 target mRNA into a corresponding GAM337414 target protein.

The mechanism of the translational inhibition exerted by GAM337414 RNA, herein designated GAM RNA, on one or more GAM337414 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337414 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337414 RNA, herein designated GAM RNA, of

GAM337414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337414 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337414 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337414 RNA correlate with, and may be deduced from, the identity of the GAM337414 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337415 7183 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACTCGGGAG Messenger 337415 (GAM337415) oligonucleotides modulates expression of respective target

GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337415 is a novel bioinformatically detectable regulatory, non protein

GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337415 was detected

CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337415 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCA GAM337415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337415 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337415 precursor RNA is designated SEQ ID:7183, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7183 is located from position 110894746 to position 110894848 relative to chromosome 2 on the `-` strand.

GAM337415 precursor RNA folds onto itself, forming GAM337415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337415 precursor RNA, designated SEQ ID NO: 7183, and a schematic representation of a predicted secondary folding of GAM337415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337415 folded precursor RNA yielding a GAM337415 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337415 RNA, hereby incorporated herein. Expression of GAM337415 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337415 target RNA, herein designated GAM TARGET RNA.

GAM337415 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337415 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337415 RNA, herein designated GAM RNA, to target binding sites on GAM337415 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337415 target RNA into GAM337415 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337415 target genes. The mRNA of each one of this plurality of GAM337415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337415 RNA, herein designated GAM RNA, and which when bound by GAM337415 RNA causes inhibition of translation of the GAM337415 target mRNA into a corresponding GAM337415 target protein.

The mechanism of the translational inhibition exerted by GAM337415 RNA, herein designated GAM RNA, on one or more GAM337415 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337415 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337415 RNA, herein designated GAM RNA, of GAM337415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337415 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337415 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337415 RNA correlate with, and may be deduced from, the identity of the GAM337415 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337416 6661 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGGGAGGC Messenger 337416 (GAM337416) oligonucleotides modulates expression of respective target
TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337416 is a novel bioinformatically detectable regulatory, non protein
CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337416 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACC encoded by the human genome.

GAM337416 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337416 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337416 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337416 precursor RNA is designated SEQ ID:6661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6661 is located from position 110894755 to position 110894841 relative to chromosome 2 on the `-` strand.

GAM337416 precursor RNA folds onto itself, forming GAM337416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337416 precursor RNA, designated SEQ ID NO: 6661, and a schematic representation of a predicted secondary folding of GAM337416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337416 folded precursor RNA yielding a GAM337416 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337416 RNA, hereby incorporated herein. Expression of GAM337416 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337416 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337416 target RNA, herein designated GAM TARGET RNA.

GAM337416 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337416 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337416 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337416 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337416 RNA, herein designated GAM RNA, to target binding sites on GAM337416 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337416 target RNA into GAM337416 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337416 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337416 target genes. The mRNA of each one of this plurality of GAM337416 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337416 RNA, herein designated GAM RNA, and which when bound by GAM337416 RNA causes inhibition of translation of the GAM337416 target mRNA into a corresponding GAM337416 target protein.

The mechanism of the translational inhibition exerted by GAM337416 RNA, herein designated GAM RNA, on one or more GAM337416 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337416 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337416 RNA, herein designated GAM RNA, of GAM337416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337416 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337416 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337416 RNA correlate with, and may be deduced from, the identity of the GAM337416 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337417 7057 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGCTGCAGT Messenger 337417 (GAM337417) oligonucleotides modulates expression of respective target

GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337417 is a novel bioinformatically detectable regulatory, non protein

TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337417 was detected

CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337417 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337417 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337417 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337417 precursor RNA is designated SEQ ID:7057, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7057 is located from position 110894759 to position 110894835 relative to chromosome 2 on the `-` strand.

GAM337417 precursor RNA folds onto itself, forming GAM337417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337417 precursor RNA, designated SEQ ID NO: 7057, and a schematic representation of a predicted secondary folding of GAM337417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337417 folded precursor RNA yielding a GAM337417 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337417 RNA, hereby incorporated herein. Expression of GAM337417 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337417 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337417 target RNA, herein designated GAM TARGET RNA.

GAM337417 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337417 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337417 RNA, herein designated GAM RNA, to target binding sites on GAM337417 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337417 target RNA into GAM337417 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337417 target genes. The mRNA of each one of this plurality of GAM337417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337417 RNA, herein designated GAM RNA, and which when bound by GAM337417 RNA causes inhibition of translation of the GAM337417 target mRNA into a corresponding GAM337417 target protein.

The mechanism of the translational inhibition exerted by GAM337417 RNA, herein designated GAM RNA, on one or more GAM337417 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337417 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337417 RNA, herein designated GAM RNA, of GAM337417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337417 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337417 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337417 RNA correlate with, and may be deduced from, the identity of the GAM337417 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337418 6178 CTCTGTCACC CAGGCTGGAG TGAGTGTGAT CTTGGCTCAC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337418 (GAM337418) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GGCAACCTTT GAM337418 is a novel bioinformatically detectable regulatory, non protein
GCCTCCTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337418 was detected
TTCAAGCAAT is described with additional reference to Figs. 9-15.

TCTCCTGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAGCCTCCCG encoded by the human genome.

AGTAGCAGAG GAM337418 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337418 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337418 precursor RNA is designated SEQ ID:6178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6178 is located from position 111066449 to position 111066548 relative to chromosome 12 on the `+` strand.

GAM337418 precursor RNA folds onto itself, forming GAM337418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337418 precursor RNA, designated SEQ ID NO: 6178, and a schematic representation of a predicted secondary folding of GAM337418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337418 folded precursor RNA yielding a GAM337418 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337418 RNA, hereby incorporated herein.

GAM337418 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337418 target RNA, herein designated GAM TARGET RNA.

GAM337418 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337418 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337418 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337418 RNA, herein designated GAM RNA, to target binding sites on GAM337418 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337418 target RNA into GAM337418 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337418 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337418 target genes. The mRNA of each one of this plurality of GAM337418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337418 RNA, herein designated GAM RNA, and which when bound by GAM337418 RNA causes inhibition of translation of the GAM337418 target mRNA into a corresponding GAM337418 target protein.

The mechanism of the translational inhibition exerted by GAM337418 RNA, herein designated GAM RNA, on one or more GAM337418 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337418 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337418 RNA, herein designated GAM RNA, of GAM337418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337418 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337418 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337418 RNA correlate with, and may be deduced from, the identity of the GAM337418 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337419 7294 TTCAGGTTTT Fig. 8 further provides a conceptual description of another novel bioinformatically

CAGACACCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGTAGTAGA Messenger 337419 (GAM337419) oligonucleotides modulates expression of respective target

ACAGAATATT genes whose function and utility is known in the art.

TTAGCTCTGA GAM337419 is a novel bioinformatically detectable regulatory, non protein

GGACAATCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337419 was detected

AGTTATGAAT is described with additional reference to Figs. 9-15.

AGTCTGGTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGTAAGGATT encoded by the human genome.

TGCATAGTTT GAM337419 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GGAGAAATGA GAM337419 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

A GAM337419 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337419 precursor RNA is designated SEQ ID:7294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7294 is located from position 111125711 to position 111125821 relative to chromosome 9 on the `+` strand.

GAM337419 precursor RNA folds onto itself, forming GAM337419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337419 precursor RNA, designated SEQ ID NO: 7294, and a schematic representation of a predicted secondary folding of GAM337419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337419 folded precursor RNA yielding a GAM337419 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337419 RNA, hereby incorporated herein.

GAM337419 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337419 target RNA, herein designated GAM TARGET RNA.

GAM337419 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337419 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337419 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337419 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337419 RNA, herein designated GAM RNA, to target binding sites on GAM337419 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337419 target RNA into GAM337419 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337419 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337419 target genes. The mRNA of each one of this plurality of GAM337419 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337419 RNA, herein designated GAM RNA, and which when bound by GAM337419 RNA causes inhibition of translation of the GAM337419 target mRNA into a corresponding GAM337419 target protein.

The mechanism of the translational inhibition exerted by GAM337419 RNA, herein designated GAM RNA, on one or more GAM337419 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337419 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337419 RNA, herein designated GAM RNA, of GAM337419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337419 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337419 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337419 RNA correlate with, and may be deduced from, the identity of the GAM337419 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337420 6748 GGCCCAGCGT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTCCTGAC detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGGAGGATA Messenger 337420 (GAM337420) oligonucleotides modulates expression of respective target
ACAATGATAA genes whose function and utility is known in the art.

TGGAAGTGCT GAM337420 is a novel bioinformatically detectable regulatory, non protein
GTTAAAAGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337420 was detected
AGAATGACTA is described with additional reference to Figs. 9-15.

TGAGTTATTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGTTTTTCAT encoded by the human genome.

CTGCTCAGGC GAM337420 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ACCGTGCTGG GAM337420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GCC GAM337420 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337420 precursor RNA is designated SEQ ID:6748, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6748 is located from position 111321485 to position 111321597 relative to chromosome 11 on the `-` strand.

GAM337420 precursor RNA folds onto itself, forming GAM337420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337420 precursor RNA, designated SEQ ID NO: 6748, and a schematic representation of a predicted secondary folding of GAM337420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337420 folded precursor

RNA yielding a GAM337420 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337420 RNA, hereby incorporated herein.

GAM337420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337420 target RNA, herein designated GAM TARGET RNA.

GAM337420 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337420 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337420 RNA, herein designated GAM RNA, to target binding sites on GAM337420 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337420 target RNA into GAM337420 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337420 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337420 target genes. The mRNA of each one of this plurality of GAM337420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337420 RNA, herein designated GAM RNA, and which when bound by GAM337420 RNA causes inhibition of translation of the GAM337420 target mRNA into a corresponding GAM337420 target protein.

The mechanism of the translational inhibition exerted by GAM337420 RNA, herein designated GAM RNA, on one or more GAM337420 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337420 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337420 RNA, herein designated GAM RNA, of GAM337420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337420 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337420 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337420 RNA correlate with, and may be deduced from, the identity of the GAM337420 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337421 7078 TCTTCATTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTCTATATC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATTGCTATGC Messenger 337421 (GAM337421) oligonucleotides modulates expression of respective target

CCTGGTGTTG genes whose function and utility is known in the art.

TGCCCGGGGT GAM337421 is a novel bioinformatically detectable regulatory, non protein

ACAACACGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337421 was detected

GTAGGTGTTC is described with additional reference to Figs. 9-15.

GATAAACTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTTGGATAA encoded by the human genome.

ATGGAAGA GAM337421 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337421 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337421 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337421 precursor RNA is designated SEQ ID:7078, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7078 is located from position 111340859 to position 111340956 relative to chromosome 12 on the `+` strand.

GAM337421 precursor RNA folds onto itself, forming GAM337421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337421 precursor RNA, designated SEQ ID NO: 7078, and a schematic representation of a predicted secondary folding of GAM337421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337421 folded precursor RNA yielding a GAM337421 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337421 RNA, hereby incorporated herein.

GAM337421 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337421 target RNA, herein designated GAM TARGET RNA.

GAM337421 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337421 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337421 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337421 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337421 RNA, herein designated GAM RNA, to target binding sites on GAM337421 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337421 target RNA into GAM337421 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337421 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337421 target genes. The mRNA of each one of this plurality of GAM337421 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337421 RNA, herein designated GAM RNA, and which when bound by GAM337421 RNA causes inhibition of translation of the GAM337421 target mRNA into a corresponding GAM337421 target protein.

The mechanism of the translational inhibition exerted by GAM337421 RNA, herein designated GAM RNA, on one or more GAM337421 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337421 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337421 RNA, herein designated GAM RNA, of GAM337421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337421 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337421 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337421 RNA correlate with, and may be deduced from, the identity of the GAM337421 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337424 6720 GGATGGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTCCAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGGAGGTTG Messenger 337424 (GAM337424) oligonucleotides modulates expression of respective target
CAGTGAACAG genes whose function and utility is known in the art.

AGATTGTGTC GAM337424 is a novel bioinformatically detectable regulatory, non protein
ACTGCACTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337424 was detected
AGCCTGGGCA is described with additional reference to Figs. 9-15.

ACAGAGCGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACC encoded by the human genome.

GAM337424 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337424 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337424 precursor RNA is designated SEQ ID:6720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6720 is located from position 111702787 to position 111702869 relative to chromosome 11 on the `+` strand.

GAM337424 precursor RNA folds onto itself, forming GAM337424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337424 precursor RNA, designated SEQ ID NO: 6720, and a schematic representation of a predicted secondary folding of GAM337424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337424 folded precursor RNA yielding a GAM337424 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337424 RNA, hereby incorporated herein.

GAM337424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337424 target RNA, herein designated GAM TARGET RNA.

GAM337424 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337424 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337424 RNA, herein designated GAM RNA, to target binding sites on GAM337424 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337424 target RNA into GAM337424 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337424 target genes. The mRNA of each one of this

plurality of GAM337424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337424 RNA, herein designated GAM RNA, and which when bound by GAM337424 RNA causes inhibition of translation of the GAM337424 target mRNA into a corresponding GAM337424 target protein.

The mechanism of the translational inhibition exerted by GAM337424 RNA, herein designated GAM RNA, on one or more GAM337424 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337424 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337424 RNA, herein designated GAM RNA, of GAM337424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337424 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337424 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337424 RNA correlate with, and may be deduced from, the identity of the GAM337424 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337425 6564 GCTTGAGTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGAGGTGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTGCAGTG Messenger 337425 (GAM337425) oligonucleotides modulates expression of respective target

AACAGAGATT genes whose function and utility is known in the art.

GTGTCACTGC GAM337425 is a novel bioinformatically detectable regulatory, non protein

ACTCTAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337425 was detected

GGGCAACAGA is described with additional reference to Figs. 9-15.

GC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337425 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337425 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337425 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337425 precursor RNA is designated SEQ ID:6564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6564 is located from position 111702792 to position 111702863 relative to chromosome 11 on the `+` strand.

GAM337425 precursor RNA folds onto itself, forming GAM337425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337425 precursor RNA, designated SEQ ID NO: 6564, and a schematic representation of a predicted secondary folding of GAM337425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337425 folded precursor RNA yielding a GAM337425 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337425 RNA, hereby incorporated herein.

GAM337425 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337425 target RNA, herein designated GAM TARGET RNA.

GAM337425 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337425 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337425 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337425 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337425 RNA, herein designated GAM RNA, to target binding sites on GAM337425 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337425 target RNA into GAM337425 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337425 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337425 target genes. The mRNA of each one of this plurality of GAM337425 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337425 RNA, herein designated GAM RNA, and which when bound by GAM337425 RNA causes inhibition of translation of the GAM337425 target mRNA into a corresponding GAM337425 target protein.

The mechanism of the translational inhibition exerted by GAM337425 RNA, herein designated GAM RNA, on one or more GAM337425 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337425 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337425 RNA, herein designated GAM RNA, of GAM337425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337425 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337425 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337425 RNA correlate with, and may be deduced from, the identity of the GAM337425 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337426 5916 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337426 (GAM337426) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337426 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337426 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337426 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337426 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337426 precursor RNA is designated SEQ ID:5916, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5916 is located from position 111728469 to position 111728550 relative to chromosome 7 on the `+` strand.

GAM337426 precursor RNA folds onto itself, forming GAM337426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337426 precursor RNA, designated SEQ ID NO: 5916, and a schematic representation of a predicted secondary folding of GAM337426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337426 folded precursor RNA yielding a GAM337426 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337426 RNA, hereby incorporated herein.

GAM337426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337426 target RNA, herein designated GAM TARGET RNA.

GAM337426 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337426 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337426 RNA, herein designated GAM RNA, to target binding sites on GAM337426 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337426 target RNA into GAM337426 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337426 target genes. The mRNA of each one of this plurality of GAM337426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337426 RNA, herein designated GAM RNA, and which when bound by GAM337426 RNA causes inhibition of translation of the GAM337426 target mRNA into a corresponding GAM337426 target protein.

The mechanism of the translational inhibition exerted by GAM337426 RNA, herein designated GAM RNA, on one or more GAM337426 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337426 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337426 RNA, herein designated GAM RNA, of GAM337426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337426 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337426 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337426 RNA correlate with, and may be deduced from, the identity of the GAM337426 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337428 6344 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 337428 (GAM337428) oligonucleotides modulates expression of respective target

CAGAGGTTGC genes whose function and utility is known in the art.

GGTTAGCCAA GAM337428 is a novel bioinformatically detectable regulatory, non protein
GATTGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337428 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

TGGGTGACAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGAGAGACTC encoded by the human genome.

TGTCTC GAM337428 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337428 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337428 precursor RNA is designated SEQ ID:6344, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6344 is located from position 112035396 to position 112035491 relative to chromosome 12 on the `+` strand.

GAM337428 precursor RNA folds onto itself, forming GAM337428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337428 precursor RNA, designated SEQ ID NO: 6344, and a schematic representation of a predicted secondary folding of GAM337428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337428 folded precursor RNA yielding a GAM337428 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337428 RNA, hereby incorporated herein.

GAM337428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337428 target RNA, herein designated GAM TARGET RNA.

GAM337428 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337428 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337428 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337428 RNA, herein designated GAM RNA, to target binding sites on GAM337428 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337428 target RNA into GAM337428 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337428 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337428 target genes. The mRNA of each one of this plurality of GAM337428 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337428 RNA, herein designated GAM RNA, and which when bound by GAM337428 RNA causes inhibition of translation of the GAM337428 target mRNA into a corresponding GAM337428 target protein.

The mechanism of the translational inhibition exerted by GAM337428 RNA, herein designated GAM RNA, on one or more GAM337428 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337428 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337428 RNA, herein designated GAM RNA, of GAM337428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337428 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337428 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337428 RNA correlate with, and may be deduced from, the identity of the GAM337428 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337429 6152 CTAGAGTCCC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTCAGCTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGGGGAGCTT Messenger 337429 (GAM337429) oligonucleotides modulates expression of respective target
TCAAATTTGA genes whose function and utility is known in the art.

AATCAGGAGA GAM337429 is a novel bioinformatically detectable regulatory, non protein
CTCGAATTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337429 was detected
AGTTTTTCCT is described with additional reference to Figs. 9-15.

ACCCCTTAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTGTGGGAC encoded by the human genome.

TTTAG GAM337429 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337429 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337429 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337429 precursor RNA is designated SEQ ID:6152, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6152 is located from position 112396737 to position 112396831 relative to chromosome 9 on the `+` strand.

GAM337429 precursor RNA folds onto itself, forming GAM337429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337429 precursor RNA, designated SEQ ID NO: 6152, and a schematic representation of a predicted secondary folding of GAM337429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337429 folded precursor RNA yielding a GAM337429 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337429 RNA, hereby incorporated herein.

GAM337429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337429 target RNA, herein designated GAM TARGET RNA.

GAM337429 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337429 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337429 RNA, herein designated GAM RNA, to target binding sites on GAM337429 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337429 target RNA into GAM337429 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337429 target genes. The mRNA of each one of this plurality of GAM337429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337429 RNA, herein designated GAM RNA, and which when bound by GAM337429 RNA causes inhibition of translation of the GAM337429 target mRNA into a corresponding GAM337429 target protein.

The mechanism of the translational inhibition exerted by GAM337429 RNA, herein designated GAM RNA, on one or more GAM337429 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337429 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337429 RNA, herein designated GAM RNA, of GAM337429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337429 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337429 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337429 RNA correlate with, and may be deduced from, the identity of the GAM337429 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337430 6900 GTGATTCAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGACGTGAT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGAGGAAATG Messenger 337430 (GAM337430) oligonucleotides modulates expression of respective target
GTGGTATCTT genes whose function and utility is known in the art.

GTGTTATTAA GAM337430 is a novel bioinformatically detectable regulatory, non protein
GCACTTGAAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337430 was detected
TTGGTTGATG is described with additional reference to Figs. 9-15.

CACTGCAGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCTAATAAAT encoded by the human genome.

TTCCAATATC GAM337430 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AAGAAGAACA GAM337430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TGCTGAAGAA GAM337430 precursor RNA does not encode a protein. A nucleotide sequence identical or

T highly similar to the nucleotide sequence of GAM337430 precursor RNA is designated SEQ ID:6900, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6900 is located from position 112469045 to position 112469165 relative to chromosome 12 on the `-` strand.

GAM337430 precursor RNA folds onto itself, forming GAM337430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337430 precursor RNA, designated SEQ ID NO: 6900, and a schematic representation of a predicted secondary folding of GAM337430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337430 folded precursor RNA yielding a GAM337430 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337430 RNA, hereby incorporated herein.

GAM337430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337430 target RNA, herein designated GAM TARGET RNA.

GAM337430 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337430 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337430 RNA, herein designated GAM RNA, to target binding sites on GAM337430 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337430 target RNA into GAM337430 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337430 target genes. The mRNA of each one of this plurality of GAM337430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337430 RNA, herein designated GAM RNA, and which when bound by GAM337430 RNA causes inhibition of translation of the GAM337430 target mRNA into a corresponding GAM337430 target protein.

The mechanism of the translational inhibition exerted by GAM337430 RNA, herein designated GAM RNA, on one or more GAM337430 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337430 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337430 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337430 RNA, herein designated GAM RNA, of GAM337430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337430 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337430 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337430 RNA correlate with, and may be deduced from, the identity of the GAM337430 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337431 7292 TTCAGCCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

CGTGATGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAAATGGTGG Messenger 337431 (GAM337431) oligonucleotides modulates expression of respective target

TATCTTGTGT genes whose function and utility is known in the art.

TATTAAGCAC GAM337431 is a novel bioinformatically detectable regulatory, non protein

TTGAACTTGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337431 was detected

TTGATGCACT is described with additional reference to Figs. 9-15.

GCAGTCTCTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATAAATTTCC encoded by the human genome.

AATATCAAGA GAM337431 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

AGAACATGCT GAM337431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAA GAM337431 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337431 precursor RNA is designated SEQ ID:7292, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7292 is located from position 112469049 to position 112469161 relative to chromosome 12 on the `-` strand.

GAM337431 precursor RNA folds onto itself, forming GAM337431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337431 precursor RNA, designated SEQ ID NO: 7292, and a schematic representation of a predicted secondary folding of GAM337431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337431 folded precursor RNA yielding a GAM337431 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337431 RNA, hereby incorporated herein.

GAM337431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337431 target RNA, herein designated GAM TARGET RNA.

GAM337431 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337431 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337431 RNA, herein designated GAM RNA, to target binding sites on GAM337431 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337431 target RNA into GAM337431 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337431 target genes. The mRNA of each one of this plurality of GAM337431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337431 RNA, herein designated GAM RNA, and which when bound by GAM337431 RNA causes inhibition of translation of the GAM337431 target mRNA into a corresponding GAM337431 target protein.

The mechanism of the translational inhibition exerted by GAM337431 RNA, herein designated GAM RNA, on one or more GAM337431 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337431 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337431 RNA, herein designated GAM RNA, of GAM337431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337431 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337431 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337431 RNA correlate with, and may be deduced from, the identity of the GAM337431 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337432 7009 TCAGCCAGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

GTGATGGAGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAATGGTGGT Messenger 337432 (GAM337432) oligonucleotides modulates expression of respective target

ATCTTGTGTT genes whose function and utility is known in the art.

ATTAAGCACT GAM337432 is a novel bioinformatically detectable regulatory, non protein

TGAACTTGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337432 was detected

TGATGCACTG is described with additional reference to Figs. 9-15.

CAGTCTCTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TAAATTTCCA encoded by the human genome.

ATATCAAGAA GAM337432 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAACATGCTG GAM337432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

A GAM337432 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337432 precursor RNA is designated SEQ

ID:7009, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7009 is located from position 112469050 to position 112469160 relative to chromosome 12 on the `-` strand.

GAM337432 precursor RNA folds onto itself, forming GAM337432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337432 precursor RNA, designated SEQ ID NO: 7009, and a schematic representation of a predicted secondary folding of GAM337432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337432 folded precursor RNA yielding a GAM337432 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337432 RNA, hereby incorporated herein.

GAM337432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337432 target RNA, herein designated GAM TARGET RNA.

GAM337432 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337432 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337432 RNA, herein designated GAM RNA, to target binding sites on GAM337432 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337432 target RNA into GAM337432 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337432 target genes. The mRNA of each one of this plurality of GAM337432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337432 RNA, herein designated GAM RNA, and which when bound by GAM337432 RNA causes inhibition of translation of the GAM337432 target mRNA into a corresponding GAM337432 target protein.

The mechanism of the translational inhibition exerted by GAM337432 RNA, herein designated GAM RNA, on one or more GAM337432 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337432 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337432 RNA, herein designated GAM RNA, of GAM337432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337432 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337432 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337432 RNA correlate with, and may be deduced from, the identity of the GAM337432 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337433 7191 TGATGGAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AATGGTGGTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTGTGTTA Messenger 337433 (GAM337433) oligonucleotides modulates expression of respective target

TTAAGCACTT genes whose function and utility is known in the art.

GAACTTGGTT GAM337433 is a novel bioinformatically detectable regulatory, non protein

GATGCACTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337433 was detected

AGTCTCTAAT is described with additional reference to Figs. 9-15.

AAATTTCCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TATCA encoded by the human genome.

GAM337433 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337433 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337433 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337433 precursor RNA is designated SEQ ID:7191, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7191 is located from position 112469065 to position 112469149 relative to chromosome 12 on the `-` strand.

GAM337433 precursor RNA folds onto itself, forming GAM337433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337433 precursor RNA, designated SEQ ID NO: 7191, and a schematic representation of a predicted secondary folding of GAM337433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337433 folded precursor RNA yielding a GAM337433 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337433 RNA, hereby incorporated herein.

GAM337433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337433 target RNA, herein designated GAM TARGET RNA.

GAM337433 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337433 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337433 RNA, herein designated GAM RNA, to target binding sites on GAM337433 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337433 target RNA into GAM337433 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337433 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337433 target genes. The mRNA of each one of this plurality of GAM337433 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337433 RNA, herein designated GAM RNA, and which when bound by GAM337433 RNA causes inhibition of translation of the GAM337433 target mRNA into a corresponding GAM337433 target protein.

The mechanism of the translational inhibition exerted by GAM337433 RNA, herein designated GAM RNA, on one or more GAM337433 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337433 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337433 RNA, herein designated GAM RNA, of GAM337433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337433 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337433 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337433 RNA correlate with, and may be deduced from, the identity of the GAM337433 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337435 5917 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337435 (GAM337435) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337435 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337435 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337435 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337435 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337435 precursor RNA is designated SEQ ID:5917, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5917 is located from position 112801451 to position 112801532 relative to chromosome 11 on the `+` strand.

GAM337435 precursor RNA folds onto itself, forming GAM337435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337435 precursor RNA, designated SEQ ID NO: 5917, and a schematic representation of a predicted secondary folding of GAM337435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337435 folded precursor RNA yielding a GAM337435 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337435 RNA, hereby incorporated herein.

GAM337435 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337435 target RNA, herein designated GAM TARGET RNA.

GAM337435 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337435 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337435 RNA, herein designated GAM RNA, to target binding sites on GAM337435 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337435 target RNA into GAM337435 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337435 target genes. The mRNA of each one of this plurality of GAM337435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337435 RNA, herein designated GAM RNA, and which when bound by GAM337435 RNA causes inhibition of translation of the GAM337435 target mRNA into a corresponding GAM337435 target protein.

The mechanism of the translational inhibition exerted by GAM337435 RNA, herein designated GAM RNA, on one or more GAM337435 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337435 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337435 RNA, herein designated GAM RNA, of GAM337435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337435 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337435 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337435 RNA correlate with, and may be deduced from, the identity of the GAM337435 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337437 7219 TGGAGCTGCT Fig. 8 further provides a conceptual description of another novel bioinformatically
GGGTAAAATA detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGTGTACTT Messenger 337437 (GAM337437) oligonucleotides modulates expression of respective target
GTCTTAGTTT genes whose function and utility is known in the art.

GCTCTTTTCC GAM337437 is a novel bioinformatically detectable regulatory, non protein
AAGTTGAAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337437 was detected
CTGGCAGATT is described with additional reference to Figs. 9-15.

TCACCAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGTGTCTG encoded by the human genome.

CCCCCACCTC GAM337437 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM337437 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337437 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337437 precursor RNA is designated SEQ ID:7219, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7219 is located from position 112997384 to position 112997485 relative to chromosome 13 on the `+` strand.

GAM337437 precursor RNA folds onto itself, forming GAM337437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337437 precursor RNA, designated SEQ ID NO: 7219, and a schematic representation of a predicted secondary folding of GAM337437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337437 folded precursor RNA yielding a GAM337437 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337437 RNA, hereby incorporated herein.

GAM337437 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337437 target RNA, herein designated GAM TARGET RNA.

GAM337437 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337437 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337437 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337437 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337437 RNA, herein designated GAM RNA, to target binding sites on GAM337437 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337437 target RNA into GAM337437 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337437 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337437 target genes. The mRNA of each one of this plurality of GAM337437 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337437 RNA, herein designated GAM RNA, and which when bound by GAM337437 RNA causes inhibition of translation of the GAM337437 target mRNA into a corresponding GAM337437 target protein.

The mechanism of the translational inhibition exerted by GAM337437 RNA, herein designated GAM RNA, on one or more GAM337437 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337437 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337437 RNA, herein designated GAM RNA, of GAM337437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337437 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337437 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337437 RNA correlate with, and may be deduced from, the identity of the GAM337437 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337438 7184 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACTCGGGAG Messenger 337438 (GAM337438) oligonucleotides modulates expression of respective target
GGGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCAA GAM337438 is a novel bioinformatically detectable regulatory, non protein
GATCACACAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337438 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAAAGTGA encoded by the human genome.

GACCCCCATC GAM337438 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TCA GAM337438 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337438 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337438 precursor RNA is designated SEQ ID:7184, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7184 is located from position 113030916 to position 113031018 relative to chromosome 2 on the `-` strand.

GAM337438 precursor RNA folds onto itself, forming GAM337438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337438 precursor RNA, designated SEQ ID NO: 7184, and a schematic representation of a predicted secondary folding of GAM337438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337438 folded precursor RNA yielding a GAM337438 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337438 RNA, hereby incorporated herein. Expression of GAM337438 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337438 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337438 target RNA, herein designated GAM TARGET RNA.

GAM337438 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337438 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337438 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337438 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337438 RNA, herein designated GAM RNA, to target binding sites on GAM337438 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337438 target RNA into GAM337438 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337438 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337438 target genes. The mRNA of each one of this plurality of GAM337438 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337438 RNA, herein designated GAM RNA, and which when bound by GAM337438 RNA causes inhibition of translation of the GAM337438 target mRNA into a corresponding GAM337438 target protein.

The mechanism of the translational inhibition exerted by GAM337438 RNA, herein designated GAM RNA, on one or more GAM337438 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337438 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337438 RNA, herein designated GAM RNA, of GAM337438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337438 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337438 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337438 RNA correlate with, and may be deduced from, the identity of the GAM337438 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337439 6662 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGGGAGGC Messenger 337439 (GAM337439) oligonucleotides modulates expression of respective target

TGCAGTGAGC genes whose function and utility is known in the art.

CAAGATCACA GAM337439 is a novel bioinformatically detectable regulatory, non protein

CACCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337439 was detected

CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGAGACC encoded by the human genome.

GAM337439 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337439 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337439 precursor RNA is designated SEQ ID:6662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6662 is located from position 113030925 to position 113031011 relative to chromosome 2 on the `-` strand.

GAM337439 precursor RNA folds onto itself, forming GAM337439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337439 precursor RNA, designated SEQ ID NO: 6662, and a schematic representation of a predicted secondary folding of GAM337439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337439 folded precursor RNA yielding a GAM337439 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337439 RNA, hereby incorporated herein. Expression of GAM337439 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337439 target RNA, herein designated GAM TARGET RNA.

GAM337439 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337439 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337439 RNA, herein designated GAM RNA, to target binding sites on GAM337439 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337439 target RNA into GAM337439 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337439 target genes. The mRNA of each one of this plurality of GAM337439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337439 RNA, herein designated GAM RNA, and which when bound by GAM337439 RNA causes inhibition of translation of the GAM337439 target mRNA into a corresponding GAM337439 target protein.

The mechanism of the translational inhibition exerted by GAM337439 RNA, herein

designated GAM RNA, on one or more GAM337439 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337439 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337439 RNA, herein designated GAM RNA, of GAM337439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337439 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337439 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337439 RNA correlate with, and may be deduced from, the identity of the GAM337439 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337440 7058 TCGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TCGGGAGGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCTGCAGT Messenger 337440 (GAM337440) oligonucleotides modulates expression of respective target
GAGCCAAGAT genes whose function and utility is known in the art.

CACACACCAC GAM337440 is a novel bioinformatically detectable regulatory, non protein
TGCACTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337440 was detected
CCTGGGCAAC is described with additional reference to Figs. 9-15.

AAAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337440 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337440 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337440 precursor RNA is designated SEQ ID:7058, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7058 is located from position 113030929 to position 113031005

relative to chromosome 2 on the `-` strand.

GAM337440 precursor RNA folds onto itself, forming GAM337440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337440 precursor RNA, designated SEQ ID NO: 7058, and a schematic representation of a predicted secondary folding of GAM337440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337440 folded precursor RNA yielding a GAM337440 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337440 RNA, hereby incorporated herein. Expression of GAM337440 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337440 target RNA, herein designated GAM TARGET RNA.

GAM337440 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337440 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337440 RNA, herein designated GAM RNA, to target binding sites on GAM337440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337440 target RNA into GAM337440 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337440 target genes. The mRNA of each one of this plurality of GAM337440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337440 RNA, herein designated GAM RNA, and which when bound by GAM337440 RNA causes inhibition of translation of the GAM337440 target mRNA into a corresponding GAM337440 target protein.

The mechanism of the translational inhibition exerted by GAM337440 RNA, herein designated GAM RNA, on one or more GAM337440 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337440 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337440 RNA, herein designated GAM RNA, of GAM337440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337440 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337440 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337440 RNA correlate with, and may be deduced from, the identity of the GAM337440 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337441 5789 AGGGGTTGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTTAAGTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTGCCTGC Messenger 337441 (GAM337441) oligonucleotides modulates expression of respective target

AGTCCTGCTT genes whose function and utility is known in the art.

TGTTTTGGAC GAM337441 is a novel bioinformatically detectable regulatory, non protein

AAGTAGGAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337441 was detected

GACAAGCAGG is described with additional reference to Figs. 9-15.

TCAGCACAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CCTT encoded by the human genome.

GAM337441 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337441 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337441 precursor RNA is designated SEQ ID:5789, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5789 is located from position 113128395 to position 113128478 relative to chromosome 11 on the `+` strand.

GAM337441 precursor RNA folds onto itself, forming GAM337441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337441 precursor RNA, designated SEQ ID NO: 5789, and a schematic representation of a predicted secondary folding of GAM337441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337441 folded precursor RNA yielding a GAM337441 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337441 RNA, hereby incorporated herein.

GAM337441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337441 target RNA, herein designated GAM TARGET RNA.

GAM337441 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337441 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337441 RNA, herein designated GAM RNA, to target binding sites on GAM337441 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337441 target RNA into GAM337441 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337441 target genes. The mRNA of each one of this plurality of GAM337441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337441 RNA, herein designated GAM RNA, and which when bound by GAM337441 RNA causes inhibition of translation of the GAM337441 target mRNA into a corresponding GAM337441 target protein.

The mechanism of the translational inhibition exerted by GAM337441 RNA, herein designated GAM RNA, on one or more GAM337441 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337441 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337441 RNA, herein designated GAM RNA, of GAM337441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337441 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337441 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337441 RNA correlate with, and may be deduced from, the identity of the GAM337441 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337442 6819 GGGGTTGTCC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTAAGTTCCC detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTGCCTGCA Messenger 337442 (GAM337442) oligonucleotides modulates expression of respective target

GTCCTGCTTT genes whose function and utility is known in the art.

GTTTTGGACA AGTAGGAGTG ACAAGCAGGT CAGCACAGCC CT

GAM337442 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337442 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337442 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337442 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337442 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337442 precursor RNA is designated SEQ ID:6819, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6819 is located from position 113128396 to position 113128477 relative to chromosome 11 on the `+` strand.

GAM337442 precursor RNA folds onto itself, forming GAM337442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337442 precursor RNA, designated SEQ ID NO: 6819, and a schematic representation of a predicted secondary folding of GAM337442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337442 folded precursor RNA yielding a GAM337442 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337442 RNA, hereby incorporated herein.

GAM337442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337442 target RNA, herein designated GAM TARGET RNA.

GAM337442 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337442 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337442 RNA, herein designated GAM RNA, to target binding sites on GAM337442 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337442 target RNA into GAM337442 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337442 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337442 target genes. The mRNA of each one of this plurality of GAM337442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337442 RNA, herein designated GAM RNA, and which when bound by GAM337442 RNA causes inhibition of translation of the GAM337442 target mRNA into a corresponding GAM337442 target protein.

The mechanism of the translational inhibition exerted by GAM337442 RNA, herein designated GAM RNA, on one or more GAM337442 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337442 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337442 RNA, herein designated GAM RNA, of GAM337442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337442 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337442 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337442 RNA correlate with, and may be deduced from, the identity of the GAM337442 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337443 6827 GGGTTGTCCT Fig. 8 further provides a conceptual description of another novel bioinformatically
TAAGTTCCCT detected oligonucleotides of the present invention, referred to here as Genomic Address
CTGCCTGCAG Messenger 337443 (GAM337443) oligonucleotides modulates expression of respective target
TCCTGCTTTG genes whose function and utility is known in the art.

TTTTGGACAA GAM337443 is a novel bioinformatically detectable regulatory, non protein
GTAGGAGTGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337443 was detected
CAAGCAGGTC is described with additional reference to Figs. 9-15.

AGCACAGCCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337443 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337443 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337443 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337443 precursor RNA is designated SEQ ID:6827, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6827 is located from position 113128397 to position 113128476 relative to chromosome 11 on the `+` strand.

GAM337443 precursor RNA folds onto itself, forming GAM337443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337443 precursor RNA, designated SEQ ID NO: 6827, and a schematic representation of a predicted secondary folding of GAM337443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337443 folded precursor RNA yielding a GAM337443 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337443 RNA, hereby incorporated herein.

GAM337443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337443 target RNA, herein designated GAM TARGET RNA.

GAM337443 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337443 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337443 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337443 RNA, herein designated GAM RNA, to target binding sites on GAM337443 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337443 target RNA into GAM337443 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337443 target genes. The mRNA of each one of this plurality of GAM337443 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337443 RNA, herein designated GAM RNA, and which when bound by GAM337443 RNA causes inhibition of translation of the GAM337443 target mRNA into a corresponding GAM337443 target protein.

The mechanism of the translational inhibition exerted by GAM337443 RNA, herein designated GAM RNA, on one or more GAM337443 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337443 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337443 RNA, herein designated GAM RNA, of GAM337443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337443 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337443 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337443 RNA correlate with, and may be deduced from, the identity of the GAM337443 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337445 7041 TCCTGACGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCCTCTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGCATTTAGG Messenger 337445 (GAM337445) oligonucleotides modulates expression of respective target
AACAAGGAGC genes whose function and utility is known in the art.

TCCCCGAGTA GAM337445 is a novel bioinformatically detectable regulatory, non protein
ACCTGAAGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337445 was detected
CACTCTGCCC is described with additional reference to Figs. 9-15.

AGAGGCCCCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAACTTACAG encoded by the human genome.

GA GAM337445 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337445 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337445 precursor RNA is designated SEQ ID:7041, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7041 is located from position 113838652 to position 113838743 relative to chromosome 13 on the `+` strand.

GAM337445 precursor RNA folds onto itself, forming GAM337445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337445 precursor RNA, designated SEQ ID NO: 7041, and a schematic representation of a predicted secondary folding of GAM337445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337445 folded precursor RNA yielding a GAM337445 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337445 RNA, hereby incorporated herein.

GAM337445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337445 target RNA, herein designated GAM TARGET RNA.

GAM337445 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337445 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337445 RNA, herein designated GAM RNA, to target binding sites on GAM337445 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337445 target RNA into GAM337445 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337445 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337445 target genes. The mRNA of each one of this plurality of GAM337445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337445 RNA, herein designated GAM RNA, and which when bound by GAM337445 RNA causes inhibition of translation of the GAM337445 target mRNA into a corresponding GAM337445 target protein.

The mechanism of the translational inhibition exerted by GAM337445 RNA, herein designated GAM RNA, on one or more GAM337445 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337445 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337445 RNA, herein designated GAM RNA, of GAM337445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337445 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337445 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337445 RNA correlate with, and may be deduced from, the identity of the GAM337445 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337446 6611 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAAGGCGGAG Messenger 337446 (GAM337446) oligonucleotides modulates expression of respective target
GTTGCAGTGA genes whose function and utility is known in the art.

GCCGAGATCG GAM337446 is a novel bioinformatically detectable regulatory, non protein
TGCCACTGCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337446 was detected
CTCCAGCCTG is described with additional reference to Figs. 9-15.

GGCAACAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GTGAGACTCC encoded by the human genome.

GAM337446 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337446 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337446 precursor RNA is designated SEQ ID:6611, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6611 is located from position 113861407 to position 113861496 relative to chromosome 7 on the `+` strand.

GAM337446 precursor RNA folds onto itself, forming GAM337446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337446 precursor RNA, designated SEQ ID NO: 6611, and a schematic representation of a predicted secondary folding of GAM337446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337446 folded precursor RNA yielding a GAM337446 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337446 RNA, hereby incorporated herein. Expression of GAM337446 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337446 target RNA, herein designated GAM TARGET RNA.

GAM337446 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337446 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337446 RNA, herein designated GAM RNA, to target binding sites on GAM337446 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337446 target RNA into GAM337446 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337446 target genes. The mRNA of each one of this plurality of GAM337446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337446 RNA, herein designated GAM RNA, and which when bound by GAM337446 RNA causes inhibition of translation of the GAM337446 target mRNA into a corresponding GAM337446 target protein.

The mechanism of the translational inhibition exerted by GAM337446 RNA, herein designated GAM RNA, on one or more GAM337446 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337446 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337446 RNA, herein designated GAM RNA, of GAM337446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337446 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337446 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337446 RNA correlate with, and may be deduced from, the identity of the GAM337446 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337447 7001 TCACTTGAAC CCGGGAAGGC GGAGGTTGCA GTGAGCCGAG ATCGTGCCAC TGCACTCCAG CCTGGGCAAC AAGAGTGA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337447 (GAM337447) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337447 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337447 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337447 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337447 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337447 precursor RNA is designated SEQ ID:7001, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7001 is located from position 113861413 to position 113861490 relative to chromosome 7 on the `+` strand.

GAM337447 precursor RNA folds onto itself, forming GAM337447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337447 precursor RNA, designated SEQ ID NO: 7001, and a schematic representation of a predicted secondary folding of GAM337447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337447 folded precursor RNA yielding a GAM337447 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337447 RNA, hereby incorporated herein. Expression of GAM337447 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337447 target RNA, herein designated GAM TARGET RNA.

GAM337447 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337447 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337447 RNA, herein designated GAM RNA, to target binding sites on GAM337447 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337447 target RNA into GAM337447 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337447 target genes. The mRNA of each one of this plurality of GAM337447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337447 RNA,

herein designated GAM RNA, and which when bound by GAM337447 RNA causes inhibition of translation of the GAM337447 target mRNA into a corresponding GAM337447 target protein.

The mechanism of the translational inhibition exerted by GAM337447 RNA, herein designated GAM RNA, on one or more GAM337447 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337447 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337447 RNA, herein designated GAM RNA, of GAM337447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337447 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337447 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337447 RNA correlate with, and may be deduced from, the identity of the GAM337447 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337448 6260 CTTGAACCCG Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAGGCGGA detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTGCAGTG Messenger 337448 (GAM337448) oligonucleotides modulates expression of respective target

AGCCGAGATC genes whose function and utility is known in the art.

GTGCCACTGC GAM337448 is a novel bioinformatically detectable regulatory, non protein

ACTCCAGCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337448 was detected

GGGCAACAAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337448 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337448 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337448 precursor RNA is designated SEQ ID:6260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6260 is located from position 113861416 to position 113861485 relative to chromosome 7 on the `+` strand.

GAM337448 precursor RNA folds onto itself, forming GAM337448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337448 precursor RNA, designated SEQ ID NO: 6260, and a schematic representation of a predicted secondary folding of GAM337448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337448 folded precursor RNA yielding a GAM337448 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337448 RNA, hereby incorporated herein. Expression of GAM337448 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337448 target RNA, herein designated GAM TARGET RNA.

GAM337448 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337448 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337448 RNA, herein designated GAM RNA, to target binding sites on GAM337448 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337448 target RNA into GAM337448 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337448 target genes. The mRNA of each one of this plurality of GAM337448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337448 RNA, herein designated GAM RNA, and which when bound by GAM337448 RNA causes inhibition of translation of the GAM337448 target mRNA into a corresponding GAM337448 target protein.

The mechanism of the translational inhibition exerted by GAM337448 RNA, herein designated GAM RNA, on one or more GAM337448 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337448 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337448 RNA, herein designated GAM RNA, of GAM337448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337448 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337448 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337448 RNA correlate with, and may be deduced from, the identity of the GAM337448 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337449 5918 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337449 (GAM337449) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337449 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337449 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337449 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337449 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337449 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337449 precursor RNA is designated SEQ ID:5918, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5918 is located from position 114300062 to position 114300143 relative to chromosome X on the `-` strand.

GAM337449 precursor RNA folds onto itself, forming GAM337449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337449 precursor RNA, designated SEQ ID NO: 5918, and a schematic representation of a predicted secondary folding of GAM337449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337449 folded precursor RNA yielding a GAM337449 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337449 RNA, hereby incorporated herein.

GAM337449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337449 target RNA, herein designated GAM TARGET RNA.

GAM337449 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337449 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337449 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337449 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337449 RNA, herein designated GAM RNA, to target binding sites on GAM337449 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337449 target RNA into GAM337449 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337449 target genes. The mRNA of each one of this plurality of GAM337449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337449 RNA, herein designated GAM RNA, and which when bound by GAM337449 RNA causes inhibition of translation of the GAM337449 target mRNA into a corresponding GAM337449 target protein.

The mechanism of the translational inhibition exerted by GAM337449 RNA, herein designated GAM RNA, on one or more GAM337449 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337449 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337449 RNA, herein designated GAM RNA, of GAM337449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337449 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337449 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337449 RNA correlate with, and may be deduced from, the identity of the GAM337449 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337450 7200 TGCCTGAATA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAGCTAGACG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTCATTGACC Messenger 337450 (GAM337450) oligonucleotides modulates expression of respective target

AGCAGAGTCT genes whose function and utility is known in the art.

TTTATAACTA GAM337450 is a novel bioinformatically detectable regulatory, non protein
CCCCAGTTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337450 was detected
GTGGAAAACT is described with additional reference to Figs. 9-15.

TGGGCTGGTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TAAGTACTGT encoded by the human genome.

CCAGGCA GAM337450 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337450 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337450 precursor RNA is designated SEQ ID:7200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7200 is located from position 114520290 to position 114520386 relative to chromosome 12 on the `+` strand.

GAM337450 precursor RNA folds onto itself, forming GAM337450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337450 precursor RNA, designated SEQ ID NO: 7200, and a schematic representation of a predicted secondary folding of GAM337450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337450 folded precursor RNA yielding a GAM337450 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337450 RNA, hereby incorporated herein.

GAM337450 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337450 target RNA, herein designated GAM TARGET RNA.

GAM337450 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337450 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337450 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337450 RNA, herein designated GAM RNA, to target binding sites on GAM337450 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337450 target RNA into GAM337450 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337450 target genes. The mRNA of each one of this plurality of GAM337450 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337450 RNA, herein designated GAM RNA, and which when bound by GAM337450 RNA causes inhibition of translation of the GAM337450 target mRNA into a corresponding GAM337450 target protein.

The mechanism of the translational inhibition exerted by GAM337450 RNA, herein designated GAM RNA, on one or more GAM337450 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337450 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337450 RNA, herein designated GAM RNA, of GAM337450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337450 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337450 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337450 RNA correlate with, and may be deduced from, the identity of the GAM337450 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337452 6808 GGGCTTTTGC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTAGATGGA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAAGTTCAAA Messenger 337452 (GAM337452) oligonucleotides modulates expression of respective target
TCCTGGCTCA genes whose function and utility is known in the art.

GTCACTTAGG GAM337452 is a novel bioinformatically detectable regulatory, non protein
AAATTTGGCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337452 was detected
GTTTGTCTTG is described with additional reference to Figs. 9-15.

GGCAAGTTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TC encoded by the human genome.

GAM337452 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337452 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337452 precursor RNA is designated SEQ ID:6808, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6808 is located from position 115482747 to position 115482828 relative to chromosome 10 on the `-` strand.

GAM337452 precursor RNA folds onto itself, forming GAM337452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337452 precursor RNA, designated SEQ ID NO: 6808, and a schematic representation of a predicted secondary folding of GAM337452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337452 folded precursor RNA yielding a GAM337452 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337452 RNA, hereby incorporated herein.

GAM337452 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337452 target RNA, herein designated GAM TARGET RNA.

GAM337452 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337452 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337452 RNA, herein designated GAM RNA, to target binding sites on GAM337452 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337452 target RNA into GAM337452 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337452 target genes. The mRNA of each one of this plurality of GAM337452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337452 RNA, herein designated GAM RNA, and which when bound by GAM337452 RNA causes inhibition of translation of the GAM337452 target mRNA into a corresponding GAM337452 target protein.

The mechanism of the translational inhibition exerted by GAM337452 RNA, herein designated GAM RNA, on one or more GAM337452 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337452 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337452 RNA, herein designated GAM RNA, of GAM337452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337452 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337452 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337452 RNA correlate with, and may be deduced from, the identity of the GAM337452 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337453 7151 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGGTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337453 (GAM337453) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCCG GAM337453 is a novel bioinformatically detectable regulatory, non protein
AGATCGTACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337453 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCAA encoded by the human genome.

AACTCCGTCT GAM337453 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM337453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337453 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337453 precursor RNA is designated SEQ ID:7151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7151 is located from position 116189890 to position 116189991 relative to chromosome 1 on the `-` strand.

GAM337453 precursor RNA folds onto itself, forming GAM337453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337453 precursor RNA, designated SEQ ID NO: 7151, and a schematic representation of a predicted secondary folding of GAM337453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337453 folded precursor

RNA yielding a GAM337453 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337453 RNA, hereby incorporated herein. Expression of GAM337453 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337453 target RNA, herein designated GAM TARGET RNA.

GAM337453 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337453 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337453 RNA, herein designated GAM RNA, to target binding sites on GAM337453 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337453 target RNA into GAM337453 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337453 target genes. The mRNA of each one of this plurality of GAM337453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337453 RNA, herein designated GAM RNA, and which when bound by GAM337453 RNA causes inhibition of translation of the GAM337453 target mRNA into a corresponding GAM337453 target protein.

The mechanism of the translational inhibition exerted by GAM337453 RNA, herein designated GAM RNA, on one or more GAM337453 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337453 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337453 folded precursor RNA, herein

designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337453 RNA, herein designated GAM RNA, of GAM337453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337453 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337453 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337453 RNA correlate with, and may be deduced from, the identity of the GAM337453 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337454 6405 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATCGGTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 337454 (GAM337454) oligonucleotides modulates expression of respective target
CAGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCGA GAM337454 is a novel bioinformatically detectable regulatory, non protein
GATCGTACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337454 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAAGAGCAAA encoded by the human genome.

ACTCCGTCTC GAM337454 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337454 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337454 precursor RNA is designated SEQ ID:6405, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6405 is located from position 116189891 to position 116189990 relative to chromosome 1 on the `-` strand.

GAM337454 precursor RNA folds onto itself, forming GAM337454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337454 precursor RNA, designated SEQ ID NO: 6405, and a schematic representation of a predicted secondary folding of GAM337454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337454 folded precursor RNA yielding a GAM337454 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337454 RNA, hereby incorporated herein. Expression of GAM337454 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337454 target RNA, herein designated GAM TARGET RNA.

GAM337454 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337454 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337454 RNA, herein designated GAM RNA, to target binding sites on GAM337454 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337454 target RNA into GAM337454 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337454 target genes. The mRNA of each one of this plurality of GAM337454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337454 RNA, herein designated GAM RNA, and which when bound by GAM337454 RNA causes inhibition of

translation of the GAM337454 target mRNA into a corresponding GAM337454 target protein.

The mechanism of the translational inhibition exerted by GAM337454 RNA, herein designated GAM RNA, on one or more GAM337454 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337454 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337454 RNA, herein designated GAM RNA, of GAM337454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337454 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337454 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337454 RNA correlate with, and may be deduced from, the identity of the GAM337454 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337456 7123 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
CAATCACTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337456 (GAM337456) oligonucleotides modulates expression of respective target
TTTGAGGCTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM337456 is a novel bioinformatically detectable regulatory, non protein
AGATCACGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337456 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

ACCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGCAAG encoded by the human genome.

ATCTTGTCTC GAM337456 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

G GAM337456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337456 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337456 precursor RNA is designated SEQ ID:7123, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7123 is located from position 116582532 to position 116582632 relative to chromosome 12 on the `-` strand.

GAM337456 precursor RNA folds onto itself, forming GAM337456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337456 precursor RNA, designated SEQ ID NO: 7123, and a schematic representation of a predicted secondary folding of GAM337456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337456 folded precursor RNA yielding a GAM337456 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337456 RNA, hereby incorporated herein.

GAM337456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337456 target RNA, herein designated GAM TARGET RNA.

GAM337456 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337456 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337456 RNA, herein designated GAM RNA, to target binding sites on GAM337456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337456 target RNA

into GAM337456 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337456 target genes. The mRNA of each one of this plurality of GAM337456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337456 RNA, herein designated GAM RNA, and which when bound by GAM337456 RNA causes inhibition of translation of the GAM337456 target mRNA into a corresponding GAM337456 target protein.

The mechanism of the translational inhibition exerted by GAM337456 RNA, herein designated GAM RNA, on one or more GAM337456 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337456 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337456 RNA, herein designated GAM RNA, of GAM337456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337456 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337456 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337456 RNA correlate with, and may be deduced from, the identity of the GAM337456 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337457 6379 GAGGCAGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCACTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGT Messenger 337457 (GAM337457) oligonucleotides modulates expression of respective target

TTGAGGCTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337457 is a novel bioinformatically detectable regulatory, non protein

GATCACGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337457 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

CCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGCAAGA encoded by the human genome.

TCTTGTCTC GAM337457 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337457 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337457 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337457 precursor RNA is designated SEQ ID:6379, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6379 is located from position 116582533 to position 116582631 relative to chromosome 12 on the `-` strand.

GAM337457 precursor RNA folds onto itself, forming GAM337457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337457 precursor RNA, designated SEQ ID NO: 6379, and a schematic representation of a predicted secondary folding of GAM337457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337457 folded precursor RNA yielding a GAM337457 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337457 RNA, hereby incorporated herein.

GAM337457 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337457 target RNA, herein designated GAM TARGET RNA.

GAM337457 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337457 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337457 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337457 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337457 RNA, herein designated GAM RNA, to target binding sites on GAM337457 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337457 target RNA into GAM337457 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337457 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337457 target genes. The mRNA of each one of this plurality of GAM337457 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337457 RNA, herein designated GAM RNA, and which when bound by GAM337457 RNA causes inhibition of translation of the GAM337457 target mRNA into a corresponding GAM337457 target protein.

The mechanism of the translational inhibition exerted by GAM337457 RNA, herein designated GAM RNA, on one or more GAM337457 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337457 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337457 RNA, herein designated GAM RNA, of GAM337457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337457 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337457 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337457 RNA correlate with, and may be deduced from, the identity of the GAM337457 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337458 5962 ATGAAGTGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCACATTGGC detected oligonucleotides of the present invention, referred to here as Genomic Address

TACTGGTGAG Messenger 337458 (GAM337458) oligonucleotides modulates expression of respective target

GAAGGAGCAG genes whose function and utility is known in the art.

AGTTGTGGGC GAM337458 is a novel bioinformatically detectable regulatory, non protein
TGAGACTGAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337458 was detected
GCTGTTCAGC is described with additional reference to Figs. 9-15.

ATCTGTCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTGTCACCA encoded by the human genome.

ACATAGATGA GAM337458 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CCACTAGCAT GAM337458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337458 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337458 precursor RNA is designated SEQ ID:5962, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5962 is located from position 116689623 to position 116689732 relative to chromosome 11 on the `-` strand.

GAM337458 precursor RNA folds onto itself, forming GAM337458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337458 precursor RNA, designated SEQ ID NO: 5962, and a schematic representation of a predicted secondary folding of GAM337458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337458 folded precursor RNA yielding a GAM337458 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337458 RNA, hereby incorporated herein.

GAM337458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337458 target RNA, herein designated GAM TARGET RNA.

GAM337458 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337458 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337458 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337458 RNA, herein designated GAM RNA, to target binding sites on GAM337458 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337458 target RNA into GAM337458 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337458 target genes. The mRNA of each one of this plurality of GAM337458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337458 RNA, herein designated GAM RNA, and which when bound by GAM337458 RNA causes inhibition of translation of the GAM337458 target mRNA into a corresponding GAM337458 target protein.

The mechanism of the translational inhibition exerted by GAM337458 RNA, herein designated GAM RNA, on one or more GAM337458 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337458 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337458 RNA, herein designated GAM RNA, of GAM337458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337458 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337458 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337458 RNA correlate with, and may be deduced from, the identity of the GAM337458 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337459 5814 AGTGAGTCAC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTGGCTACT detected oligonucleotides of the present invention, referred to here as Genomic Address
GGTGAGGAAG Messenger 337459 (GAM337459) oligonucleotides modulates expression of respective target
GAGCAGAGTT genes whose function and utility is known in the art.

GTGGGCTGAG GAM337459 is a novel bioinformatically detectable regulatory, non protein
ACTGATGCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337459 was detected
TTCAGCATCT is described with additional reference to Figs. 9-15.

GTCTTCCTTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TCACCAACAT encoded by the human genome.

AGATGACCAC GAM337459 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
T GAM337459 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337459 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337459 precursor RNA is designated SEQ ID:5814, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5814 is located from position 116689628 to position 116689728 relative to chromosome 11 on the `-` strand.

GAM337459 precursor RNA folds onto itself, forming GAM337459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337459 precursor RNA, designated SEQ ID NO: 5814, and a schematic representation of a predicted secondary folding of GAM337459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337459 folded precursor RNA yielding a GAM337459 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337459 RNA, hereby incorporated herein.

GAM337459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337459 target RNA, herein designated GAM TARGET RNA.

GAM337459 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337459 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337459 RNA, herein designated GAM RNA, to target binding sites on GAM337459 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337459 target RNA into GAM337459 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337459 target genes. The mRNA of each one of this plurality of GAM337459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337459 RNA, herein designated GAM RNA, and which when bound by GAM337459 RNA causes inhibition of translation of the GAM337459 target mRNA into a corresponding GAM337459 target protein.

The mechanism of the translational inhibition exerted by GAM337459 RNA, herein designated GAM RNA, on one or more GAM337459 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337459 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337459 RNA, herein designated GAM RNA, of GAM337459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337459 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337459 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337459 RNA correlate with, and may be deduced from, the identity of the GAM337459 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337460 6999 TCACTTAAAC CCGGGAGGTG GAGGTTGCAG TGAGTGGAGA TGGTGCCACT GCACTCCAGC CTGGGTGACA GAGTGA

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337460 (GAM337460) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337460 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337460 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337460 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337460 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337460 precursor RNA is designated SEQ ID:6999, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6999 is located from position 116939053 to position 116939128 relative to chromosome 9 on the `+` strand.

GAM337460 precursor RNA folds onto itself, forming GAM337460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337460 precursor RNA, designated SEQ ID NO: 6999, and a schematic representation of a predicted secondary folding of GAM337460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337460 folded precursor

RNA yielding a GAM337460 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337460 RNA, hereby incorporated herein.

GAM337460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337460 target RNA, herein designated GAM TARGET RNA.

GAM337460 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337460 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337460 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337460 RNA, herein designated GAM RNA, to target binding sites on GAM337460 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337460 target RNA into GAM337460 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337460 target genes. The mRNA of each one of this plurality of GAM337460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337460 RNA, herein designated GAM RNA, and which when bound by GAM337460 RNA causes inhibition of translation of the GAM337460 target mRNA into a corresponding GAM337460 target protein.

The mechanism of the translational inhibition exerted by GAM337460 RNA, herein designated GAM RNA, on one or more GAM337460 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337460 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337460 RNA, herein designated GAM RNA, of GAM337460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337460 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337460 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337460 RNA correlate with, and may be deduced from, the identity of the GAM337460 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337461 6738 GGCATCTGTA ATCCCAGCTA CTCGGGAGGC TGAGGCACGA GAATTGCTTG AGCCTGGGAG GTGGAGATTG CAGTGAGTC

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337461 (GAM337461) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337461 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337461 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337461 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337461 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337461 precursor RNA is designated SEQ ID:6738, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6738 is located from position 116942975 to position 116943053 relative to chromosome X on the `-` strand.

GAM337461 precursor RNA folds onto itself, forming GAM337461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337461 precursor RNA, designated SEQ ID NO: 6738, and a schematic representation of a predicted secondary folding of GAM337461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337461 folded precursor RNA yielding a GAM337461 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337461 RNA, hereby incorporated herein.

GAM337461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337461 target RNA, herein designated GAM TARGET RNA.

GAM337461 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337461 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337461 RNA, herein designated GAM RNA, to target binding sites on GAM337461 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337461 target RNA into GAM337461 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337461 target genes. The mRNA of each one of this plurality of GAM337461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337461 RNA, herein designated GAM RNA, and which when bound by GAM337461 RNA causes inhibition of translation of the GAM337461 target mRNA into a corresponding GAM337461 target protein.

The mechanism of the translational inhibition exerted by GAM337461 RNA, herein designated GAM RNA, on one or more GAM337461 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337461 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337461 RNA, herein designated GAM RNA, of GAM337461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337461 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337461 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337461 RNA correlate with, and may be deduced from, the identity of the GAM337461 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337462 6687 GGAGAATTGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 337462 (GAM337462) oligonucleotides modulates expression of respective target

TGAGCCGAGG genes whose function and utility is known in the art.

TTGCGCCATT GAM337462 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337462 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

AGAGCGAAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TCC encoded by the human genome.

GAM337462 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337462 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337462 precursor RNA is designated SEQ ID:6687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6687 is located from position 117189825 to position 117189907 relative to chromosome 9 on the `+` strand.

GAM337462 precursor RNA folds onto itself, forming GAM337462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337462 precursor RNA, designated SEQ ID NO: 6687, and a schematic representation of a predicted secondary folding of GAM337462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337462 folded precursor RNA yielding a GAM337462 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337462 RNA, hereby incorporated herein.

GAM337462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337462 target RNA, herein designated GAM TARGET RNA.

GAM337462 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337462 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337462 RNA, herein designated GAM RNA, to target binding sites on GAM337462 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337462 target RNA into GAM337462 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337462 target genes. The mRNA of each one of this plurality of GAM337462 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM337462 RNA, herein designated GAM RNA, and which when bound by GAM337462 RNA causes inhibition of translation of the GAM337462 target mRNA into a corresponding GAM337462 target protein.

The mechanism of the translational inhibition exerted by GAM337462 RNA, herein designated GAM RNA, on one or more GAM337462 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337462 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337462 RNA, herein designated GAM RNA, of GAM337462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337462 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337462 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337462 RNA correlate with, and may be deduced from, the identity of the GAM337462 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337463 6135 CGAAGGCAGC Fig. 8 further provides a conceptual description of another novel bioinformatically
ATGGAAGAAT detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGCAGTATT Messenger 337463 (GAM337463) oligonucleotides modulates expression of respective target
GGATTTGAAA genes whose function and utility is known in the art.

TCAGGAGACT GAM337463 is a novel bioinformatically detectable regulatory, non protein
TGGAATTGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337463 was detected
TTCTGCCTCT is described with additional reference to Figs. 9-15.

TCCACTACCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTGTGAAAT encoded by the human genome.

TG GAM337463 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337463 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337463 precursor RNA is designated SEQ ID:6135, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6135 is located from position 117327121 to position 117327212 relative to chromosome 9 on the `+` strand.

GAM337463 precursor RNA folds onto itself, forming GAM337463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337463 precursor RNA, designated SEQ ID NO: 6135, and a schematic representation of a predicted secondary folding of GAM337463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337463 folded precursor RNA yielding a GAM337463 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337463 RNA, hereby incorporated herein.

GAM337463 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337463 target RNA, herein designated GAM TARGET RNA.

GAM337463 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337463 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337463 RNA, herein designated GAM RNA, to target binding sites on GAM337463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337463 target RNA

into GAM337463 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337463 target genes. The mRNA of each one of this plurality of GAM337463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337463 RNA, herein designated GAM RNA, and which when bound by GAM337463 RNA causes inhibition of translation of the GAM337463 target mRNA into a corresponding GAM337463 target protein.

The mechanism of the translational inhibition exerted by GAM337463 RNA, herein designated GAM RNA, on one or more GAM337463 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337463 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337463 RNA, herein designated GAM RNA, of GAM337463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337463 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337463 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337463 RNA correlate with, and may be deduced from, the identity of the GAM337463 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337464 6489 GCAGCATGGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAATAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTATTGGATT Messenger 337464 (GAM337464) oligonucleotides modulates expression of respective target
TGAAATCAGG genes whose function and utility is known in the art.

AGACTTGGAA GAM337464 is a novel bioinformatically detectable regulatory, non protein
TTGAATTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337464 was detected
CCTCTTCCAC is described with additional reference to Figs. 9-15.

TACCAGCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337464 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337464 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337464 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337464 precursor RNA is designated SEQ ID:6489, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6489 is located from position 117327126 to position 117327205 relative to chromosome 9 on the `+` strand.

GAM337464 precursor RNA folds onto itself, forming GAM337464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337464 precursor RNA, designated SEQ ID NO: 6489, and a schematic representation of a predicted secondary folding of GAM337464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337464 folded precursor RNA yielding a GAM337464 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337464 RNA, hereby incorporated herein.

GAM337464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337464 target RNA, herein designated GAM TARGET RNA.

GAM337464 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337464 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337464 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337464 RNA, herein designated GAM RNA, to target binding sites on GAM337464 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337464 target RNA into GAM337464 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337464 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337464 target genes. The mRNA of each one of this plurality of GAM337464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337464 RNA, herein designated GAM RNA, and which when bound by GAM337464 RNA causes inhibition of translation of the GAM337464 target mRNA into a corresponding GAM337464 target protein.

The mechanism of the translational inhibition exerted by GAM337464 RNA, herein designated GAM RNA, on one or more GAM337464 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337464 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337464 RNA, herein designated GAM RNA, of GAM337464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337464 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337464 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337464 RNA correlate with, and may be deduced from, the identity of the GAM337464 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337465 5919 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337465 (GAM337465) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337465 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337465 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337465 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337465 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337465 precursor RNA is designated SEQ ID:5919, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5919 is located from position 117891472 to position 117891553 relative to chromosome 7 on the `-` strand.

GAM337465 precursor RNA folds onto itself, forming GAM337465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337465 precursor RNA, designated SEQ ID NO: 5919, and a schematic representation of a predicted secondary folding of GAM337465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337465 folded precursor RNA yielding a GAM337465 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337465 RNA, hereby incorporated herein.

GAM337465 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337465 target RNA, herein designated GAM TARGET RNA.

GAM337465 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337465 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337465 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337465 RNA, herein designated GAM RNA, to target binding sites on GAM337465 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337465 target RNA into GAM337465 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337465 target genes. The mRNA of each one of this plurality of GAM337465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337465 RNA, herein designated GAM RNA, and which when bound by GAM337465 RNA causes inhibition of translation of the GAM337465 target mRNA into a corresponding GAM337465 target protein.

The mechanism of the translational inhibition exerted by GAM337465 RNA, herein designated GAM RNA, on one or more GAM337465 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337465 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337465 RNA, herein designated GAM RNA, of GAM337465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337465 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337465 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337465 RNA correlate with, and may be deduced from, the identity of the GAM337465 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337466 5920 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337466 (GAM337466) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337466 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337466 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337466 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337466 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337466 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337466 precursor RNA is designated SEQ ID:5920, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5920 is located from position 118241872 to position 118241953 relative to chromosome 8 on the `+` strand.

GAM337466 precursor RNA folds onto itself, forming GAM337466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337466 precursor RNA, designated SEQ ID NO: 5920, and a schematic representation of a predicted secondary folding of GAM337466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337466 folded precursor RNA yielding a GAM337466 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337466 RNA, hereby incorporated herein.

GAM337466 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337466 target RNA, herein designated GAM TARGET RNA.

GAM337466 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337466 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337466 RNA, herein designated GAM RNA, to target binding sites on GAM337466 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337466 target RNA into GAM337466 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337466 target genes. The mRNA of each one of this plurality of GAM337466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337466 RNA, herein designated GAM RNA, and which when bound by GAM337466 RNA causes inhibition of translation of the GAM337466 target mRNA into a corresponding GAM337466 target protein.

The mechanism of the translational inhibition exerted by GAM337466 RNA, herein designated GAM RNA, on one or more GAM337466 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337466 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337466 RNA, herein designated GAM RNA, of GAM337466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337466 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337466 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337466 RNA correlate with, and may be deduced from, the identity of the GAM337466 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337469 6454 GAGGTCATAA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTGAATGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTATGCAGTG Messenger 337469 (GAM337469) oligonucleotides modulates expression of respective target
GCCATGTCAT genes whose function and utility is known in the art.

CAGAACAGGT GAM337469 is a novel bioinformatically detectable regulatory, non protein
GTGCCAGCCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337469 was detected
CCTGCATGGA is described with additional reference to Figs. 9-15.

ACATGTACAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCTTC encoded by the human genome.

GAM337469 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337469 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337469 precursor RNA is designated SEQ ID:6454, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6454 is located from position 118785414 to position 118785498 relative to chromosome 8 on the `-` strand.

GAM337469 precursor RNA folds onto itself, forming GAM337469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337469 precursor RNA, designated SEQ ID NO: 6454, and a schematic representation of a predicted secondary folding of GAM337469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337469 folded precursor RNA yielding a GAM337469 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337469 RNA, hereby incorporated herein.

GAM337469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337469 target RNA, herein designated GAM TARGET RNA.

GAM337469 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337469 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337469 RNA, herein designated GAM RNA, to target binding sites on GAM337469 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337469 target RNA into GAM337469 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337469 target genes. The mRNA of each one of this plurality of GAM337469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337469 RNA, herein designated GAM RNA, and which when bound by GAM337469 RNA causes inhibition of translation of the GAM337469 target mRNA into a corresponding GAM337469 target protein.

The mechanism of the translational inhibition exerted by GAM337469 RNA, herein designated GAM RNA, on one or more GAM337469 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337469 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337469 RNA, herein designated GAM RNA, of GAM337469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337469 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337469 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337469 RNA correlate with, and may be deduced from, the identity of the GAM337469 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337470 6197 CTGAGAGGTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGATTCCACA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCCCAAGTTG Messenger 337470 (GAM337470) oligonucleotides modulates expression of respective target
CACAGCTGGG genes whose function and utility is known in the art.

GAGAGACAGT GAM337470 is a novel bioinformatically detectable regulatory, non protein
GTCAGGACAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337470 was detected
TATCGCCTGT is described with additional reference to Figs. 9-15.

GCTGAGGTCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCTCCCCAG encoded by the human genome.

CTAGACTGAA GAM337470 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCTTTATGAG GAM337470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GATTTTATTC GAM337470 precursor RNA does not encode a protein. A nucleotide sequence identical or

ATTTCAAG highly similar to the nucleotide sequence of GAM337470 precursor RNA is designated SEQ

ID:6197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6197 is located from position 119479486 to position 119479613 relative to chromosome 12 on the `-` strand.

GAM337470 precursor RNA folds onto itself, forming GAM337470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337470 precursor RNA, designated SEQ ID NO: 6197, and a schematic representation of a predicted secondary folding of GAM337470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337470 folded precursor RNA yielding a GAM337470 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337470 RNA, hereby incorporated herein.

GAM337470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337470 target RNA, herein designated GAM TARGET RNA.

GAM337470 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337470 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337470 RNA, herein designated GAM RNA, to target binding sites on GAM337470 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337470 target RNA into GAM337470 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337470 target genes. The mRNA of each one of this plurality of GAM337470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337470 RNA, herein designated GAM RNA, and which when bound by GAM337470 RNA causes inhibition of translation of the GAM337470 target mRNA into a corresponding GAM337470 target protein.

The mechanism of the translational inhibition exerted by GAM337470 RNA, herein designated GAM RNA, on one or more GAM337470 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337470 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337470 RNA, herein designated GAM RNA, of GAM337470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337470 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337470 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337470 RNA correlate with, and may be deduced from, the identity of the GAM337470 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337472 6289 GAACTGGGTC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTATCAAA detected oligonucleotides of the present invention, referred to here as Genomic Address

CTCTGTGTTT Messenger 337472 (GAM337472) oligonucleotides modulates expression of respective target

ATGTGGCCTT genes whose function and utility is known in the art.

TAGAATATTA GAM337472 is a novel bioinformatically detectable regulatory, non protein

TCCCTCAGTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337472 was detected

AGTTAGAGGC is described with additional reference to Figs. 9-15.

ACAGATTAAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGAGTTTGAA encoded by the human genome.

GGTTGTCACT GAM337472 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGGTTT GAM337472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337472 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337472 precursor RNA is designated SEQ ID:6289, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6289 is located from position 120043180 to position 120043285 relative to chromosome 12 on the `-` strand.

GAM337472 precursor RNA folds onto itself, forming GAM337472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337472 precursor RNA, designated SEQ ID NO: 6289, and a schematic representation of a predicted secondary folding of GAM337472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337472 folded precursor RNA yielding a GAM337472 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337472 RNA, hereby incorporated herein.

GAM337472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337472 target RNA, herein designated GAM TARGET RNA.

GAM337472 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337472 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337472 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337472 RNA, herein designated GAM RNA, to target binding sites on GAM337472 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337472 target RNA into GAM337472 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337472 target genes. The mRNA of each one of this plurality of GAM337472 target genes comprises one or more target binding sites, each

having a nucleotide sequence which is at least partly complementary to GAM337472 RNA, herein designated GAM RNA, and which when bound by GAM337472 RNA causes inhibition of translation of the GAM337472 target mRNA into a corresponding GAM337472 target protein.

The mechanism of the translational inhibition exerted by GAM337472 RNA, herein designated GAM RNA, on one or more GAM337472 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337472 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337472 RNA, herein designated GAM RNA, of GAM337472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337472 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337472 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337472 RNA correlate with, and may be deduced from, the identity of the GAM337472 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337473 5921 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337473 (GAM337473) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337473 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337473 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337473 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337473 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337473 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337473 precursor RNA is designated SEQ ID:5921, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5921 is located from position 120076221 to position 120076302 relative to chromosome 6 on the `+` strand.

GAM337473 precursor RNA folds onto itself, forming GAM337473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337473 precursor RNA, designated SEQ ID NO: 5921, and a schematic representation of a predicted secondary folding of GAM337473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337473 folded precursor RNA yielding a GAM337473 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337473 RNA, hereby incorporated herein.

GAM337473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337473 target RNA, herein designated GAM TARGET RNA.

GAM337473 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337473 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337473 RNA, herein designated GAM RNA, to target binding sites on GAM337473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337473 target RNA

into GAM337473 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337473 target genes. The mRNA of each one of this plurality of GAM337473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337473 RNA, herein designated GAM RNA, and which when bound by GAM337473 RNA causes inhibition of translation of the GAM337473 target mRNA into a corresponding GAM337473 target protein.

The mechanism of the translational inhibition exerted by GAM337473 RNA, herein designated GAM RNA, on one or more GAM337473 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337473 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337473 RNA, herein designated GAM RNA, of GAM337473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337473 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337473 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337473 RNA correlate with, and may be deduced from, the identity of the GAM337473 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337476 7137 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 337476 (GAM337476) oligonucleotides modulates expression of respective target

GCGGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCGA GAM337476 is a novel bioinformatically detectable regulatory, non protein

AGATCGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337476 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCAA encoded by the human genome.

AACTCTGTCT GAM337476 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM337476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337476 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337476 precursor RNA is designated SEQ ID:7137, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7137 is located from position 120997503 to position 120997604 relative to chromosome X on the `+` strand.

GAM337476 precursor RNA folds onto itself, forming GAM337476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337476 precursor RNA, designated SEQ ID NO: 7137, and a schematic representation of a predicted secondary folding of GAM337476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337476 folded precursor RNA yielding a GAM337476 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337476 RNA, hereby incorporated herein. Expression of GAM337476 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337476 target RNA, herein designated GAM TARGET RNA.

GAM337476 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337476 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING

SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337476 RNA, herein designated GAM RNA, to target binding sites on GAM337476 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337476 target RNA into GAM337476 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337476 target genes. The mRNA of each one of this plurality of GAM337476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337476 RNA, herein designated GAM RNA, and which when bound by GAM337476 RNA causes inhibition of translation of the GAM337476 target mRNA into a corresponding GAM337476 target protein.

The mechanism of the translational inhibition exerted by GAM337476 RNA, herein designated GAM RNA, on one or more GAM337476 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337476 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337476 RNA, herein designated GAM RNA, of GAM337476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337476 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337476 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337476 RNA correlate with, and may be deduced from, the identity of the GAM337476 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337477 5922 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337477 (GAM337477) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337477 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337477 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337477 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337477 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337477 precursor RNA is designated SEQ ID:5922, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5922 is located from position 121175114 to position 121175195 relative to chromosome 9 on the `-` strand.

GAM337477 precursor RNA folds onto itself, forming GAM337477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337477 precursor RNA, designated SEQ ID NO: 5922, and a schematic representation of a predicted secondary folding of GAM337477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337477 folded precursor RNA yielding a GAM337477 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337477 RNA, hereby incorporated herein.

GAM337477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337477 target RNA, herein designated GAM TARGET RNA.

GAM337477 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337477 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337477 RNA, herein designated GAM RNA, to target binding sites on GAM337477 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337477 target RNA into GAM337477 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337477 target genes. The mRNA of each one of this plurality of GAM337477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337477 RNA, herein designated GAM RNA, and which when bound by GAM337477 RNA causes inhibition of translation of the GAM337477 target mRNA into a corresponding GAM337477 target protein.

The mechanism of the translational inhibition exerted by GAM337477 RNA, herein designated GAM RNA, on one or more GAM337477 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337477 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337477 RNA, herein designated GAM RNA, of GAM337477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337477 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337477 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337477

RNA correlate with, and may be deduced from, the identity of the GAM337477 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337478 5673 AATCAAAAAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GTTTGAGCAA detected oligonucleotides of the present invention, referred to here as Genomic Address
AGGATGAACA Messenger 337478 (GAM337478) oligonucleotides modulates expression of respective target
CAATCTACAG genes whose function and utility is known in the art.

TCAGATTATG GAM337478 is a novel bioinformatically detectable regulatory, non protein
TCACTCCTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337478 was detected
GCCCAGACCT is described with additional reference to Figs. 9-15.

TCTTGATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337478 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337478 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337478 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337478 precursor RNA is designated SEQ ID:5673, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5673 is located from position 121180039 to position 121180116 relative to chromosome 8 on the `+` strand.

GAM337478 precursor RNA folds onto itself, forming GAM337478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337478 precursor RNA, designated SEQ ID NO: 5673, and a schematic representation of a predicted secondary folding of GAM337478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337478 folded precursor RNA yielding a GAM337478 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337478 RNA, hereby incorporated herein.

GAM337478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337478 target RNA, herein designated GAM TARGET RNA.

GAM337478 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337478 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337478 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337478 RNA, herein designated GAM RNA, to target binding sites on GAM337478 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337478 target RNA into GAM337478 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337478 target genes. The mRNA of each one of this plurality of GAM337478 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337478 RNA, herein designated GAM RNA, and which when bound by GAM337478 RNA causes inhibition of translation of the GAM337478 target mRNA into a corresponding GAM337478 target protein.

The mechanism of the translational inhibition exerted by GAM337478 RNA, herein designated GAM RNA, on one or more GAM337478 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337478 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337478 RNA, herein designated GAM RNA, of GAM337478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337478 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337478 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337478 RNA correlate with, and may be deduced from, the identity of the GAM337478 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337479 6198 CTGAGCAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAATCTCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GATCCCAGGA Messenger 337479 (GAM337479) oligonucleotides modulates expression of respective target
GGTCAAGGCT genes whose function and utility is known in the art.

GCAGTGAGCC GAM337479 is a novel bioinformatically detectable regulatory, non protein
ACAATTTTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337479 was detected
CACTGCACTC is described with additional reference to Figs. 9-15.

CAGCCTGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AACAGAGCAA encoded by the human genome.

GACCCTGTCT GAM337479 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CAG GAM337479 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337479 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337479 precursor RNA is designated SEQ ID:6198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6198 is located from position 121585232 to position 121585334 relative to chromosome 12 on the `+` strand.

GAM337479 precursor RNA folds onto itself, forming GAM337479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337479 precursor RNA, designated SEQ ID NO: 6198, and a schematic representation of a predicted secondary folding of GAM337479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337479 folded precursor RNA yielding a GAM337479 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337479 RNA, hereby incorporated herein. Expression of GAM337479 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337479 target RNA, herein designated GAM TARGET RNA.

GAM337479 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337479 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337479 RNA, herein designated GAM RNA, to target binding sites on GAM337479 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337479 target RNA into GAM337479 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337479 target genes. The mRNA of each one of this plurality of GAM337479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337479 RNA, herein designated GAM RNA, and which when bound by GAM337479 RNA causes inhibition of translation of the GAM337479 target mRNA into a corresponding GAM337479 target protein.

The mechanism of the translational inhibition exerted by GAM337479 RNA, herein designated GAM RNA, on one or more GAM337479 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337479 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337479 RNA, herein designated GAM RNA, of GAM337479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337479 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337479 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337479 RNA correlate with, and may be deduced from, the identity of the GAM337479 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337480 5923 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337480 (GAM337480) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337480 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337480 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337480 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337480 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337480 precursor RNA is designated SEQ ID:5923, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5923 is located from position 121875870 to position 121875951 relative to chromosome 10 on the `+` strand.

GAM337480 precursor RNA folds onto itself, forming GAM337480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337480 precursor RNA, designated SEQ ID NO: 5923, and a schematic representation of a predicted secondary folding of GAM337480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337480 folded precursor RNA yielding a GAM337480 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337480 RNA, hereby incorporated herein.

GAM337480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337480 target RNA, herein designated GAM TARGET RNA.

GAM337480 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337480 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337480 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337480 RNA, herein designated GAM RNA, to target binding sites on GAM337480 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337480 target RNA into GAM337480 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337480 target genes. The mRNA of each one of this plurality of GAM337480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337480 RNA, herein designated GAM RNA, and which when bound by GAM337480 RNA causes inhibition of translation of the GAM337480 target mRNA into a corresponding GAM337480 target protein.

The mechanism of the translational inhibition exerted by GAM337480 RNA, herein designated GAM RNA, on one or more GAM337480 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337480 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337480 RNA, herein designated GAM RNA, of GAM337480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337480 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337480 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337480 RNA correlate with, and may be deduced from, the identity of the GAM337480 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337481 5644 AAAAATGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGAAAAGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGAGGCAGA Messenger 337481 (GAM337481) oligonucleotides modulates expression of respective target

TGGGAAGATG genes whose function and utility is known in the art.

ACCCTTTTAC GAM337481 is a novel bioinformatically detectable regulatory, non protein

AAATGTTTCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337481 was detected

TCTCCTTTTT is described with additional reference to Figs. 9-15.

CTTTCTGTTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TT encoded by the human genome.

GAM337481 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337481 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337481 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337481 precursor RNA is designated SEQ

ID:5644, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5644 is located from position 122005663 to position 122005744 relative to chromosome 11 on the `+` strand.

GAM337481 precursor RNA folds onto itself, forming GAM337481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337481 precursor RNA, designated SEQ ID NO: 5644, and a schematic representation of a predicted secondary folding of GAM337481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337481 folded precursor RNA yielding a GAM337481 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337481 RNA, hereby incorporated herein.

GAM337481 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337481 target RNA, herein designated GAM TARGET RNA.

GAM337481 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337481 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337481 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337481 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337481 RNA, herein designated GAM RNA, to target binding sites on GAM337481 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337481 target RNA into GAM337481 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337481 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337481 target genes. The mRNA of each one of this plurality of GAM337481 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337481 RNA, herein designated GAM RNA, and which when bound by GAM337481 RNA causes inhibition of translation of the GAM337481 target mRNA into a corresponding GAM337481 target protein.

The mechanism of the translational inhibition exerted by GAM337481 RNA, herein designated GAM RNA, on one or more GAM337481 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337481 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337481 RNA, herein designated GAM RNA, of GAM337481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337481 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337481 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337481 RNA correlate with, and may be deduced from, the identity of the GAM337481 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337482 6657 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGGCGGACG Messenger 337482 (GAM337482) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATCGC GAM337482 is a novel bioinformatically detectable regulatory, non protein

ACCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337482 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAATCTCC encoded by the human genome.

GAM337482 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337482 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337482 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337482 precursor RNA is designated SEQ ID:6657, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6657 is located from position 122221602 to position 122221690 relative to chromosome 4 on the `+` strand.

GAM337482 precursor RNA folds onto itself, forming GAM337482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337482 precursor RNA, designated SEQ ID NO: 6657, and a schematic representation of a predicted secondary folding of GAM337482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337482 folded precursor RNA yielding a GAM337482 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337482 RNA, hereby incorporated herein. Expression of GAM337482 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337482 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337482 target RNA, herein designated GAM TARGET RNA.

GAM337482 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337482 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337482 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337482 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337482 RNA, herein designated GAM RNA, to target binding sites on GAM337482 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337482 target RNA into GAM337482 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337482 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337482 target genes. The mRNA of each one of this plurality of GAM337482 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337482 RNA, herein designated GAM RNA, and which when bound by GAM337482 RNA causes inhibition of translation of the GAM337482 target mRNA into a corresponding GAM337482 target protein.

The mechanism of the translational inhibition exerted by GAM337482 RNA, herein designated GAM RNA, on one or more GAM337482 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337482 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337482 RNA, herein designated GAM RNA, of GAM337482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337482 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337482 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337482 RNA correlate with, and may be deduced from, the identity of the GAM337482 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337485 7071 TCTGAGTCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

TGGGCTGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGCTGCCC Messenger 337485 (GAM337485) oligonucleotides modulates expression of respective target

ACCTTTCATC genes whose function and utility is known in the art.

TAGGTGGGCA GAM337485 is a novel bioinformatically detectable regulatory, non protein
CAACGTAATC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337485 was
detected
AGCTGCCAGC is described with additional reference to Figs. 9-15.

TTGACCAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a
humen gene
encoded by the human genome.

GAM337485 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337485 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA
genes
GAM337485 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337485 precursor RNA is designated SEQ ID:7071, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7071 is located from position 122598663 to position 122598741 relative to chromosome 12 on the `+` strand.

GAM337485 precursor RNA folds onto itself, forming GAM337485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337485 precursor RNA, designated SEQ ID NO: 7071, and a schematic representation of a predicted secondary folding of GAM337485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337485 folded precursor RNA yielding a GAM337485 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337485 RNA, hereby incorporated herein.

GAM337485 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337485 target RNA, herein designated GAM TARGET RNA.

GAM337485 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337485 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337485 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337485 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337485 RNA, herein designated GAM RNA, to target binding sites on GAM337485 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337485 target RNA into GAM337485 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337485 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337485 target genes. The mRNA of each one of this plurality of GAM337485 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337485 RNA, herein designated GAM RNA, and which when bound by GAM337485 RNA causes inhibition of translation of the GAM337485 target mRNA into a corresponding GAM337485 target protein.

The mechanism of the translational inhibition exerted by GAM337485 RNA, herein designated GAM RNA, on one or more GAM337485 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337485 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337485 RNA, herein designated GAM RNA, of GAM337485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337485 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337485 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337485 RNA correlate with, and may be deduced from, the identity of the GAM337485 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337486 7106 TGAGATTTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGGCACTGC detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCTAAGTAG Messenger 337486 (GAM337486) oligonucleotides modulates expression of respective target
GAATCACACT genes whose function and utility is known in the art.

GCAGTGGGTT GAM337486 is a novel bioinformatically detectable regulatory, non protein
AGTGACACCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337486 was detected
TGCTCAGAAA is described with additional reference to Figs. 9-15.

TGGTGCCTGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GCAAAATGTT encoded by the human genome.

TCA GAM337486 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337486 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337486 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337486 precursor RNA is designated SEQ ID:7106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7106 is located from position 122851359 to position 122851451 relative to chromosome 8 on the `-` strand.

GAM337486 precursor RNA folds onto itself, forming GAM337486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337486 precursor RNA, designated SEQ ID NO: 7106, and a schematic representation of a predicted secondary folding of GAM337486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337486 folded precursor RNA yielding a GAM337486 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337486 RNA, hereby incorporated herein.

GAM337486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337486 target RNA, herein designated GAM TARGET RNA.

GAM337486 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337486 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337486 RNA, herein designated GAM RNA, to target binding sites on GAM337486 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337486 target RNA into GAM337486 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337486 target genes. The mRNA of each one of this plurality of GAM337486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337486 RNA, herein designated GAM RNA, and which when bound by GAM337486 RNA causes inhibition of translation of the GAM337486 target mRNA into a corresponding GAM337486 target protein.

The mechanism of the translational inhibition exerted by GAM337486 RNA, herein designated GAM RNA, on one or more GAM337486 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337486 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337486 RNA, herein designated GAM RNA, of GAM337486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337486 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337486 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337486 RNA correlate with, and may be deduced from, the identity of the GAM337486 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337488 5692 ACATTATTAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATTTCAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
AGCTGGGCAT Messenger 337488 (GAM337488) oligonucleotides modulates expression of respective target
GTTGGAGTAT genes whose function and utility is known in the art.

GCCTGTGATC GAM337488 is a novel bioinformatically detectable regulatory, non protein
TCAGTTACTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337488 was detected
AGGAGGCTGA is described with additional reference to Figs. 9-15.

GGCAGAAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTACTTGAGG encoded by the human genome.

CCAGGAGTTT GAM337488 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAGTCTGTAG GAM337488 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TGT GAM337488 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337488 precursor RNA is designated SEQ ID:5692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5692 is located from position 123179192 to position 123179304 relative to chromosome 7 on the `+` strand.

GAM337488 precursor RNA folds onto itself, forming GAM337488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337488 precursor RNA, designated SEQ ID NO: 5692, and a schematic representation of a predicted secondary folding of GAM337488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337488 folded precursor RNA yielding a GAM337488 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337488 RNA, hereby incorporated herein.

GAM337488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337488 target RNA, herein designated GAM TARGET RNA.

GAM337488 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337488 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337488 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337488 RNA, herein designated GAM RNA, to target binding sites on GAM337488 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337488 target RNA into GAM337488 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337488 target genes. The mRNA of each one of this plurality of GAM337488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337488 RNA, herein designated GAM RNA, and which when bound by GAM337488 RNA causes inhibition of translation of the GAM337488 target mRNA into a corresponding GAM337488 target protein.

The mechanism of the translational inhibition exerted by GAM337488 RNA, herein designated GAM RNA, on one or more GAM337488 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337488 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337488 RNA, herein designated GAM RNA, of

GAM337488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337488 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337488 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337488 RNA correlate with, and may be deduced from, the identity of the GAM337488 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337489 7221 TGGAGGAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGCTGGTGCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGTTAAATAC Messenger 337489 (GAM337489) oligonucleotides modulates expression of respective target

AACCTAAATC genes whose function and utility is known in the art.

AAACCACAGT GAM337489 is a novel bioinformatically detectable regulatory, non protein

TGACCAACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337489 was detected

CCACATCCAG is described with additional reference to Figs. 9-15.

CTTCTCCTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CA encoded by the human genome.

GAM337489 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337489 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337489 precursor RNA is designated SEQ ID:7221, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7221 is located from position 123330334 to position 123330415 relative to chromosome 11 on the `-` strand.

GAM337489 precursor RNA folds onto itself, forming GAM337489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337489 precursor RNA, designated SEQ ID NO: 7221, and

a schematic representation of a predicted secondary folding of GAM337489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337489 folded precursor RNA yielding a GAM337489 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337489 RNA, hereby incorporated herein.

GAM337489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337489 target RNA, herein designated GAM TARGET RNA.

GAM337489 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337489 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337489 RNA, herein designated GAM RNA, to target binding sites on GAM337489 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337489 target RNA into GAM337489 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337489 target genes. The mRNA of each one of this plurality of GAM337489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337489 RNA, herein designated GAM RNA, and which when bound by GAM337489 RNA causes inhibition of translation of the GAM337489 target mRNA into a corresponding GAM337489 target protein.

The mechanism of the translational inhibition exerted by GAM337489 RNA, herein designated GAM RNA, on one or more GAM337489 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337489 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337489 RNA, herein designated GAM RNA, of GAM337489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337489 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337489 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337489 RNA correlate with, and may be deduced from, the identity of the GAM337489 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337490 6337 GAGACAGGAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CTGGCTTCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GACTGTGGAC Messenger 337490 (GAM337490) oligonucleotides modulates expression of respective target

TGGGCTGCTG genes whose function and utility is known in the art.

GCCTGCTTGC GAM337490 is a novel bioinformatically detectable regulatory, non protein

TTCCTCCCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337490 was detected

CCCCATTCCT is described with additional reference to Figs. 9-15.

AGCAGGGCCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGGCCCTCC encoded by the human genome.

TCTTCTC GAM337490 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337490 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337490 precursor RNA is designated SEQ ID:6337, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6337 is located from position 123435499 to position 123435595 relative to chromosome 9 on the `+` strand.

GAM337490 precursor RNA folds onto itself, forming GAM337490 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337490 precursor RNA, designated SEQ ID NO: 6337, and a schematic representation of a predicted secondary folding of GAM337490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337490 folded precursor RNA yielding a GAM337490 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337490 RNA, hereby incorporated herein.

GAM337490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337490 target RNA, herein designated GAM TARGET RNA.

GAM337490 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337490 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337490 RNA, herein designated GAM RNA, to target binding sites on GAM337490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337490 target RNA into GAM337490 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337490 target genes. The mRNA of each one of this plurality of GAM337490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337490 RNA,

herein designated GAM RNA, and which when bound by GAM337490 RNA causes inhibition of translation of the GAM337490 target mRNA into a corresponding GAM337490 target protein.

The mechanism of the translational inhibition exerted by GAM337490 RNA, herein designated GAM RNA, on one or more GAM337490 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337490 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337490 RNA, herein designated GAM RNA, of GAM337490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337490 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337490 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337490 RNA correlate with, and may be deduced from, the identity of the GAM337490 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337495 6793 GGGAGGCCAA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTGGGAAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGCTTGAGC Messenger 337495 (GAM337495) oligonucleotides modulates expression of respective target

CCTGGAGGTT genes whose function and utility is known in the art.

GAGACAAGCC GAM337495 is a novel bioinformatically detectable regulatory, non protein

TGGGCAACAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337495 was detected

AGCAATACCC is described with additional reference to Figs. 9-15.

CATTTGTTTC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TT encoded by the human genome.

GAM337495 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337495 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337495 precursor RNA is designated SEQ ID:6793, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6793 is located from position 123734213 to position 123734294 relative to chromosome 12 on the `-` strand.

GAM337495 precursor RNA folds onto itself, forming GAM337495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337495 precursor RNA, designated SEQ ID NO: 6793, and a schematic representation of a predicted secondary folding of GAM337495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337495 folded precursor RNA yielding a GAM337495 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337495 RNA, hereby incorporated herein.

GAM337495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337495 target RNA, herein designated GAM TARGET RNA.

GAM337495 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337495 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337495 RNA, herein designated GAM RNA, to target binding sites on GAM337495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337495 target RNA

into GAM337495 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337495 target genes. The mRNA of each one of this plurality of GAM337495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337495 RNA, herein designated GAM RNA, and which when bound by GAM337495 RNA causes inhibition of translation of the GAM337495 target mRNA into a corresponding GAM337495 target protein.

The mechanism of the translational inhibition exerted by GAM337495 RNA, herein designated GAM RNA, on one or more GAM337495 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337495 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337495 RNA, herein designated GAM RNA, of GAM337495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337495 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337495 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337495 RNA correlate with, and may be deduced from, the identity of the GAM337495 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337496 6607 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGAAGG Messenger 337496 (GAM337496) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CTAAGATCGC GAM337496 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337496 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GACATTCT encoded by the human genome.

GAM337496 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337496 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337496 precursor RNA is designated SEQ ID:6607, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6607 is located from position 124130227 to position 124130314 relative to chromosome 12 on the `-` strand.

GAM337496 precursor RNA folds onto itself, forming GAM337496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337496 precursor RNA, designated SEQ ID NO: 6607, and a schematic representation of a predicted secondary folding of GAM337496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337496 folded precursor RNA yielding a GAM337496 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337496 RNA, hereby incorporated herein. Expression of GAM337496 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337496 target RNA, herein designated GAM TARGET RNA.

GAM337496 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337496 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337496 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337496 RNA, herein designated GAM RNA, to target binding sites on GAM337496 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337496 target RNA into GAM337496 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337496 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337496 target genes. The mRNA of each one of this plurality of GAM337496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337496 RNA, herein designated GAM RNA, and which when bound by GAM337496 RNA causes inhibition of translation of the GAM337496 target mRNA into a corresponding GAM337496 target protein.

The mechanism of the translational inhibition exerted by GAM337496 RNA, herein designated GAM RNA, on one or more GAM337496 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337496 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337496 RNA, herein designated GAM RNA, of GAM337496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337496 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337496 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337496 RNA correlate with, and may be deduced from, the identity of the GAM337496 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337497 6199 CTGAGCTTAG Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTTATGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCTTTCTGG Messenger 337497 (GAM337497) oligonucleotides modulates expression of respective target
TCTGTGTATC genes whose function and utility is known in the art.

CCAGGACTGT GAM337497 is a novel bioinformatically detectable regulatory, non protein
TCATCTCCTA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337497 was detected
TGTGATGCTG is described with additional reference to Figs. 9-15.

AAGACCAAGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGTGACCAA encoded by the human genome.

GAAGGCTCAG GAM337497 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337497 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337497 precursor RNA is designated SEQ ID:6199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6199 is located from position 124151674 to position 124151773 relative to chromosome 9 on the `-` strand.

GAM337497 precursor RNA folds onto itself, forming GAM337497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337497 precursor RNA, designated SEQ ID NO: 6199, and a schematic representation of a predicted secondary folding of GAM337497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337497 folded precursor RNA yielding a GAM337497 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337497 RNA, hereby incorporated herein.

GAM337497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337497 target RNA, herein designated GAM TARGET RNA.

GAM337497 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337497 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337497 RNA, herein designated GAM RNA, to target binding sites on GAM337497 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337497 target RNA into GAM337497 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337497 target genes. The mRNA of each one of this plurality of GAM337497 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337497 RNA, herein designated GAM RNA, and which when bound by GAM337497 RNA causes inhibition of translation of the GAM337497 target mRNA into a corresponding GAM337497 target protein.

The mechanism of the translational inhibition exerted by GAM337497 RNA, herein designated GAM RNA, on one or more GAM337497 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337497 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337497 RNA, herein designated GAM RNA, of GAM337497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337497 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337497 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337497

RNA correlate with, and may be deduced from, the identity of the GAM337497 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337498 6086 CCCTGAACTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGGGGCTTCG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCACTGATTG Messenger 337498 (GAM337498) oligonucleotides modulates expression of respective target
TCCAAACGCA genes whose function and utility is known in the art.

ATTCTTGTAC GAM337498 is a novel bioinformatically detectable regulatory, non protein
GAGTCTGCGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337498 was detected
CCAACCGAGA is described with additional reference to Figs. 9-15.

ATTGTGGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GACATCTGTG encoded by the human genome.

GCTGAGCTCC GAM337498 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GGGCGCAACA GAM337498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GGG GAM337498 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337498 precursor RNA is designated SEQ ID:6086, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6086 is located from position 124608557 to position 124608669 relative to chromosome 9 on the `-` strand.

GAM337498 precursor RNA folds onto itself, forming GAM337498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337498 precursor RNA, designated SEQ ID NO: 6086, and a schematic representation of a predicted secondary folding of GAM337498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337498 folded precursor RNA yielding a GAM337498 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly

similar to the nucleotide sequence of GAM337498 RNA, hereby incorporated herein.

GAM337498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337498 target RNA, herein designated GAM TARGET RNA.

GAM337498 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337498 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337498 RNA, herein designated GAM RNA, to target binding sites on GAM337498 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337498 target RNA into GAM337498 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337498 target genes. The mRNA of each one of this plurality of GAM337498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337498 RNA, herein designated GAM RNA, and which when bound by GAM337498 RNA causes inhibition of translation of the GAM337498 target mRNA into a corresponding GAM337498 target protein.

The mechanism of the translational inhibition exerted by GAM337498 RNA, herein designated GAM RNA, on one or more GAM337498 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337498 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337498 RNA, herein designated GAM RNA, of GAM337498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337498 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337498 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337498 RNA correlate with, and may be deduced from, the identity of the GAM337498 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337499 6507 GCCCTGAACT Fig. 8 further provides a conceptual description of another novel bioinformatically
CAGGGGCTTC detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCACTGATT Messenger 337499 (GAM337499) oligonucleotides modulates expression of respective target
GTCCAAACGC genes whose function and utility is known in the art.

AATTCTTGTA GAM337499 is a novel bioinformatically detectable regulatory, non protein
CGAGTCTGCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337499 was detected
GCCAACCGAG is described with additional reference to Figs. 9-15.

AATTGTGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGACATCTGT encoded by the human genome.

GGCTGAGCTC GAM337499 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CGGGC GAM337499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337499 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337499 precursor RNA is designated SEQ ID:6507, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6507 is located from position 124608566 to position 124608670 relative to chromosome 9 on the `-` strand.

GAM337499 precursor RNA folds onto itself, forming GAM337499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337499 precursor RNA, designated SEQ ID NO: 6507, and a schematic representation of a predicted secondary folding of GAM337499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337499 folded precursor RNA yielding a GAM337499 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337499 RNA, hereby incorporated herein.

GAM337499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337499 target RNA, herein designated GAM TARGET RNA.

GAM337499 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337499 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337499 RNA, herein designated GAM RNA, to target binding sites on GAM337499 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337499 target RNA into GAM337499 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337499 target genes. The mRNA of each one of this plurality of GAM337499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337499 RNA, herein designated GAM RNA, and which when bound by GAM337499 RNA causes inhibition of translation of the GAM337499 target mRNA into a corresponding GAM337499 target protein.

The mechanism of the translational inhibition exerted by GAM337499 RNA, herein designated GAM RNA, on one or more GAM337499 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337499 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337499 RNA, herein designated GAM RNA, of GAM337499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337499 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337499 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337499 RNA correlate with, and may be deduced from, the identity of the GAM337499 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337500 6161 CTCAGGGGCT Fig. 8 further provides a conceptual description of another novel bioinformatically

TCGCCACTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTCCAAAC Messenger 337500 (GAM337500) oligonucleotides modulates expression of respective target

GCAATTCTTG genes whose function and utility is known in the art.

TACGAGTCTG GAM337500 is a novel bioinformatically detectable regulatory, non protein

CGGCCAACCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337500 was detected

AGAATTGTGG is described with additional reference to Figs. 9-15.

CTGGACATCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGGCTGAGC encoded by the human genome.

TCCGGG GAM337500 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337500 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337500 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337500 precursor RNA is designated SEQ ID:6161, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6161 is located from position 124608567 to position 124608662 relative to chromosome 9 on the `-` strand.

GAM337500 precursor RNA folds onto itself, forming GAM337500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337500 precursor RNA, designated SEQ ID NO: 6161, and a schematic representation of a predicted secondary folding of GAM337500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337500 folded precursor RNA yielding a GAM337500 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337500 RNA, hereby incorporated herein.

GAM337500 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337500 target RNA, herein designated GAM TARGET RNA.

GAM337500 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337500 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337500 RNA, herein designated GAM RNA, to target binding sites on GAM337500 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337500 target RNA into GAM337500 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337500 target genes. The mRNA of each one of this plurality of GAM337500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337500 RNA, herein designated GAM RNA, and which when bound by GAM337500 RNA causes inhibition of translation of the GAM337500 target mRNA into a corresponding GAM337500 target protein.

The mechanism of the translational inhibition exerted by GAM337500 RNA, herein designated GAM RNA, on one or more GAM337500 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337500 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337500 RNA, herein designated GAM RNA, of GAM337500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337500 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337500 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337500 RNA correlate with, and may be deduced from, the identity of the GAM337500 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337501 6813 GGGGCTTCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

CACTGATTGT detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAAACGCAA Messenger 337501 (GAM337501) oligonucleotides modulates expression of respective target

TTCTTGTACG genes whose function and utility is known in the art.

AGTCTGCGGC GAM337501 is a novel bioinformatically detectable regulatory, non protein

CAACCGAGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337501 was detected

TTGTGGCTGG is described with additional reference to Figs. 9-15.

ACATCTGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CTGAGCTCC encoded by the human genome.

GAM337501 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337501 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337501 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337501 precursor RNA is designated SEQ

ID:6813, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6813 is located from position 124608570 to position 124608658 relative to chromosome 9 on the `-` strand.

GAM337501 precursor RNA folds onto itself, forming GAM337501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337501 precursor RNA, designated SEQ ID NO: 6813, and a schematic representation of a predicted secondary folding of GAM337501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337501 folded precursor RNA yielding a GAM337501 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337501 RNA, hereby incorporated herein.

GAM337501 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337501 target RNA, herein designated GAM TARGET RNA.

GAM337501 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337501 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337501 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337501 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337501 RNA, herein designated GAM RNA, to target binding sites on GAM337501 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337501 target RNA into GAM337501 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337501 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337501 target genes. The mRNA of each one of this plurality of GAM337501 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337501 RNA, herein designated GAM RNA, and which when bound by GAM337501 RNA causes inhibition of translation of the GAM337501 target mRNA into a corresponding GAM337501 target protein.

The mechanism of the translational inhibition exerted by GAM337501 RNA, herein designated GAM RNA, on one or more GAM337501 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337501 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337501 RNA, herein designated GAM RNA, of GAM337501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337501 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337501 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337501 RNA correlate with, and may be deduced from, the identity of the GAM337501 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337502 5924 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337502 (GAM337502) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337502 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337502 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337502 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337502 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337502 precursor RNA is designated SEQ ID:5924, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5924 is located from position 124663501 to position 124663582 relative to chromosome 6 on the `+` strand.

GAM337502 precursor RNA folds onto itself, forming GAM337502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337502 precursor RNA, designated SEQ ID NO: 5924, and a schematic representation of a predicted secondary folding of GAM337502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337502 folded precursor RNA yielding a GAM337502 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337502 RNA, hereby incorporated herein.

GAM337502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337502 target RNA, herein designated GAM TARGET RNA.

GAM337502 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337502 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337502 RNA, herein designated GAM RNA, to target binding sites on GAM337502 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337502 target RNA into GAM337502 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337502 target genes. The mRNA of each one of this plurality of GAM337502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337502 RNA, herein designated GAM RNA, and which when bound by GAM337502 RNA causes inhibition of translation of the GAM337502 target mRNA into a corresponding GAM337502 target protein.

The mechanism of the translational inhibition exerted by GAM337502 RNA, herein designated GAM RNA, on one or more GAM337502 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337502 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337502 RNA, herein designated GAM RNA, of GAM337502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337502 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337502 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337502 RNA correlate with, and may be deduced from, the identity of the GAM337502 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337507 6075 CCCAGTGACC Fig. 8 further provides a conceptual description of another novel bioinformatically

CACAGGTAAG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTTGTGT Messenger 337507 (GAM337507) oligonucleotides modulates expression of respective target

TTTCCAGATT genes whose function and utility is known in the art.

CTGAGTGTGG GAM337507 is a novel bioinformatically detectable regulatory, non protein
CTCAGCTCGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337507 was detected
GAATGCAGTG is described with additional reference to Figs. 9-15.

GCACAAGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTCTGTGGGA encoded by the human genome.

GTGGATCTTG GAM337507 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GG GAM337507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337507 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337507 precursor RNA is designated SEQ ID:6075, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6075 is located from position 126234545 to position 126234646 relative to chromosome 11 on the `+` strand.

GAM337507 precursor RNA folds onto itself, forming GAM337507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337507 precursor RNA, designated SEQ ID NO: 6075, and a schematic representation of a predicted secondary folding of GAM337507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337507 folded precursor RNA yielding a GAM337507 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337507 RNA, hereby incorporated herein.

GAM337507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337507 target RNA, herein designated GAM TARGET RNA.

GAM337507 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337507 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337507 RNA, herein designated GAM RNA, to target binding sites on GAM337507 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337507 target RNA into GAM337507 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337507 target genes. The mRNA of each one of this plurality of GAM337507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337507 RNA, herein designated GAM RNA, and which when bound by GAM337507 RNA causes inhibition of translation of the GAM337507 target mRNA into a corresponding GAM337507 target protein.

The mechanism of the translational inhibition exerted by GAM337507 RNA, herein designated GAM RNA, on one or more GAM337507 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337507 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337507 RNA, herein designated GAM RNA, of GAM337507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337507 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337507 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337507 RNA correlate with, and may be deduced from, the identity of the GAM337507 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337508 6068 CCCACAGGTA Fig. 8 further provides a conceptual description of another novel bioinformatically
AGAACCTTGT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTTTCCAGA Messenger 337508 (GAM337508) oligonucleotides modulates expression of respective target
TTCTGAGTGT genes whose function and utility is known in the art.

GGCTCAGCTC GAM337508 is a novel bioinformatically detectable regulatory, non protein
GTGAATGCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337508 was detected
TGGCACAAGG is described with additional reference to Figs. 9-15.

CACTCTGTGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
G encoded by the human genome.

GAM337508 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337508 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337508 precursor RNA is designated SEQ ID:6068, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6068 is located from position 126234553 to position 126234633 relative to chromosome 11 on the `+` strand.

GAM337508 precursor RNA folds onto itself, forming GAM337508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337508 precursor RNA, designated SEQ ID NO: 6068, and a schematic representation of a predicted secondary folding of GAM337508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337508 folded precursor RNA yielding a GAM337508 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337508 RNA, hereby incorporated herein.

GAM337508 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337508 target RNA, herein designated GAM TARGET RNA.

GAM337508 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337508 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337508 RNA, herein designated GAM RNA, to target binding sites on GAM337508 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337508 target RNA into GAM337508 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337508 target genes. The mRNA of each one of this plurality of GAM337508 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337508 RNA, herein designated GAM RNA, and which when bound by GAM337508 RNA causes inhibition of translation of the GAM337508 target mRNA into a corresponding GAM337508 target protein.

The mechanism of the translational inhibition exerted by GAM337508 RNA, herein designated GAM RNA, on one or more GAM337508 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337508 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337508 RNA, herein designated GAM RNA, of GAM337508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337508 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337508 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337508 RNA correlate with, and may be deduced from, the identity of the GAM337508 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337510 6418 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 337510 (GAM337510) oligonucleotides modulates expression of respective target
CAGAAGTTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337510 is a novel bioinformatically detectable regulatory, non protein
GATCGCATCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337510 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGCGAGA encoded by the human genome.

CTCTGTCTC GAM337510 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337510 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337510 precursor RNA is designated SEQ ID:6418, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6418 is located from position 126518661 to position 126518759 relative to chromosome 12 on the `+` strand.

GAM337510 precursor RNA folds onto itself, forming GAM337510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337510 precursor RNA, designated SEQ ID NO: 6418, and a schematic representation of a predicted secondary folding of GAM337510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337510 folded precursor RNA yielding a GAM337510 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337510 RNA, hereby incorporated herein. Expression of GAM337510 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337510 target RNA, herein designated GAM TARGET RNA.

GAM337510 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337510 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337510 RNA, herein designated GAM RNA, to target binding sites on GAM337510 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337510 target RNA into GAM337510 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337510 target genes. The mRNA of each one of this plurality of GAM337510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337510 RNA, herein designated GAM RNA, and which when bound by GAM337510 RNA causes inhibition of translation of the GAM337510 target mRNA into a corresponding GAM337510 target protein.

The mechanism of the translational inhibition exerted by GAM337510 RNA, herein designated GAM RNA, on one or more GAM337510 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337510 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337510 RNA, herein designated GAM RNA, of GAM337510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337510 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337510 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337510 RNA correlate with, and may be deduced from, the identity of the GAM337510 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337511 6029 CAGGTGTGCG Fig. 8 further provides a conceptual description of another novel bioinformatically

CCACCACACG detected oligonucleotides of the present invention, referred to here as Genomic Address

TGACTGGGAA Messenger 337511 (GAM337511) oligonucleotides modulates expression of respective target

GCCTTCTGGT genes whose function and utility is known in the art.

TTTAAGATGG GAM337511 is a novel bioinformatically detectable regulatory, non protein

CTTTAGAATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337511 was detected

AAAGGCAGTT is described with additional reference to Figs. 9-15.

CCTAGCACCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GTGGTCAATC encoded by the human genome.

ACATCTG GAM337511 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337511 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337511 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337511 precursor RNA is designated SEQ ID:6029, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6029 is located from position 126721975 to position 126722071 relative to chromosome 10 on the `+` strand.

GAM337511 precursor RNA folds onto itself, forming GAM337511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337511 precursor RNA, designated SEQ ID NO: 6029, and a schematic representation of a predicted secondary folding of GAM337511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337511 folded precursor RNA yielding a GAM337511 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337511 RNA, hereby incorporated herein.

GAM337511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337511 target RNA, herein designated GAM TARGET RNA.

GAM337511 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337511 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337511 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337511 RNA, herein designated GAM RNA, to target binding sites on GAM337511 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337511 target RNA into GAM337511 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337511 target genes. The mRNA of each one of this plurality of GAM337511 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337511 RNA, herein designated GAM RNA, and which when bound by GAM337511 RNA causes inhibition of translation of the GAM337511 target mRNA into a corresponding GAM337511 target protein.

The mechanism of the translational inhibition exerted by GAM337511 RNA, herein designated GAM RNA, on one or more GAM337511 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337511 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337511 RNA, herein designated GAM RNA, of GAM337511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337511 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337511 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337511 RNA correlate with, and may be deduced from, the identity of the GAM337511 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337512 6578 GGAACGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCTTGAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGAGGCA Messenger 337512 (GAM337512) oligonucleotides modulates expression of respective target

AAGGTTGCAG genes whose function and utility is known in the art.

TGAGTCAAGA GAM337512 is a novel bioinformatically detectable regulatory, non protein

TCATGCCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337512 was detected

GCACTCCTGC is described with additional reference to Figs. 9-15.

CTGGGTGACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGTGAGACC encoded by the human genome.

TTGTCTC GAM337512 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337512 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337512 precursor RNA is designated SEQ ID:6578, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6578 is located from position 126808650 to position 126808746

relative to chromosome 10 on the `+` strand.

GAM337512 precursor RNA folds onto itself, forming GAM337512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337512 precursor RNA, designated SEQ ID NO: 6578, and a schematic representation of a predicted secondary folding of GAM337512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337512 folded precursor RNA yielding a GAM337512 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337512 RNA, hereby incorporated herein.

GAM337512 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337512 target RNA, herein designated GAM TARGET RNA.

GAM337512 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337512 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337512 RNA, herein designated GAM RNA, to target binding sites on GAM337512 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337512 target RNA into GAM337512 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337512 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337512 target genes. The mRNA of each one of this plurality of GAM337512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337512 RNA, herein designated GAM RNA, and which when bound by GAM337512 RNA causes inhibition of translation of the GAM337512 target mRNA into a corresponding GAM337512 target protein.

The mechanism of the translational inhibition exerted by GAM337512 RNA, herein designated GAM RNA, on one or more GAM337512 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337512 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337512 RNA, herein designated GAM RNA, of GAM337512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337512 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337512 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337512 RNA correlate with, and may be deduced from, the identity of the GAM337512 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337515 6120 CCTGCTGTAT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTAGGCATT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTGCAAGGTG Messenger 337515 (GAM337515) oligonucleotides modulates expression of respective target

TTAGGGCTGA genes whose function and utility is known in the art.

TGCTTGAGCA GAM337515 is a novel bioinformatically detectable regulatory, non protein

CAGTACCTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337515 was detected

ACATCTGCAG is described with additional reference to Figs. 9-15.

TATGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337515 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337515 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337515 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337515 precursor RNA is designated SEQ ID:6120, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6120 is located from position 127715522 to position 127715596 relative to chromosome 7 on the `+` strand.

GAM337515 precursor RNA folds onto itself, forming GAM337515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337515 precursor RNA, designated SEQ ID NO: 6120, and a schematic representation of a predicted secondary folding of GAM337515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337515 folded precursor RNA yielding a GAM337515 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337515 RNA, hereby incorporated herein.

GAM337515 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337515 target RNA, herein designated GAM TARGET RNA.

GAM337515 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337515 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337515 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337515 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337515 RNA, herein designated GAM RNA, to target

binding sites on GAM337515 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337515 target RNA into GAM337515 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337515 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337515 target genes. The mRNA of each one of this plurality of GAM337515 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337515 RNA, herein designated GAM RNA, and which when bound by GAM337515 RNA causes inhibition of translation of the GAM337515 target mRNA into a corresponding GAM337515 target protein.

The mechanism of the translational inhibition exerted by GAM337515 RNA, herein designated GAM RNA, on one or more GAM337515 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337515 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337515 RNA, herein designated GAM RNA, of GAM337515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337515 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337515 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337515 RNA correlate with, and may be deduced from, the identity of the GAM337515 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337516 6143 CGCTTGCAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TGAAAGGCGG detected oligonucleotides of the present invention, referred to here as Genomic Address

AGGTTGCAGT Messenger 337516 (GAM337516) oligonucleotides modulates expression of respective target

GAACCAAGAT genes whose function and utility is known in the art.

CGCACCACTG GAM337516 is a novel bioinformatically detectable regulatory, non protein

CACTCCAGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337516 was detected

TGGGCAACAA is described with additional reference to Figs. 9-15.

AAGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337516 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337516 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337516 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337516 precursor RNA is designated SEQ ID:6143, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6143 is located from position 127763749 to position 127763823 relative to chromosome 7 on the `-` strand.

GAM337516 precursor RNA folds onto itself, forming GAM337516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337516 precursor RNA, designated SEQ ID NO: 6143, and a schematic representation of a predicted secondary folding of GAM337516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337516 folded precursor RNA yielding a GAM337516 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337516 RNA, hereby incorporated herein. Expression of GAM337516 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337516 target RNA, herein designated GAM TARGET RNA.

GAM337516 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337516 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337516 RNA, herein designated GAM RNA, to target binding sites on GAM337516 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337516 target RNA into GAM337516 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337516 target genes. The mRNA of each one of this plurality of GAM337516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337516 RNA, herein designated GAM RNA, and which when bound by GAM337516 RNA causes inhibition of translation of the GAM337516 target mRNA into a corresponding GAM337516 target protein.

The mechanism of the translational inhibition exerted by GAM337516 RNA, herein designated GAM RNA, on one or more GAM337516 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337516 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337516 RNA, herein designated GAM RNA, of GAM337516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337516 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337516 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337516 RNA correlate with, and may be deduced from, the identity of the GAM337516 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337518 6001 CACTAGGCTA Fig. 8 further provides a conceptual description of another novel bioinformatically

GACATACAAA detected oligonucleotides of the present invention, referred to here as Genomic Address
GACCCCTTGC Messenger 337518 (GAM337518) oligonucleotides modulates expression of respective target
CCGTGGCTCC genes whose function and utility is known in the art.

CATTTCAAAT GAM337518 is a novel bioinformatically detectable regulatory, non protein
ATATCTCATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337518 was detected
ACCAGGGTGT is described with additional reference to Figs. 9-15.

GGGAGCACGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGGAGGT encoded by the human genome.

AAGAGTTTAA GAM337518 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

ACTGTG GAM337518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337518 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337518 precursor RNA is designated SEQ ID:6001, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6001 is located from position 127854074 to position 127854179 relative to chromosome 10 on the `+` strand.

GAM337518 precursor RNA folds onto itself, forming GAM337518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337518 precursor RNA, designated SEQ ID NO: 6001, and a schematic representation of a predicted secondary folding of GAM337518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337518 folded precursor RNA yielding a GAM337518 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337518 RNA, hereby incorporated herein.

GAM337518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337518 target RNA, herein designated GAM TARGET RNA.

GAM337518 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region,

designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337518 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337518 RNA, herein designated GAM RNA, to target binding sites on GAM337518 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337518 target RNA into GAM337518 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337518 target genes. The mRNA of each one of this plurality of GAM337518 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337518 RNA, herein designated GAM RNA, and which when bound by GAM337518 RNA causes inhibition of translation of the GAM337518 target mRNA into a corresponding GAM337518 target protein.

The mechanism of the translational inhibition exerted by GAM337518 RNA, herein designated GAM RNA, on one or more GAM337518 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337518 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337518 RNA, herein designated GAM RNA, of GAM337518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337518 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337518 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337518 RNA correlate with, and may be deduced from, the identity of the GAM337518 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337520 6093 CCCTTATGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
ATTCTGGAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGTGGCTAC Messenger 337520 (GAM337520) oligonucleotides modulates expression of respective target
ACGGATGTAC genes whose function and utility is known in the art.

ATGAGTGTGA GAM337520 is a novel bioinformatically detectable regulatory, non protein
AAAAATCATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337520 was detected
AAACTGTATG is described with additional reference to Figs. 9-15.

CTCTGTGAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTTACTGTAT encoded by the human genome.

CTGTTATCCT GAM337520 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TCCTAATGGG GAM337520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337520 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337520 precursor RNA is designated SEQ ID:6093, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6093 is located from position 128242511 to position 128242620 relative to chromosome 9 on the `+` strand.

GAM337520 precursor RNA folds onto itself, forming GAM337520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337520 precursor RNA, designated SEQ ID NO: 6093, and a schematic representation of a predicted secondary folding of GAM337520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337520 folded precursor RNA yielding a GAM337520 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337520 RNA, hereby incorporated herein.

GAM337520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337520 target RNA, herein designated GAM TARGET RNA.

GAM337520 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337520 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337520 RNA, herein designated GAM RNA, to target binding sites on GAM337520 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337520 target RNA into GAM337520 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337520 target genes. The mRNA of each one of this plurality of GAM337520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337520 RNA, herein designated GAM RNA, and which when bound by GAM337520 RNA causes inhibition of translation of the GAM337520 target mRNA into a corresponding GAM337520 target protein.

The mechanism of the translational inhibition exerted by GAM337520 RNA, herein designated GAM RNA, on one or more GAM337520 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337520 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337520 RNA, herein designated GAM RNA, of GAM337520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337520 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337520 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337520 RNA correlate with, and may be deduced from, the identity of the GAM337520 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337521 6011 CAGACCCTCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CTCTTTCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGCTTCCTGT Messenger 337521 (GAM337521) oligonucleotides modulates expression of respective target
CCTTCAGCAA genes whose function and utility is known in the art.

GGCCACCTGA GAM337521 is a novel bioinformatically detectable regulatory, non protein
GAACTGAATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337521 was detected
GTAAATTCCA is described with additional reference to Figs. 9-15.

GCCTTGCAAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAAGGGGAGG encoded by the human genome.

AGGCTGAAAG GAM337521 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
ACAAGATAAA GAM337521 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
TG GAM337521 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337521 precursor RNA is designated SEQ ID:6011, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6011 is located from position 128399235 to position 128399346 relative to chromosome 9 on the `+` strand.

GAM337521 precursor RNA folds onto itself, forming GAM337521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337521 precursor RNA, designated SEQ ID NO: 6011, and a schematic representation of a predicted secondary folding of GAM337521 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337521 folded precursor RNA yielding a GAM337521 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337521 RNA, hereby incorporated herein.

GAM337521 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337521 target RNA, herein designated GAM TARGET RNA.

GAM337521 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337521 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337521 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337521 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337521 RNA, herein designated GAM RNA, to target binding sites on GAM337521 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337521 target RNA into GAM337521 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337521 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337521 target genes. The mRNA of each one of this plurality of GAM337521 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337521 RNA, herein designated GAM RNA, and which when bound by GAM337521 RNA causes inhibition of translation of the GAM337521 target mRNA into a corresponding GAM337521 target protein.

The mechanism of the translational inhibition exerted by GAM337521 RNA, herein designated GAM RNA, on one or more GAM337521 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337521 precursor RNA, herein designated GAM PRECURSOR

RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337521 RNA, herein designated GAM RNA, of GAM337521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337521 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337521 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337521 RNA correlate with, and may be deduced from, the identity of the GAM337521 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337522 7066 TCTCTCTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
CCAGGCTTCC detected oligonucleotides of the present invention, referred to here as Genomic Address
TGTCCTTCAG Messenger 337522 (GAM337522) oligonucleotides modulates expression of respective target
CAAGGCCACC genes whose function and utility is known in the art.

TGAGAACTGA GAM337522 is a novel bioinformatically detectable regulatory, non protein
ATTGTAAATT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337522 was detected
CCAGCCTTGC is described with additional reference to Figs. 9-15.

AAGGAAGGGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGAGGCTGA encoded by the human genome.

AAGACAAGA GAM337522 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337522 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337522 precursor RNA is designated SEQ ID:7066, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7066 is located from position 128399242 to position 128399340 relative to chromosome 9 on the `+` strand.

GAM337522 precursor RNA folds onto itself, forming GAM337522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337522 precursor RNA, designated SEQ ID NO: 7066, and a schematic representation of a predicted secondary folding of GAM337522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337522 folded precursor RNA yielding a GAM337522 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337522 RNA, hereby incorporated herein.

GAM337522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337522 target RNA, herein designated GAM TARGET RNA.

GAM337522 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337522 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337522 RNA, herein designated GAM RNA, to target binding sites on GAM337522 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337522 target RNA into GAM337522 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337522 target genes. The mRNA of each one of this plurality of GAM337522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337522 RNA, herein designated GAM RNA, and which when bound by GAM337522 RNA causes inhibition of translation of the GAM337522 target mRNA into a corresponding GAM337522 target protein.

The mechanism of the translational inhibition exerted by GAM337522 RNA, herein designated GAM RNA, on one or more GAM337522 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337522 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337522 RNA, herein designated GAM RNA, of GAM337522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337522 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337522 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337522 RNA correlate with, and may be deduced from, the identity of the GAM337522 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337523 7080 TCTTTCCCAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCTTCCTGTC detected oligonucleotides of the present invention, referred to here as Genomic Address

CTTCAGCAAG Messenger 337523 (GAM337523) oligonucleotides modulates expression of respective target

GCCACCTGAG genes whose function and utility is known in the art.

AACTGAATTG GAM337523 is a novel bioinformatically detectable regulatory, non protein

TAAATTCCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337523 was detected

CCTTGCAAGG is described with additional reference to Figs. 9-15.

AAGGGGAGGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGCTGAAAGA encoded by the human genome.

GAM337523 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337523 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337523 precursor RNA is designated SEQ

ID:7080, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7080 is located from position 128399246 to position 128399335 relative to chromosome 9 on the `+` strand.

GAM337523 precursor RNA folds onto itself, forming GAM337523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337523 precursor RNA, designated SEQ ID NO: 7080, and a schematic representation of a predicted secondary folding of GAM337523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337523 folded precursor RNA yielding a GAM337523 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337523 RNA, hereby incorporated herein.

GAM337523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337523 target RNA, herein designated GAM TARGET RNA.

GAM337523 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337523 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337523 RNA, herein designated GAM RNA, to target binding sites on GAM337523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337523 target RNA into GAM337523 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337523 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337523 target genes. The mRNA of each one of this plurality of GAM337523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337523 RNA, herein designated GAM RNA, and which when bound by GAM337523 RNA causes inhibition of translation of the GAM337523 target mRNA into a corresponding GAM337523 target protein.

The mechanism of the translational inhibition exerted by GAM337523 RNA, herein designated GAM RNA, on one or more GAM337523 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337523 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337523 RNA, herein designated GAM RNA, of GAM337523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337523 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337523 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337523 RNA correlate with, and may be deduced from, the identity of the GAM337523 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337524 6799 GGGATTACAG Fig. 8 further provides a conceptual description of another novel bioinformatically

GCACCTGCTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAAGTCTGG Messenger 337524 (GAM337524) oligonucleotides modulates expression of respective target

CTAATTTTTG genes whose function and utility is known in the art.

TATTTTTAAT GAM337524 is a novel bioinformatically detectable regulatory, non protein

AGAGACGGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337524 was detected

TTTCGCTATG is described with additional reference to Figs. 9-15.

TTGGCCAGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGGTCTCGAA encoded by the human genome.

CTCCTGATCT GAM337524 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM337524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337524 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337524 precursor RNA is designated SEQ ID:6799, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6799 is located from position 128497045 to position 128497145 relative to chromosome 8 on the `+` strand.

GAM337524 precursor RNA folds onto itself, forming GAM337524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337524 precursor RNA, designated SEQ ID NO: 6799, and a schematic representation of a predicted secondary folding of GAM337524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337524 folded precursor RNA yielding a GAM337524 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337524 RNA, hereby incorporated herein.

GAM337524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337524 target RNA, herein designated GAM TARGET RNA.

GAM337524 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337524 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337524 RNA, herein designated GAM RNA, to target binding sites on GAM337524 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337524 target RNA into GAM337524 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337524 target genes. The mRNA of each one of this plurality of GAM337524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337524 RNA, herein designated GAM RNA, and which when bound by GAM337524 RNA causes inhibition of translation of the GAM337524 target mRNA into a corresponding GAM337524 target protein.

The mechanism of the translational inhibition exerted by GAM337524 RNA, herein designated GAM RNA, on one or more GAM337524 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337524 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337524 RNA, herein designated GAM RNA, of GAM337524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337524 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337524 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337524 RNA correlate with, and may be deduced from, the identity of the GAM337524 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337525 6533 GCTCCTGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically

GCATATGCAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GGGTACACAG Messenger 337525 (GAM337525) oligonucleotides modulates expression of respective target

CCTGTAACTA genes whose function and utility is known in the art.

CATGTGTGTG GAM337525 is a novel bioinformatically detectable regulatory, non protein
AGCCTGTGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337525 was detected
TATGTGAGGG is described with additional reference to Figs. 9-15.

GAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337525 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337525 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337525 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337525 precursor RNA is designated SEQ ID:6533, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6533 is located from position 128533191 to position 128533264 relative to chromosome 8 on the `+` strand.

GAM337525 precursor RNA folds onto itself, forming GAM337525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337525 precursor RNA, designated SEQ ID NO: 6533, and a schematic representation of a predicted secondary folding of GAM337525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337525 folded precursor RNA yielding a GAM337525 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337525 RNA, hereby incorporated herein.

GAM337525 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337525 target RNA, herein designated GAM TARGET RNA.

GAM337525 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337525 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337525 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337525 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337525 RNA, herein designated GAM RNA, to target binding sites on GAM337525 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337525 target RNA into GAM337525 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337525 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337525 target genes. The mRNA of each one of this plurality of GAM337525 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337525 RNA, herein designated GAM RNA, and which when bound by GAM337525 RNA causes inhibition of translation of the GAM337525 target mRNA into a corresponding GAM337525 target protein.

The mechanism of the translational inhibition exerted by GAM337525 RNA, herein designated GAM RNA, on one or more GAM337525 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337525 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337525 RNA, herein designated GAM RNA, of GAM337525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337525 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337525 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337525 RNA correlate with, and may be deduced from, the identity of the GAM337525 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337526 6288 GAACCTTTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
TGTTACTCTA detected oligonucleotides of the present invention, referred to here as Genomic Address
TCGTCTGGAT Messenger 337526 (GAM337526) oligonucleotides modulates expression of respective target
CTCTTTTGCC genes whose function and utility is known in the art.

TGTGAGGGAG GAM337526 is a novel bioinformatically detectable regulatory, non protein
GCAGAGAGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337526 was detected
ATTTAGGCAT is described with additional reference to Figs. 9-15.

GAGGCAGCAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGGTTT encoded by the human genome.

GAM337526 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337526 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337526 precursor RNA is designated SEQ ID:6288, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6288 is located from position 128779961 to position 128780046 relative to chromosome 11 on the `+` strand.

GAM337526 precursor RNA folds onto itself, forming GAM337526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337526 precursor RNA, designated SEQ ID NO: 6288, and a schematic representation of a predicted secondary folding of GAM337526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337526 folded precursor RNA yielding a GAM337526 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337526 RNA, hereby incorporated herein.

GAM337526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337526 target RNA, herein designated GAM TARGET RNA.

GAM337526 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337526 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337526 RNA, herein designated GAM RNA, to target binding sites on GAM337526 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337526 target RNA into GAM337526 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337526 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337526 target genes. The mRNA of each one of this plurality of GAM337526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337526 RNA, herein designated GAM RNA, and which when bound by GAM337526 RNA causes inhibition of translation of the GAM337526 target mRNA into a corresponding GAM337526 target protein.

The mechanism of the translational inhibition exerted by GAM337526 RNA, herein designated GAM RNA, on one or more GAM337526 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337526 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337526 RNA, herein designated GAM RNA, of GAM337526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337526 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337526 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337526 RNA correlate with, and may be deduced from, the identity of the GAM337526 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337528 6576 GGAACAGCAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GGCTAGAAAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CCAGAGAGAC Messenger 337528 (GAM337528) oligonucleotides modulates expression of respective target
AGGGGCTCTG genes whose function and utility is known in the art.

GCCCTTTCTG GAM337528 is a novel bioinformatically detectable regulatory, non protein
ATGCTGTTTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337528 was detected
TAGCACCTGC is described with additional reference to Figs. 9-15.

TTTCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337528 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337528 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337528 precursor RNA is designated SEQ ID:6576, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6576 is located from position 129138656 to position 129138730 relative to chromosome 12 on the `+` strand.

GAM337528 precursor RNA folds onto itself, forming GAM337528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337528 precursor RNA, designated SEQ ID NO: 6576, and a schematic representation of a predicted secondary folding of GAM337528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337528 folded precursor RNA yielding a GAM337528 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337528 RNA, hereby incorporated herein.

GAM337528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337528 target RNA, herein designated GAM TARGET RNA.

GAM337528 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337528 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337528 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337528 RNA, herein designated GAM RNA, to target binding sites on GAM337528 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337528 target RNA into GAM337528 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337528 target genes. The mRNA of each one of this plurality of GAM337528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337528 RNA, herein designated GAM RNA, and which when bound by GAM337528 RNA causes inhibition of translation of the GAM337528 target mRNA into a corresponding GAM337528 target protein.

The mechanism of the translational inhibition exerted by GAM337528 RNA, herein designated GAM RNA, on one or more GAM337528 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337528 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337528 RNA, herein designated GAM RNA, of GAM337528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337528 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337528 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337528 RNA correlate with, and may be deduced from, the identity of the GAM337528 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337529 5751 AGCGGTGAAG ACCAAGGCCA GAGCTTAAAC TCATAGGGGT CATTCAACTC TGTTTTTATT AGTTGTCCTT GGTTTATACT GTT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337529 (GAM337529) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337529 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337529 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337529 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337529 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337529 precursor RNA is designated SEQ ID:5751, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5751 is located from position 129198494 to position 129198576 relative to chromosome 7 on the `-` strand.

GAM337529 precursor RNA folds onto itself, forming GAM337529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337529 precursor RNA, designated SEQ ID NO: 5751, and a schematic representation of a predicted secondary folding of GAM337529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337529 folded precursor RNA yielding a GAM337529 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337529 RNA, hereby incorporated herein.

GAM337529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337529 target RNA, herein designated GAM TARGET RNA.

GAM337529 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337529 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337529 RNA, herein designated GAM RNA, to target binding sites on GAM337529 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337529 target RNA into GAM337529 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337529 target genes. The mRNA of each one of this plurality of GAM337529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337529 RNA, herein designated GAM RNA, and which when bound by GAM337529 RNA causes inhibition of translation of the GAM337529 target mRNA into a corresponding GAM337529 target protein.

The mechanism of the translational inhibition exerted by GAM337529 RNA, herein designated GAM RNA, on one or more GAM337529 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337529 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337529 RNA, herein designated GAM RNA, of GAM337529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337529 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337529 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337529 RNA correlate with, and may be deduced from, the identity of the GAM337529 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337530 6112 CCTCCTCCAT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCGTCTCCCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GGGTGCCTTT Messenger 337530 (GAM337530) oligonucleotides modulates expression of respective target
GTTTTGAATC genes whose function and utility is known in the art.

ATTTTTGATT GAM337530 is a novel bioinformatically detectable regulatory, non protein
TCAATTTAAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337530 was detected
AAGAGAAAGA is described with additional reference to Figs. 9-15.

AGAGGCTGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACGAAGGAAG encoded by the human genome.

GAGG GAM337530 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337530 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337530 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337530 precursor RNA is designated SEQ ID:6112, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6112 is located from position 129432365 to position 129432458 relative to chromosome 12 on the `+` strand.

GAM337530 precursor RNA folds onto itself, forming GAM337530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337530 precursor RNA, designated SEQ ID NO: 6112, and a schematic representation of a predicted secondary folding of GAM337530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337530 folded precursor RNA yielding a GAM337530 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337530 RNA, hereby incorporated herein.

GAM337530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337530 target RNA, herein designated GAM TARGET RNA.

GAM337530 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337530 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337530 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337530 RNA, herein designated GAM RNA, to target binding sites on GAM337530 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337530 target RNA into GAM337530 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337530 target genes. The mRNA of each one of this plurality of GAM337530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337530 RNA, herein designated GAM RNA, and which when bound by GAM337530 RNA causes inhibition of translation of the GAM337530 target mRNA into a corresponding GAM337530 target protein.

The mechanism of the translational inhibition exerted by GAM337530 RNA, herein designated GAM RNA, on one or more GAM337530 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337530 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337530 RNA, herein designated GAM RNA, of GAM337530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337530 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337530 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337530 RNA correlate with, and may be deduced from, the identity of the GAM337530 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337531 5925 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337531 (GAM337531) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337531 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337531 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337531 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337531 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337531 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337531 precursor RNA is designated SEQ

ID:5925, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5925 is located from position 129487964 to position 129488045 relative to chromosome 2 on the `+` strand.

GAM337531 precursor RNA folds onto itself, forming GAM337531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337531 precursor RNA, designated SEQ ID NO: 5925, and a schematic representation of a predicted secondary folding of GAM337531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337531 folded precursor RNA yielding a GAM337531 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337531 RNA, hereby incorporated herein.

GAM337531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337531 target RNA, herein designated GAM TARGET RNA.

GAM337531 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337531 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337531 RNA, herein designated GAM RNA, to target binding sites on GAM337531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337531 target RNA into GAM337531 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337531 target genes. The mRNA of each one of this plurality of GAM337531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337531 RNA, herein designated GAM RNA, and which when bound by GAM337531 RNA causes inhibition of translation of the GAM337531 target mRNA into a corresponding GAM337531 target protein.

The mechanism of the translational inhibition exerted by GAM337531 RNA, herein designated GAM RNA, on one or more GAM337531 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337531 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337531 RNA, herein designated GAM RNA, of GAM337531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337531 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337531 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337531 RNA correlate with, and may be deduced from, the identity of the GAM337531 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337533 5926 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337533 (GAM337533) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337533 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337533 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337533 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337533 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337533 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337533 precursor RNA is designated SEQ ID:5926, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5926 is located from position 129681005 to position 129681086 relative to chromosome 12 on the `-` strand.

GAM337533 precursor RNA folds onto itself, forming GAM337533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337533 precursor RNA, designated SEQ ID NO: 5926, and a schematic representation of a predicted secondary folding of GAM337533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337533 folded precursor RNA yielding a GAM337533 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337533 RNA, hereby incorporated herein.

GAM337533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337533 target RNA, herein designated GAM TARGET RNA.

GAM337533 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337533 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337533 RNA, herein designated GAM RNA, to target binding sites on GAM337533 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337533 target RNA into GAM337533 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337533 target genes. The mRNA of each one of this plurality of GAM337533 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337533 RNA, herein designated GAM RNA, and which when bound by GAM337533 RNA causes inhibition of translation of the GAM337533 target mRNA into a corresponding GAM337533 target protein.

The mechanism of the translational inhibition exerted by GAM337533 RNA, herein designated GAM RNA, on one or more GAM337533 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337533 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337533 RNA, herein designated GAM RNA, of GAM337533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337533 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337533 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337533 RNA correlate with, and may be deduced from, the identity of the GAM337533 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337534 5927 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337534 (GAM337534) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337534 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337534 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337534 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337534 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337534 precursor RNA is designated SEQ ID:5927, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5927 is located from position 129687004 to position 129687085 relative to chromosome 12 on the `+` strand.

GAM337534 precursor RNA folds onto itself, forming GAM337534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337534 precursor RNA, designated SEQ ID NO: 5927, and a schematic representation of a predicted secondary folding of GAM337534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337534 folded precursor RNA yielding a GAM337534 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337534 RNA, hereby incorporated herein.

GAM337534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337534 target RNA, herein designated GAM TARGET RNA.

GAM337534 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337534 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337534 RNA, herein designated GAM RNA, to target binding sites on GAM337534 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337534 target RNA into GAM337534 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337534 target genes. The mRNA of each one of this plurality of GAM337534 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337534 RNA, herein designated GAM RNA, and which when bound by GAM337534 RNA causes inhibition of translation of the GAM337534 target mRNA into a corresponding GAM337534 target protein.

The mechanism of the translational inhibition exerted by GAM337534 RNA, herein designated GAM RNA, on one or more GAM337534 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337534 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337534 RNA, herein designated GAM RNA, of GAM337534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337534 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337534 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337534 RNA correlate with, and may be deduced from, the identity of the GAM337534 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337541 6420 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
ACCCAGGAGG Messenger 337541 (GAM337541) oligonucleotides modulates expression of respective target
TGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM337541 is a novel bioinformatically detectable regulatory, non protein
GACCATGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337541 was detected
TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGA encoded by the human genome.

CTTGGTGTC GAM337541 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337541 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337541 precursor RNA is designated SEQ ID:6420, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6420 is located from position 130940694 to position 130940792 relative to chromosome 10 on the `+` strand.

GAM337541 precursor RNA folds onto itself, forming GAM337541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337541 precursor RNA, designated SEQ ID NO: 6420, and a schematic representation of a predicted secondary folding of GAM337541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337541 folded precursor RNA yielding a GAM337541 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337541 RNA, hereby incorporated herein. Expression of GAM337541 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337541 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337541 target RNA, herein designated GAM TARGET RNA.

GAM337541 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337541 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337541 RNA, herein designated GAM RNA, to target binding sites on GAM337541 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337541 target RNA into GAM337541 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337541 target genes. The mRNA of each one of this plurality of GAM337541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337541 RNA, herein designated GAM RNA, and which when bound by GAM337541 RNA causes inhibition of translation of the GAM337541 target mRNA into a corresponding GAM337541 target protein.

The mechanism of the translational inhibition exerted by GAM337541 RNA, herein designated GAM RNA, on one or more GAM337541 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337541 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337541 RNA, herein designated GAM RNA, of GAM337541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337541 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337541 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337541 RNA correlate with, and may be deduced from, the identity of the GAM337541 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337542 6329 GAGAATTGCT TGAACCCAGG AGGTGGAGGT TGCAGTGAGC TGAGACCATG CCATTGCACT CCAGCCTGGG CAACAGAGTG AGACTT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337542 (GAM337542) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337542 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337542 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337542 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337542 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337542 precursor RNA is designated SEQ ID:6329, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6329 is located from position 130940701 to position 130940786 relative to chromosome 10 on the `+` strand.

GAM337542 precursor RNA folds onto itself, forming GAM337542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337542 precursor RNA, designated SEQ ID NO: 6329, and a schematic representation of a predicted secondary folding of GAM337542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337542 folded precursor RNA yielding a GAM337542 RNA, herein designated GAM RNA, in the form of a single stranded

~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337542 RNA, hereby incorporated herein. Expression of GAM337542 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337542 target RNA, herein designated GAM TARGET RNA.

GAM337542 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337542 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337542 RNA, herein designated GAM RNA, to target binding sites on GAM337542 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337542 target RNA into GAM337542 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337542 target genes. The mRNA of each one of this plurality of GAM337542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337542 RNA, herein designated GAM RNA, and which when bound by GAM337542 RNA causes inhibition of translation of the GAM337542 target mRNA into a corresponding GAM337542 target protein.

The mechanism of the translational inhibition exerted by GAM337542 RNA, herein designated GAM RNA, on one or more GAM337542 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337542 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337542 RNA, herein designated GAM RNA, of GAM337542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337542 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337542 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337542 RNA correlate with, and may be deduced from, the identity of the GAM337542 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337543 5928 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337543 (GAM337543) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337543 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337543 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337543 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337543 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337543 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337543 precursor RNA is designated SEQ ID:5928, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5928 is located from position 131254288 to position 131254369 relative to chromosome 5 on the `+` strand.

GAM337543 precursor RNA folds onto itself, forming GAM337543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337543 precursor RNA, designated SEQ ID NO: 5928, and a schematic representation of a predicted secondary folding of GAM337543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337543 folded precursor RNA yielding a GAM337543 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337543 RNA, hereby incorporated herein.

GAM337543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337543 target RNA, herein designated GAM TARGET RNA.

GAM337543 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337543 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337543 RNA, herein designated GAM RNA, to target binding sites on GAM337543 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337543 target RNA into GAM337543 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337543 target genes. The mRNA of each one of this plurality of GAM337543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337543 RNA, herein designated GAM RNA, and which when bound by GAM337543 RNA causes inhibition of translation of the GAM337543 target mRNA into a corresponding GAM337543 target protein.

The mechanism of the translational inhibition exerted by GAM337543 RNA, herein designated GAM RNA, on one or more GAM337543 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337543 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337543 RNA, herein designated GAM RNA, of GAM337543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337543 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337543 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337543 RNA correlate with, and may be deduced from, the identity of the GAM337543 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337544 5929 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337544 (GAM337544) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337544 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337544 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337544 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337544 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337544 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337544 precursor RNA is designated SEQ ID:5929, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5929 is located from position 131317013 to position 131317094 relative to chromosome 9 on the `+` strand.

GAM337544 precursor RNA folds onto itself, forming GAM337544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337544 precursor RNA, designated SEQ ID NO: 5929, and a schematic representation of a predicted secondary folding of GAM337544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337544 folded precursor RNA yielding a GAM337544 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337544 RNA, hereby incorporated herein.

GAM337544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337544 target RNA, herein designated GAM TARGET RNA.

GAM337544 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337544 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337544 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337544 RNA, herein designated GAM RNA, to target binding sites on GAM337544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337544 target RNA into GAM337544 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337544 target genes. The mRNA of each one of this

plurality of GAM337544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337544 RNA, herein designated GAM RNA, and which when bound by GAM337544 RNA causes inhibition of translation of the GAM337544 target mRNA into a corresponding GAM337544 target protein.

The mechanism of the translational inhibition exerted by GAM337544 RNA, herein designated GAM RNA, on one or more GAM337544 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337544 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337544 RNA, herein designated GAM RNA, of GAM337544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337544 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337544 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337544 RNA correlate with, and may be deduced from, the identity of the GAM337544 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337545 6616 GGAGAATCAC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 337545 (GAM337545) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGAGATTGA GAM337545 is a novel bioinformatically detectable regulatory, non protein

GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337545 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

ACATCAGGGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337545 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337545 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337545 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337545 precursor RNA is designated SEQ ID:6616, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6616 is located from position 131445968 to position 131446055 relative to chromosome X on the `+` strand.

GAM337545 precursor RNA folds onto itself, forming GAM337545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337545 precursor RNA, designated SEQ ID NO: 6616, and a schematic representation of a predicted secondary folding of GAM337545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337545 folded precursor RNA yielding a GAM337545 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337545 RNA, hereby incorporated herein.

GAM337545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337545 target RNA, herein designated GAM TARGET RNA.

GAM337545 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337545 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337545 RNA, herein designated GAM RNA, to target binding sites on GAM337545 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337545 target RNA into GAM337545 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337545 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337545 target genes. The mRNA of each one of this plurality of GAM337545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337545 RNA, herein designated GAM RNA, and which when bound by GAM337545 RNA causes inhibition of translation of the GAM337545 target mRNA into a corresponding GAM337545 target protein.

The mechanism of the translational inhibition exerted by GAM337545 RNA, herein designated GAM RNA, on one or more GAM337545 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337545 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337545 RNA, herein designated GAM RNA, of GAM337545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337545 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337545 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337545 RNA correlate with, and may be deduced from, the identity of the GAM337545 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337547 6074 CCCAGGTTTC Fig. 8 further provides a conceptual description of another novel bioinformatically
AGTTTGGTAG detected oligonucleotides of the present invention, referred to here as Genomic Address
CATGAATCCT Messenger 337547 (GAM337547) oligonucleotides modulates expression of respective target
TAGCATTTAG genes whose function and utility is known in the art.

TGACTCCAGT GAM337547 is a novel bioinformatically detectable regulatory, non protein
TTTGGTCTGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337547 was detected
TGTCTTTCTT is described with additional reference to Figs. 9-15.

AAATGGATGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ATGAGGCAAC encoded by the human genome.

CATTGGGTAC GAM337547 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TGGG GAM337547 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337547 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337547 precursor RNA is designated SEQ ID:6074, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6074 is located from position 131841260 to position 131841363 relative to chromosome 10 on the `+` strand.

GAM337547 precursor RNA folds onto itself, forming GAM337547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337547 precursor RNA, designated SEQ ID NO: 6074, and a schematic representation of a predicted secondary folding of GAM337547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337547 folded precursor RNA yielding a GAM337547 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337547 RNA, hereby incorporated herein.

GAM337547 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337547 target RNA, herein designated GAM TARGET RNA.

GAM337547 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337547 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337547 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337547 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337547 RNA, herein designated GAM RNA, to target binding sites on GAM337547 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337547 target RNA into GAM337547 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337547 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337547 target genes. The mRNA of each one of this plurality of GAM337547 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337547 RNA, herein designated GAM RNA, and which when bound by GAM337547 RNA causes inhibition of translation of the GAM337547 target mRNA into a corresponding GAM337547 target protein.

The mechanism of the translational inhibition exerted by GAM337547 RNA, herein designated GAM RNA, on one or more GAM337547 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337547 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337547 RNA, herein designated GAM RNA, of GAM337547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337547 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337547 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337547 RNA correlate with, and may be deduced from, the identity of the GAM337547 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337548 7140 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGTG Messenger 337548 (GAM337548) oligonucleotides modulates expression of respective target

GCAAGGCTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM337548 is a novel bioinformatically detectable regulatory, non protein

AGATCGCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337548 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGAGCGAG encoded by the human genome.

ACTCCAGCTC GAM337548 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337548 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337548 precursor RNA is designated SEQ ID:7140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7140 is located from position 131845700 to position 131845800 relative to chromosome 2 on the `+` strand.

GAM337548 precursor RNA folds onto itself, forming GAM337548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337548 precursor RNA, designated SEQ ID NO: 7140, and a schematic representation of a predicted secondary folding of GAM337548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337548 folded precursor RNA yielding a GAM337548 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337548 RNA, hereby incorporated herein. Expression of GAM337548 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337548 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337548 target RNA, herein designated GAM TARGET RNA.

GAM337548 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337548 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337548 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337548 RNA, herein designated GAM RNA, to target binding sites on GAM337548 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337548 target RNA into GAM337548 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337548 target genes. The mRNA of each one of this plurality of GAM337548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337548 RNA, herein designated GAM RNA, and which when bound by GAM337548 RNA causes inhibition of translation of the GAM337548 target mRNA into a corresponding GAM337548 target protein.

The mechanism of the translational inhibition exerted by GAM337548 RNA, herein designated GAM RNA, on one or more GAM337548 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337548 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337548 RNA, herein designated GAM RNA, of GAM337548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337548 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337548 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337548 RNA correlate with, and may be deduced from, the identity of the GAM337548 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337549 6641 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGGCAAGGC Messenger 337549 (GAM337549) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CTGAGATCGC GAM337549 is a novel bioinformatically detectable regulatory, non protein
ACTACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337549 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM337549 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337549 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337549 precursor RNA is designated SEQ ID:6641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6641 is located from position 131845707 to position 131845794 relative to chromosome 2 on the `+` strand.

GAM337549 precursor RNA folds onto itself, forming GAM337549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337549 precursor RNA, designated SEQ ID NO: 6641, and a schematic representation of a predicted secondary folding of GAM337549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337549 folded precursor RNA yielding a GAM337549 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337549 RNA, hereby incorporated herein. Expression of GAM337549 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337549 target RNA, herein designated GAM TARGET RNA.

GAM337549 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337549 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337549 RNA, herein designated GAM RNA, to target binding sites on GAM337549 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337549 target RNA into GAM337549 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337549 target genes. The mRNA of each one of this plurality of GAM337549 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337549 RNA, herein designated GAM RNA, and which when bound by GAM337549 RNA causes inhibition of translation of the GAM337549 target mRNA into a corresponding GAM337549 target protein.

The mechanism of the translational inhibition exerted by GAM337549 RNA, herein designated GAM RNA, on one or more GAM337549 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337549 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337549 RNA, herein designated GAM RNA, of

GAM337549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337549 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337549 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337549 RNA correlate with, and may be deduced from, the identity of the GAM337549 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337552 7117 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAATGGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 337552 (GAM337552) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCTG GAM337552 is a novel bioinformatically detectable regulatory, non protein

AGATTGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337552 was detected

ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCAA encoded by the human genome.

AACTCCGTCT GAM337552 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM337552 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337552 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337552 precursor RNA is designated SEQ ID:7117, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7117 is located from position 132503685 to position 132503786 relative to chromosome 12 on the `-` strand.

GAM337552 precursor RNA folds onto itself, forming GAM337552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337552 precursor RNA, designated SEQ ID NO: 7117, and a schematic representation of a predicted secondary folding of GAM337552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337552 folded precursor RNA yielding a GAM337552 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337552 RNA, hereby incorporated herein. Expression of GAM337552 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337552 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337552 target RNA, herein designated GAM TARGET RNA.

GAM337552 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337552 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337552 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337552 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337552 RNA, herein designated GAM RNA, to target binding sites on GAM337552 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337552 target RNA into GAM337552 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337552 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337552 target genes. The mRNA of each one of this plurality of GAM337552 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337552 RNA, herein designated GAM RNA, and which when bound by GAM337552 RNA causes inhibition of translation of the GAM337552 target mRNA into a corresponding GAM337552 target protein.

The mechanism of the translational inhibition exerted by GAM337552 RNA, herein designated GAM RNA, on one or more GAM337552 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337552 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337552 RNA, herein designated GAM RNA, of GAM337552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337552 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337552 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337552 RNA correlate with, and may be deduced from, the identity of the GAM337552 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337553 5694 ACCAGTGGTT Fig. 8 further provides a conceptual description of another novel bioinformatically
AGCAGATGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGAAAGAGA Messenger 337553 (GAM337553) oligonucleotides modulates expression of respective target
TGGGACAGTG genes whose function and utility is known in the art.

ACTGTATCTG GAM337553 is a novel bioinformatically detectable regulatory, non protein
TTCTGATGAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337553 was detected
GGAGATTGTG is described with additional reference to Figs. 9-15.

CAGTTACATG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CGTAACGTCA encoded by the human genome.

TTAAACTTCA GAM337553 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTCTTCCAGG GAM337553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
T GAM337553 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337553 precursor RNA is designated SEQ ID:5694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5694 is located from position 132744616 to position 132744726

relative to chromosome 8 on the `-` strand.

GAM337553 precursor RNA folds onto itself, forming GAM337553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337553 precursor RNA, designated SEQ ID NO: 5694, and a schematic representation of a predicted secondary folding of GAM337553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337553 folded precursor RNA yielding a GAM337553 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337553 RNA, hereby incorporated herein.

GAM337553 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337553 target RNA, herein designated GAM TARGET RNA.

GAM337553 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337553 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337553 RNA, herein designated GAM RNA, to target binding sites on GAM337553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337553 target RNA into GAM337553 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337553 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337553 target genes. The mRNA of each one of this plurality of GAM337553 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337553 RNA, herein designated GAM RNA, and which when bound by GAM337553 RNA causes inhibition of translation of the GAM337553 target mRNA into a corresponding GAM337553 target protein.

The mechanism of the translational inhibition exerted by GAM337553 RNA, herein designated GAM RNA, on one or more GAM337553 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337553 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337553 RNA, herein designated GAM RNA, of GAM337553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337553 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337553 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337553 RNA correlate with, and may be deduced from, the identity of the GAM337553 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337554 6473 GATGAGGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAGAGATGGG detected oligonucleotides of the present invention, referred to here as Genomic Address
ACAGTGACTG Messenger 337554 (GAM337554) oligonucleotides modulates expression of respective target
TATCTGTTCT genes whose function and utility is known in the art.

GATGAAGGAG GAM337554 is a novel bioinformatically detectable regulatory, non protein
ATTGTGCAGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337554 was detected
TACATGCGTA is described with additional reference to Figs. 9-15.

ACGTCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACTTCATT encoded by the human genome.

GAM337554 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337554 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337554 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337554 precursor RNA is designated SEQ ID:6473, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6473 is located from position 132744625 to position 132744712 relative to chromosome 8 on the `-` strand.

GAM337554 precursor RNA folds onto itself, forming GAM337554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337554 precursor RNA, designated SEQ ID NO: 6473, and a schematic representation of a predicted secondary folding of GAM337554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337554 folded precursor RNA yielding a GAM337554 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337554 RNA, hereby incorporated herein.

GAM337554 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337554 target RNA, herein designated GAM TARGET RNA.

GAM337554 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337554 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337554 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337554 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337554 RNA, herein designated GAM RNA, to target

binding sites on GAM337554 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337554 target RNA into GAM337554 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337554 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337554 target genes. The mRNA of each one of this plurality of GAM337554 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337554 RNA, herein designated GAM RNA, and which when bound by GAM337554 RNA causes inhibition of translation of the GAM337554 target mRNA into a corresponding GAM337554 target protein.

The mechanism of the translational inhibition exerted by GAM337554 RNA, herein designated GAM RNA, on one or more GAM337554 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337554 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337554 RNA, herein designated GAM RNA, of GAM337554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337554 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337554 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337554 RNA correlate with, and may be deduced from, the identity of the GAM337554 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337555 6430 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAAG Messenger 337555 (GAM337555) oligonucleotides modulates expression of respective target

CGGAGGTTGC genes whose function and utility is known in the art.

AGTGAGCTGA GAM337555 is a novel bioinformatically detectable regulatory, non protein

GATTGCCTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337555 was detected

CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAGAGTGAAA encoded by the human genome.

CAATGTCTC GAM337555 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337555 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337555 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337555 precursor RNA is designated SEQ ID:6430, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6430 is located from position 132911257 to position 132911355 relative to chromosome 12 on the `-` strand.

GAM337555 precursor RNA folds onto itself, forming GAM337555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337555 precursor RNA, designated SEQ ID NO: 6430, and a schematic representation of a predicted secondary folding of GAM337555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337555 folded precursor RNA yielding a GAM337555 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337555 RNA, hereby incorporated herein. Expression of GAM337555 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337555 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337555 target RNA, herein designated GAM TARGET RNA.

GAM337555 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337555 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337555 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337555 RNA is a partial or fully complementary sequence of the

nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337555 RNA, herein designated GAM RNA, to target binding sites on GAM337555 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337555 target RNA into GAM337555 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337555 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337555 target genes. The mRNA of each one of this plurality of GAM337555 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337555 RNA, herein designated GAM RNA, and which when bound by GAM337555 RNA causes inhibition of translation of the GAM337555 target mRNA into a corresponding GAM337555 target protein.

The mechanism of the translational inhibition exerted by GAM337555 RNA, herein designated GAM RNA, on one or more GAM337555 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337555 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337555 RNA, herein designated GAM RNA, of GAM337555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337555 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337555 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337555 RNA correlate with, and may be deduced from, the identity of the GAM337555 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337556 6257 CTTGAACCCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GGAAGCGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTTGCAGTGA Messenger 337556 (GAM337556) oligonucleotides modulates expression of respective target
GCTGAGATTG genes whose function and utility is known in the art.

CCTCACTGCA GAM337556 is a novel bioinformatically detectable regulatory, non protein
CTCCAGCCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337556 was detected
GGCAACAGAG is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337556 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337556 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337556 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337556 precursor RNA is designated SEQ ID:6257, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6257 is located from position 132911271 to position 132911340 relative to chromosome 12 on the `-` strand.

GAM337556 precursor RNA folds onto itself, forming GAM337556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337556 precursor RNA, designated SEQ ID NO: 6257, and a schematic representation of a predicted secondary folding of GAM337556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337556 folded precursor RNA yielding a GAM337556 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337556 RNA, hereby incorporated herein. Expression of GAM337556 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337556 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337556 target RNA, herein designated GAM TARGET RNA.

GAM337556 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337556 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337556 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337556 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337556 RNA, herein designated GAM RNA, to target binding sites on GAM337556 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337556 target RNA into GAM337556 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337556 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337556 target genes. The mRNA of each one of this plurality of GAM337556 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337556 RNA, herein designated GAM RNA, and which when bound by GAM337556 RNA causes inhibition of translation of the GAM337556 target mRNA into a corresponding GAM337556 target protein.

The mechanism of the translational inhibition exerted by GAM337556 RNA, herein designated GAM RNA, on one or more GAM337556 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337556 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337556 RNA, herein designated GAM RNA, of GAM337556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337556 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337556 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337556 RNA correlate with, and may be deduced from, the identity of the GAM337556 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337558 5770 AGGCAGGAGA ATTGCTTGAA CCTGTGAGGC AGAGGTTGCA GTGAGCTGAG ATCATGCCAC AGCACTTCAG CCTGAGCGAC AGAGCGAGAC TCCACCT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337558 (GAM337558) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337558 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337558 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337558 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337558 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337558 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337558 precursor RNA is designated SEQ ID:5770, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5770 is located from position 133234415 to position 133234511 relative to chromosome 7 on the `+` strand.

GAM337558 precursor RNA folds onto itself, forming GAM337558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337558 precursor RNA, designated SEQ ID NO: 5770, and a schematic representation of a predicted secondary folding of GAM337558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337558 folded precursor RNA yielding a GAM337558 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337558 RNA, hereby incorporated herein.

GAM337558 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337558 target RNA, herein designated GAM TARGET RNA.

GAM337558 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337558 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337558 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337558 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337558 RNA, herein designated GAM RNA, to target binding sites on GAM337558 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337558 target RNA into GAM337558 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337558 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337558 target genes. The mRNA of each one of this plurality of GAM337558 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337558 RNA, herein designated GAM RNA, and which when bound by GAM337558 RNA causes inhibition of translation of the GAM337558 target mRNA into a corresponding GAM337558 target protein.

The mechanism of the translational inhibition exerted by GAM337558 RNA, herein designated GAM RNA, on one or more GAM337558 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337558 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337558 RNA, herein designated GAM RNA, of

GAM337558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337558 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337558 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337558 RNA correlate with, and may be deduced from, the identity of the GAM337558 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337566 5930 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337566 (GAM337566) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337566 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337566 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337566 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337566 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337566 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337566 precursor RNA is designated SEQ ID:5930, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5930 is located from position 135316221 to position 135316302 relative to chromosome 10 on the `-` strand.

GAM337566 precursor RNA folds onto itself, forming GAM337566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337566 precursor RNA, designated SEQ ID NO: 5930, and

a schematic representation of a predicted secondary folding of GAM337566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337566 folded precursor RNA yielding a GAM337566 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337566 RNA, hereby incorporated herein.

GAM337566 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337566 target RNA, herein designated GAM TARGET RNA.

GAM337566 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337566 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337566 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337566 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337566 RNA, herein designated GAM RNA, to target binding sites on GAM337566 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337566 target RNA into GAM337566 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337566 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337566 target genes. The mRNA of each one of this plurality of GAM337566 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337566 RNA, herein designated GAM RNA, and which when bound by GAM337566 RNA causes inhibition of translation of the GAM337566 target mRNA into a corresponding GAM337566 target protein.

The mechanism of the translational inhibition exerted by GAM337566 RNA, herein designated GAM RNA, on one or more GAM337566 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337566 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337566 RNA, herein designated GAM RNA, of GAM337566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337566 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337566 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337566 RNA correlate with, and may be deduced from, the identity of the GAM337566 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337567 7279 TGTTCAGAAA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTCTGTTGTT detected oligonucleotides of the present invention, referred to here as Genomic Address
GTAAACATCC Messenger 337567 (GAM337567) oligonucleotides modulates expression of respective target
CCGACTGGAA genes whose function and utility is known in the art.

GCTGTAAGAC GAM337567 is a novel bioinformatically detectable regulatory, non protein
ACAGCTAAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337567 was detected
TTTCAGTCAG is described with additional reference to Figs. 9-15.

ATGTTTGCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CTACCGGCTA encoded by the human genome.

TTCACAGACA GAM337567 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GAM337567 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337567 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337567 precursor RNA is designated SEQ ID:7279, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7279 is located from position 135501500 to position 135501599 relative to chromosome 8 on the `-` strand.

GAM337567 precursor RNA folds onto itself, forming GAM337567 folded precursor

RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337567 precursor RNA, designated SEQ ID NO: 7279, and a schematic representation of a predicted secondary folding of GAM337567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337567 folded precursor RNA yielding a GAM337567 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337567 RNA, hereby incorporated herein.

GAM337567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337567 target RNA, herein designated GAM TARGET RNA.

GAM337567 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337567 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337567 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337567 RNA, herein designated GAM RNA, to target binding sites on GAM337567 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337567 target RNA into GAM337567 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337567 target genes. The mRNA of each one of this plurality of GAM337567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337567 RNA,

herein designated GAM RNA, and which when bound by GAM337567 RNA causes inhibition of translation of the GAM337567 target mRNA into a corresponding GAM337567 target protein.

The mechanism of the translational inhibition exerted by GAM337567 RNA, herein designated GAM RNA, on one or more GAM337567 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337567 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337567 RNA, herein designated GAM RNA, of GAM337567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337567 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337567 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337567 RNA correlate with, and may be deduced from, the identity of the GAM337567 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337568 6282 GAAAGTCTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTTGTAAAC detected oligonucleotides of the present invention, referred to here as Genomic Address

ATCCCCGACT Messenger 337568 (GAM337568) oligonucleotides modulates expression of respective target

GGAAGCTGTA genes whose function and utility is known in the art.

AGACACAGCT GAM337568 is a novel bioinformatically detectable regulatory, non protein

AAGCTTTCAG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337568 was detected

TCAGATGTTT is described with additional reference to Figs. 9-15.

GCTGCTACCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTATTC encoded by the human genome.

GAM337568 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337568 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337568 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337568 precursor RNA is designated SEQ ID:6282, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6282 is located from position 135501507 to position 135501593 relative to chromosome 8 on the `-` strand.

GAM337568 precursor RNA folds onto itself, forming GAM337568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337568 precursor RNA, designated SEQ ID NO: 6282, and a schematic representation of a predicted secondary folding of GAM337568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337568 folded precursor RNA yielding a GAM337568 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337568 RNA, hereby incorporated herein.

GAM337568 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337568 target RNA, herein designated GAM TARGET RNA.

GAM337568 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337568 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337568 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337568 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337568 RNA, herein designated GAM RNA, to target binding sites on GAM337568 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337568 target RNA

into GAM337568 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337568 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337568 target genes. The mRNA of each one of this plurality of GAM337568 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337568 RNA, herein designated GAM RNA, and which when bound by GAM337568 RNA causes inhibition of translation of the GAM337568 target mRNA into a corresponding GAM337568 target protein.

The mechanism of the translational inhibition exerted by GAM337568 RNA, herein designated GAM RNA, on one or more GAM337568 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337568 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337568 RNA, herein designated GAM RNA, of GAM337568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337568 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337568 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337568 RNA correlate with, and may be deduced from, the identity of the GAM337568 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337569 5811 AGTCTGTTGT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTAAACATC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCCGACTGGA Messenger 337569 (GAM337569) oligonucleotides modulates expression of respective target

AGCTGTAAGA genes whose function and utility is known in the art.

CACAGCTAAG GAM337569 is a novel bioinformatically detectable regulatory, non protein

CTTTCAGTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337569 was detected

GATGTTTGCT is described with additional reference to Figs. 9-15.

GCTACCGGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337569 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337569 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337569 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337569 precursor RNA is designated SEQ ID:5811, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5811 is located from position 135501511 to position 135501590 relative to chromosome 8 on the `-` strand.

GAM337569 precursor RNA folds onto itself, forming GAM337569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337569 precursor RNA, designated SEQ ID NO: 5811, and a schematic representation of a predicted secondary folding of GAM337569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337569 folded precursor RNA yielding a GAM337569 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337569 RNA, hereby incorporated herein.

GAM337569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337569 target RNA, herein designated GAM TARGET RNA.

GAM337569 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337569 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337569 RNA, herein designated GAM RNA, to target binding sites on GAM337569 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337569 target RNA into GAM337569 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337569 target genes. The mRNA of each one of this plurality of GAM337569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337569 RNA, herein designated GAM RNA, and which when bound by GAM337569 RNA causes inhibition of translation of the GAM337569 target mRNA into a corresponding GAM337569 target protein.

The mechanism of the translational inhibition exerted by GAM337569 RNA, herein designated GAM RNA, on one or more GAM337569 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337569 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337569 RNA, herein designated GAM RNA, of GAM337569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337569 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337569 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337569 RNA correlate with, and may be deduced from, the identity of the GAM337569 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337570 6820 GGGTACCAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TGTGCTTCCT detected oligonucleotides of the present invention, referred to here as Genomic Address

GTCCTCAGTA Messenger 337570 (GAM337570) oligonucleotides modulates expression of respective target

AAGAACTTGG genes whose function and utility is known in the art.

AGTATGTTGT GAM337570 is a novel bioinformatically detectable regulatory, non protein
TCCTCAAATA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337570 was detected
TCTTTTGATG is described with additional reference to Figs. 9-15.

AATGGGTGCT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CCAGGAGTTT encoded by the human genome.

CTACTGACAG GAM337570 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
GCTACATTTT GAM337570 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
ATCC GAM337570 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337570 precursor RNA is designated SEQ ID:6820, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6820 is located from position 137087025 to position 137087138 relative to chromosome 7 on the `-` strand.

GAM337570 precursor RNA folds onto itself, forming GAM337570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337570 precursor RNA, designated SEQ ID NO: 6820, and a schematic representation of a predicted secondary folding of GAM337570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337570 folded precursor RNA yielding a GAM337570 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337570 RNA, hereby incorporated herein.

GAM337570 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337570 target RNA, herein designated GAM TARGET RNA.

GAM337570 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337570 RNA, herein designated GAM RNA, binds complementarily to one or more

target binding sites located in untranslated regions of GAM337570 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337570 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337570 RNA, herein designated GAM RNA, to target binding sites on GAM337570 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337570 target RNA into GAM337570 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337570 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337570 target genes. The mRNA of each one of this plurality of GAM337570 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337570 RNA, herein designated GAM RNA, and which when bound by GAM337570 RNA causes inhibition of translation of the GAM337570 target mRNA into a corresponding GAM337570 target protein.

The mechanism of the translational inhibition exerted by GAM337570 RNA, herein designated GAM RNA, on one or more GAM337570 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337570 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337570 RNA, herein designated GAM RNA, of GAM337570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337570 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337570 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337570 RNA correlate with, and may be deduced from, the identity of the GAM337570 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337571 5739 AGATGTGCTT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTGTCCTCA detected oligonucleotides of the present invention, referred to here as Genomic Address
GTAAAGAACT Messenger 337571 (GAM337571) oligonucleotides modulates expression of respective target
TGGAGTATGT genes whose function and utility is known in the art.

TGTTCCTCAA GAM337571 is a novel bioinformatically detectable regulatory, non protein
ATATCTTTTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337571 was detected
ATGAATGGGT is described with additional reference to Figs. 9-15.

GCTCCAGGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TTTCTACTGA encoded by the human genome.

CAGGCTACAT GAM337571 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
TT GAM337571 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337571 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337571 precursor RNA is designated SEQ ID:5739, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5739 is located from position 137087030 to position 137087131 relative to chromosome 7 on the `-` strand.

GAM337571 precursor RNA folds onto itself, forming GAM337571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337571 precursor RNA, designated SEQ ID NO: 5739, and a schematic representation of a predicted secondary folding of GAM337571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337571 folded precursor RNA yielding a GAM337571 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337571 RNA, hereby incorporated herein.

GAM337571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337571 target RNA, herein designated GAM TARGET RNA.

GAM337571 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337571 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337571 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337571 RNA, herein designated GAM RNA, to target binding sites on GAM337571 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337571 target RNA into GAM337571 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337571 target genes. The mRNA of each one of this plurality of GAM337571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337571 RNA, herein designated GAM RNA, and which when bound by GAM337571 RNA causes inhibition of translation of the GAM337571 target mRNA into a corresponding GAM337571 target protein.

The mechanism of the translational inhibition exerted by GAM337571 RNA, herein designated GAM RNA, on one or more GAM337571 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337571 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337571 RNA, herein designated GAM RNA, of GAM337571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337571 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337571 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337571 RNA correlate with, and may be deduced from, the identity of the GAM337571 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337572 6124 CCTGTCCTCA Fig. 8 further provides a conceptual description of another novel bioinformatically
GTAAAGAACT detected oligonucleotides of the present invention, referred to here as Genomic Address
TGGAGTATGT Messenger 337572 (GAM337572) oligonucleotides modulates expression of respective target
TGTTCCTCAA genes whose function and utility is known in the art.

ATATCTTTTG GAM337572 is a novel bioinformatically detectable regulatory, non protein
ATGAATGGGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337572 was detected
GCTCCAGGAG is described with additional reference to Figs. 9-15.

TTTCTACTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGG encoded by the human genome.

GAM337572 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337572 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337572 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337572 precursor RNA is designated SEQ ID:6124, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6124 is located from position 137087038 to position 137087121 relative to chromosome 7 on the `-` strand.

GAM337572 precursor RNA folds onto itself, forming GAM337572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337572 precursor RNA, designated SEQ ID NO: 6124, and a schematic representation of a predicted secondary folding of GAM337572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337572 folded precursor

RNA yielding a GAM337572 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337572 RNA, hereby incorporated herein.

GAM337572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337572 target RNA, herein designated GAM TARGET RNA.

GAM337572 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337572 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337572 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337572 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337572 RNA, herein designated GAM RNA, to target binding sites on GAM337572 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337572 target RNA into GAM337572 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337572 target genes. The mRNA of each one of this plurality of GAM337572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337572 RNA, herein designated GAM RNA, and which when bound by GAM337572 RNA causes inhibition of translation of the GAM337572 target mRNA into a corresponding GAM337572 target protein.

The mechanism of the translational inhibition exerted by GAM337572 RNA, herein designated GAM RNA, on one or more GAM337572 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337572 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337572 RNA, herein designated GAM RNA, of GAM337572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337572 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337572 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337572 RNA correlate with, and may be deduced from, the identity of the GAM337572 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337573 5931 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337573 (GAM337573) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337573 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337573 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337573 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337573 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337573 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337573 precursor RNA is designated SEQ ID:5931, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5931 is located from position 137116843 to position 137116924 relative to chromosome 6 on the `-` strand.

GAM337573 precursor RNA folds onto itself, forming GAM337573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337573 precursor RNA, designated SEQ ID NO: 5931, and a schematic representation of a predicted secondary folding of GAM337573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337573 folded precursor RNA yielding a GAM337573 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337573 RNA, hereby incorporated herein.

GAM337573 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337573 target RNA, herein designated GAM TARGET RNA.

GAM337573 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337573 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337573 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337573 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337573 RNA, herein designated GAM RNA, to target binding sites on GAM337573 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337573 target RNA into GAM337573 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337573 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337573 target genes. The mRNA of each one of this plurality of GAM337573 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337573 RNA, herein designated GAM RNA, and which when bound by GAM337573 RNA causes inhibition of translation of the GAM337573 target mRNA into a corresponding GAM337573 target protein.

The mechanism of the translational inhibition exerted by GAM337573 RNA, herein designated GAM RNA, on one or more GAM337573 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337573 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337573 RNA, herein designated GAM RNA, of GAM337573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337573 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337573 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337573 RNA correlate with, and may be deduced from, the identity of the GAM337573 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337574 7126 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATAGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCAGGAG Messenger 337574 (GAM337574) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGTCG GAM337574 is a novel bioinformatically detectable regulatory, non protein

AGATTGCACC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337574 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCAA encoded by the human genome.

AACTCTGTCT GAM337574 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM337574 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337574 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337574 precursor RNA is designated SEQ ID:7126, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7126 is located from position 137674434 to position 137674535 relative to chromosome 7 on the `+` strand.

GAM337574 precursor RNA folds onto itself, forming GAM337574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337574 precursor RNA, designated SEQ ID NO: 7126, and a schematic representation of a predicted secondary folding of GAM337574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337574 folded precursor RNA yielding a GAM337574 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337574 RNA, hereby incorporated herein. Expression of GAM337574 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337574 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337574 target RNA, herein designated GAM TARGET RNA.

GAM337574 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337574 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337574 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337574 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337574 RNA, herein designated GAM RNA, to target binding sites on GAM337574 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337574 target RNA into GAM337574 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337574 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337574 target genes. The mRNA of each one of this plurality of GAM337574 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337574 RNA, herein designated GAM RNA, and which when bound by GAM337574 RNA causes inhibition of translation of the GAM337574 target mRNA into a corresponding GAM337574 target protein.

The mechanism of the translational inhibition exerted by GAM337574 RNA, herein designated GAM RNA, on one or more GAM337574 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337574 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337574 RNA, herein designated GAM RNA, of GAM337574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337574 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337574 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337574 RNA correlate with, and may be deduced from, the identity of the GAM337574 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337575 6341 GAGACAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCCAGAGG Messenger 337575 (GAM337575) oligonucleotides modulates expression of respective target

TGGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCGA GAM337575 is a novel bioinformatically detectable regulatory, non protein

GATTGCACCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337575 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCGAA encoded by the human genome.

ACTCCGTCTC GAM337575 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337575 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337575 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337575 precursor RNA is designated SEQ ID:6341, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6341 is located from position 138359964 to position 138360063 relative to chromosome 7 on the `+` strand.

GAM337575 precursor RNA folds onto itself, forming GAM337575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337575 precursor RNA, designated SEQ ID NO: 6341, and a schematic representation of a predicted secondary folding of GAM337575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337575 folded precursor RNA yielding a GAM337575 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337575 RNA, hereby incorporated herein. Expression of GAM337575 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337575 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337575 target RNA, herein designated GAM TARGET RNA.

GAM337575 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337575 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337575 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337575 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in

the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337575 RNA, herein designated GAM RNA, to target binding sites on GAM337575 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337575 target RNA into GAM337575 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337575 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337575 target genes. The mRNA of each one of this plurality of GAM337575 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337575 RNA, herein designated GAM RNA, and which when bound by GAM337575 RNA causes inhibition of translation of the GAM337575 target mRNA into a corresponding GAM337575 target protein.

The mechanism of the translational inhibition exerted by GAM337575 RNA, herein designated GAM RNA, on one or more GAM337575 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337575 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337575 RNA, herein designated GAM RNA, of GAM337575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337575 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337575 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337575 RNA correlate with, and may be deduced from, the identity of the GAM337575 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337576 5932 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337576 (GAM337576) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337576 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337576 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337576 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337576 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337576 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337576 precursor RNA is designated SEQ ID:5932, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5932 is located from position 138611911 to position 138611992 relative to chromosome 6 on the `+` strand.

GAM337576 precursor RNA folds onto itself, forming GAM337576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337576 precursor RNA, designated SEQ ID NO: 5932, and a schematic representation of a predicted secondary folding of GAM337576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337576 folded precursor RNA yielding a GAM337576 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337576 RNA, hereby incorporated herein.

GAM337576 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337576 target RNA, herein designated GAM TARGET RNA.

GAM337576 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337576 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337576 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337576 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337576 RNA, herein designated GAM RNA, to target binding sites on GAM337576 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337576 target RNA into GAM337576 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337576 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337576 target genes. The mRNA of each one of this plurality of GAM337576 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337576 RNA, herein designated GAM RNA, and which when bound by GAM337576 RNA causes inhibition of translation of the GAM337576 target mRNA into a corresponding GAM337576 target protein.

The mechanism of the translational inhibition exerted by GAM337576 RNA, herein designated GAM RNA, on one or more GAM337576 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337576 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337576 RNA, herein designated GAM RNA, of GAM337576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337576 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337576 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337576 RNA correlate with, and may be deduced from, the identity of the GAM337576 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337578 5933 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337578 (GAM337578) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337578 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337578 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337578 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337578 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337578 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337578 precursor RNA is designated SEQ ID:5933, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5933 is located from position 138845677 to position 138845758 relative to chromosome 8 on the `-` strand.

GAM337578 precursor RNA folds onto itself, forming GAM337578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337578 precursor RNA, designated SEQ ID NO: 5933, and a schematic representation of a predicted secondary folding of GAM337578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337578 folded precursor RNA yielding a GAM337578 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337578 RNA, hereby incorporated herein.

GAM337578 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337578 target RNA, herein designated GAM TARGET RNA.

GAM337578 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337578 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337578 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337578 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337578 RNA, herein designated GAM RNA, to target binding sites on GAM337578 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337578 target RNA into GAM337578 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337578 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337578 target genes. The mRNA of each one of this plurality of GAM337578 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337578 RNA, herein designated GAM RNA, and which when bound by GAM337578 RNA causes inhibition of translation of the GAM337578 target mRNA into a corresponding GAM337578 target protein.

The mechanism of the translational inhibition exerted by GAM337578 RNA, herein designated GAM RNA, on one or more GAM337578 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337578 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337578 RNA, herein designated GAM RNA, of GAM337578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337578 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337578 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337578 RNA correlate with, and may be deduced from, the identity of the GAM337578 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337579 6428 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically
AATTGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
GCCCAGGAGG Messenger 337579 (GAM337579) oligonucleotides modulates expression of respective target
CGGAGATTGC genes whose function and utility is known in the art.

AGTGAGCCGA GAM337579 is a novel bioinformatically detectable regulatory, non protein
GATCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337579 was detected
CTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CAGAGTGAGA encoded by the human genome.

CTCTGTCTC GAM337579 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337579 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337579 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337579 precursor RNA is designated SEQ ID:6428, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6428 is located from position 139758518 to position 139758616 relative to chromosome 5 on the `-` strand.

GAM337579 precursor RNA folds onto itself, forming GAM337579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337579 precursor RNA, designated SEQ ID NO: 6428, and a schematic representation of a predicted secondary folding of GAM337579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337579 folded precursor RNA yielding a GAM337579 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA

precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337579 RNA, hereby incorporated herein. Expression of GAM337579 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337579 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337579 target RNA, herein designated GAM TARGET RNA.

GAM337579 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337579 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337579 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337579 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337579 RNA, herein designated GAM RNA, to target binding sites on GAM337579 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337579 target RNA into GAM337579 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337579 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337579 target genes. The mRNA of each one of this plurality of GAM337579 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337579 RNA, herein designated GAM RNA, and which when bound by GAM337579 RNA causes inhibition of translation of the GAM337579 target mRNA into a corresponding GAM337579 target protein.

The mechanism of the translational inhibition exerted by GAM337579 RNA, herein designated GAM RNA, on one or more GAM337579 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337579 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337579 RNA, herein designated GAM RNA, of GAM337579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337579 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337579 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337579 RNA correlate with, and may be deduced from, the identity of the GAM337579 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337580 6967 TAGACTTGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

AGGGAACCTT detected oligonucleotides of the present invention, referred to here as Genomic Address

ACAGTCCTCT Messenger 337580 (GAM337580) oligonucleotides modulates expression of respective target

ACTCCAGCTC genes whose function and utility is known in the art.

CCTGATTTTA GAM337580 is a novel bioinformatically detectable regulatory, non protein

CAGATCGGGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337580 was detected

ACCCACCATT is described with additional reference to Figs. 9-15.

CAGGGCTGAT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACAAACTCA encoded by the human genome.

GGTCTCTTCA GAM337580 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CCCTCAGTCT GAM337580 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

G GAM337580 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337580 precursor RNA is designated SEQ ID:6967, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6967 is located from position 140494572 to position 140494682 relative to chromosome 7 on the `+` strand.

GAM337580 precursor RNA folds onto itself, forming GAM337580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337580 precursor RNA, designated SEQ ID NO: 6967, and a schematic representation of a predicted secondary folding of GAM337580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337580 folded precursor RNA yielding a GAM337580 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337580 RNA, hereby incorporated herein.

GAM337580 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337580 target RNA, herein designated GAM TARGET RNA.

GAM337580 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337580 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337580 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337580 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337580 RNA, herein designated GAM RNA, to target binding sites on GAM337580 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337580 target RNA into GAM337580 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337580 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337580 target genes. The mRNA of each one of this plurality of GAM337580 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337580 RNA, herein designated GAM RNA, and which when bound by GAM337580 RNA causes inhibition of translation of the GAM337580 target mRNA into a corresponding GAM337580 target protein.

The mechanism of the translational inhibition exerted by GAM337580 RNA, herein designated GAM RNA, on one or more GAM337580 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337580 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337580 RNA, herein designated GAM RNA, of GAM337580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337580 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337580 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337580 RNA correlate with, and may be deduced from, the identity of the GAM337580 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337581 5663 AAGAGGCCTA Fig. 8 further provides a conceptual description of another novel bioinformatically

AAAGTTTAAT detected oligonucleotides of the present invention, referred to here as Genomic Address

GCCAGACCTT Messenger 337581 (GAM337581) oligonucleotides modulates expression of respective target

AGGGGCAGGA genes whose function and utility is known in the art.

TGGAGCAGGG GAM337581 is a novel bioinformatically detectable regulatory, non protein

CTAAAAGATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337581 was detected

TCTCTTTGGG is described with additional reference to Figs. 9-15.

CCTGTCTGCC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCTTTCCTT encoded by the human genome.

CCTTCCTTTT GAM337581 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CTTTCCTTTT GAM337581 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337581 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337581 precursor RNA is designated SEQ ID:5663, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5663 is located from position 140505904 to position 140506013

relative to chromosome 7 on the `+` strand.

GAM337581 precursor RNA folds onto itself, forming GAM337581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337581 precursor RNA, designated SEQ ID NO: 5663, and a schematic representation of a predicted secondary folding of GAM337581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337581 folded precursor RNA yielding a GAM337581 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337581 RNA, hereby incorporated herein.

GAM337581 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337581 target RNA, herein designated GAM TARGET RNA.

GAM337581 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337581 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337581 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337581 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337581 RNA, herein designated GAM RNA, to target binding sites on GAM337581 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337581 target RNA into GAM337581 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337581 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337581 target genes. The mRNA of each one of this plurality of GAM337581 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337581 RNA, herein designated GAM RNA, and which when bound by GAM337581 RNA causes inhibition of translation of the GAM337581 target mRNA into a corresponding GAM337581 target protein.

The mechanism of the translational inhibition exerted by GAM337581 RNA, herein designated GAM RNA, on one or more GAM337581 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337581 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337581 RNA, herein designated GAM RNA, of GAM337581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337581 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337581 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337581 RNA correlate with, and may be deduced from, the identity of the GAM337581 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337584 6264 CTTGACACCT Fig. 8 further provides a conceptual description of another novel bioinformatically
CCTGTCCAGT detected oligonucleotides of the present invention, referred to here as Genomic Address
ACTGTCTTGA Messenger 337584 (GAM337584) oligonucleotides modulates expression of respective target
TGCCTGCCCC genes whose function and utility is known in the art.

ATAAAGTGAC GAM337584 is a novel bioinformatically detectable regulatory, non protein
TCTGCGATGG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337584 was detected
GCAAGTGTTA is described with additional reference to Figs. 9-15.

TGATCAGATT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GGAGGGTGTA encoded by the human genome.

AAG GAM337584 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337584 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337584 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337584 precursor RNA is designated SEQ ID:6264, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6264 is located from position 141088822 to position 141088914 relative to chromosome 8 on the `-` strand.

GAM337584 precursor RNA folds onto itself, forming GAM337584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337584 precursor RNA, designated SEQ ID NO: 6264, and a schematic representation of a predicted secondary folding of GAM337584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337584 folded precursor RNA yielding a GAM337584 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337584 RNA, hereby incorporated herein.

GAM337584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337584 target RNA, herein designated GAM TARGET RNA.

GAM337584 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337584 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337584 RNA, herein designated GAM RNA, to target

binding sites on GAM337584 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337584 target RNA into GAM337584 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337584 target genes. The mRNA of each one of this plurality of GAM337584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337584 RNA, herein designated GAM RNA, and which when bound by GAM337584 RNA causes inhibition of translation of the GAM337584 target mRNA into a corresponding GAM337584 target protein.

The mechanism of the translational inhibition exerted by GAM337584 RNA, herein designated GAM RNA, on one or more GAM337584 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337584 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337584 RNA, herein designated GAM RNA, of GAM337584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337584 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337584 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337584 RNA correlate with, and may be deduced from, the identity of the GAM337584 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337585 5684 ACACCTCCTG Fig. 8 further provides a conceptual description of another novel bioinformatically

TCCAGTACTG detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTTGATGCC Messenger 337585 (GAM337585) oligonucleotides modulates expression of respective target

TGCCCCATAA genes whose function and utility is known in the art.

AGTGACTCTG GAM337585 is a novel bioinformatically detectable regulatory, non protein

CGATGGGCAA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337585 was detected

GTGTTATGAT is described with additional reference to Figs. 9-15.

CAGATTGGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GGTGT encoded by the human genome.

GAM337585 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337585 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337585 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337585 precursor RNA is designated SEQ ID:5684, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5684 is located from position 141088826 to position 141088910 relative to chromosome 8 on the `-` strand.

GAM337585 precursor RNA folds onto itself, forming GAM337585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337585 precursor RNA, designated SEQ ID NO: 5684, and a schematic representation of a predicted secondary folding of GAM337585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337585 folded precursor RNA yielding a GAM337585 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337585 RNA, hereby incorporated herein.

GAM337585 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337585 target RNA, herein designated GAM TARGET RNA.

GAM337585 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337585 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337585 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337585 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337585 RNA, herein designated GAM RNA, to target binding sites on GAM337585 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337585 target RNA into GAM337585 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337585 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337585 target genes. The mRNA of each one of this plurality of GAM337585 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337585 RNA, herein designated GAM RNA, and which when bound by GAM337585 RNA causes inhibition of translation of the GAM337585 target mRNA into a corresponding GAM337585 target protein.

The mechanism of the translational inhibition exerted by GAM337585 RNA, herein designated GAM RNA, on one or more GAM337585 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337585 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337585 RNA, herein designated GAM RNA, of GAM337585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337585 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337585 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337585 RNA correlate with, and may be deduced from, the identity of the GAM337585 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337586 6466 GAGTTTGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

TCTGTCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCTG Messenger 337586 (GAM337586) oligonucleotides modulates expression of respective target

AAACCCCAGC genes whose function and utility is known in the art.

TCTGTAAACA GAM337586 is a novel bioinformatically detectable regulatory, non protein
ATACAAAAAT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337586 was detected

TAGCTGGGCG is described with additional reference to Figs. 9-15.

TGGCGGTCTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TGCCTACAGT encoded by the human genome.

CCCAGCTACT GAM337586 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

C GAM337586 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337586 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337586 precursor RNA is designated SEQ ID:6466, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6466 is located from position 141572888 to position 141572988 relative to chromosome 8 on the `+` strand.

GAM337586 precursor RNA folds onto itself, forming GAM337586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337586 precursor RNA, designated SEQ ID NO: 6466, and a schematic representation of a predicted secondary folding of GAM337586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337586 folded precursor RNA yielding a GAM337586 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337586 RNA, hereby incorporated herein.

GAM337586 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337586 target RNA, herein designated GAM TARGET RNA.

GAM337586 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337586 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337586 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337586 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337586 RNA, herein designated GAM RNA, to target binding sites on GAM337586 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337586 target RNA into GAM337586 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337586 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337586 target genes. The mRNA of each one of this plurality of GAM337586 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337586 RNA, herein designated GAM RNA, and which when bound by GAM337586 RNA causes inhibition of translation of the GAM337586 target mRNA into a corresponding GAM337586 target protein.

The mechanism of the translational inhibition exerted by GAM337586 RNA, herein designated GAM RNA, on one or more GAM337586 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337586 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337586 RNA, herein designated GAM RNA, of GAM337586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337586 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337586 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337586

RNA correlate with, and may be deduced from, the identity of the GAM337586 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337587 6241 CTGTCTGGGC Fig. 8 further provides a conceptual description of another novel bioinformatically
AACATGCTGA detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCCAGCT Messenger 337587 (GAM337587) oligonucleotides modulates expression of respective target
CTGTAAACAA genes whose function and utility is known in the art.

TACAAAAATT GAM337587 is a novel bioinformatically detectable regulatory, non protein
AGCTGGGCGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337587 was detected
GGCGGTCTGT is described with additional reference to Figs. 9-15.

GCCTACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337587 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337587 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337587 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337587 precursor RNA is designated SEQ ID:6241, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6241 is located from position 141572899 to position 141572976 relative to chromosome 8 on the `+` strand.

GAM337587 precursor RNA folds onto itself, forming GAM337587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337587 precursor RNA, designated SEQ ID NO: 6241, and a schematic representation of a predicted secondary folding of GAM337587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337587 folded precursor RNA yielding a GAM337587 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337587 RNA, hereby incorporated herein.

GAM337587 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337587 target RNA, herein designated GAM TARGET RNA.

GAM337587 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337587 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337587 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337587 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337587 RNA, herein designated GAM RNA, to target binding sites on GAM337587 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337587 target RNA into GAM337587 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337587 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337587 target genes. The mRNA of each one of this plurality of GAM337587 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337587 RNA, herein designated GAM RNA, and which when bound by GAM337587 RNA causes inhibition of translation of the GAM337587 target mRNA into a corresponding GAM337587 target protein.

The mechanism of the translational inhibition exerted by GAM337587 RNA, herein designated GAM RNA, on one or more GAM337587 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337587 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337587 RNA, herein designated GAM RNA, of GAM337587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337587 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337587 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337587 RNA correlate with, and may be deduced from, the identity of the GAM337587 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337588 7290 TTCACGCTTG Fig. 8 further provides a conceptual description of another novel bioinformatically
AACCTGGGAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GTGGAGGTTG Messenger 337588 (GAM337588) oligonucleotides modulates expression of respective target
CAGTGAGCCG genes whose function and utility is known in the art.

AGATCATGCC GAM337588 is a novel bioinformatically detectable regulatory, non protein
ATTGCACTCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337588 was detected
AGCCTGGGCA is described with additional reference to Figs. 9-15.

ACAAGAGTGA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
A encoded by the human genome.

GAM337588 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337588 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337588 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337588 precursor RNA is designated SEQ ID:7290, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7290 is located from position 142629616 to position 142629696 relative to chromosome 1 on the `-` strand.

GAM337588 precursor RNA folds onto itself, forming GAM337588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337588 precursor RNA, designated SEQ ID NO: 7290, and a schematic representation of a predicted secondary folding of GAM337588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337588 folded precursor RNA yielding a GAM337588 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337588 RNA, hereby incorporated herein. Expression of GAM337588 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337588 target RNA, herein designated GAM TARGET RNA.

GAM337588 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337588 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337588 RNA, herein designated GAM RNA, to target binding sites on GAM337588 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337588 target RNA into GAM337588 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337588 target genes. The mRNA of each one of this plurality of GAM337588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337588 RNA, herein designated GAM RNA, and which when bound by GAM337588 RNA causes inhibition of translation of the GAM337588 target mRNA into a corresponding GAM337588 target protein.

The mechanism of the translational inhibition exerted by GAM337588 RNA, herein designated GAM RNA, on one or more GAM337588 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337588 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337588 RNA, herein designated GAM RNA, of GAM337588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337588 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337588 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337588 RNA correlate with, and may be deduced from, the identity of the GAM337588 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337589 5934 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337589 (GAM337589) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337589 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337589 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337589 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337589 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337589 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337589 precursor RNA is designated SEQ ID:5934, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5934 is located from position 142638211 to position 142638292 relative to chromosome 8 on the `-` strand.

GAM337589 precursor RNA folds onto itself, forming GAM337589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337589 precursor RNA, designated SEQ ID NO: 5934, and a schematic representation of a predicted secondary folding of GAM337589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337589 folded precursor RNA yielding a GAM337589 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337589 RNA, hereby incorporated herein.

GAM337589 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337589 target RNA, herein designated GAM TARGET RNA.

GAM337589 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337589 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337589 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337589 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337589 RNA, herein designated GAM RNA, to target binding sites on GAM337589 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337589 target RNA into GAM337589 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337589 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337589 target genes. The mRNA of each one of this plurality of GAM337589 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337589 RNA, herein designated GAM RNA, and which when bound by GAM337589 RNA causes inhibition of translation of the GAM337589 target mRNA into a corresponding GAM337589 target protein.

The mechanism of the translational inhibition exerted by GAM337589 RNA, herein designated GAM RNA, on one or more GAM337589 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337589 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337589 RNA, herein designated GAM RNA, of GAM337589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337589 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337589 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337589 RNA correlate with, and may be deduced from, the identity of the GAM337589 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337590 7177 TGAGGTAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCACATG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 337590 (GAM337590) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM337590 is a novel bioinformatically detectable regulatory, non protein

AGACCACGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337590 was detected

ATTGCACACC is described with additional reference to Figs. 9-15.

AACCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGACTGAG encoded by the human genome.

ACTCTGTCTC GAM337590 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

A GAM337590 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337590 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337590 precursor RNA is designated SEQ

ID:7177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7177 is located from position 142719208 to position 142719308 relative to chromosome 7 on the `+` strand.

GAM337590 precursor RNA folds onto itself, forming GAM337590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337590 precursor RNA, designated SEQ ID NO: 7177, and a schematic representation of a predicted secondary folding of GAM337590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337590 folded precursor RNA yielding a GAM337590 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337590 RNA, hereby incorporated herein.

GAM337590 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337590 target RNA, herein designated GAM TARGET RNA.

GAM337590 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337590 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337590 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337590 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337590 RNA, herein designated GAM RNA, to target binding sites on GAM337590 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337590 target RNA into GAM337590 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337590 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337590 target genes. The mRNA of each one of this plurality of GAM337590 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337590 RNA, herein designated GAM RNA, and which when bound by GAM337590 RNA causes inhibition of translation of the GAM337590 target mRNA into a corresponding GAM337590 target protein.

The mechanism of the translational inhibition exerted by GAM337590 RNA, herein designated GAM RNA, on one or more GAM337590 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337590 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337590 RNA, herein designated GAM RNA, of GAM337590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337590 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337590 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337590 RNA correlate with, and may be deduced from, the identity of the GAM337590 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337591 7302 TTCCGATAAA Fig. 8 further provides a conceptual description of another novel bioinformatically

AGAGTTGCCA detected oligonucleotides of the present invention, referred to here as Genomic Address

AGACCCTTGG Messenger 337591 (GAM337591) oligonucleotides modulates expression of respective target

AAGCTCCACA genes whose function and utility is known in the art.

GTAATGGGTG GAM337591 is a novel bioinformatically detectable regulatory, non protein

TCTTTCGGTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337591 was detected

TCCTGATGAG is described with additional reference to Figs. 9-15.

ATGACTGGTG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GCTGGGGGCC encoded by the human genome.

TCGAGGAGAG GAM337591 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

TTTCAAGTTG GAM337591 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAG GAM337591 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337591 precursor RNA is designated SEQ ID:7302, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7302 is located from position 143679711 to position 143679823 relative to chromosome 7 on the `+` strand.

GAM337591 precursor RNA folds onto itself, forming GAM337591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337591 precursor RNA, designated SEQ ID NO: 7302, and a schematic representation of a predicted secondary folding of GAM337591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337591 folded precursor RNA yielding a GAM337591 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337591 RNA, hereby incorporated herein.

GAM337591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337591 target RNA, herein designated GAM TARGET RNA.

GAM337591 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337591 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region

or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337591 RNA, herein designated GAM RNA, to target binding sites on GAM337591 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337591 target RNA into GAM337591 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337591 target genes. The mRNA of each one of this plurality of GAM337591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337591 RNA, herein designated GAM RNA, and which when bound by GAM337591 RNA causes inhibition of translation of the GAM337591 target mRNA into a corresponding GAM337591 target protein.

The mechanism of the translational inhibition exerted by GAM337591 RNA, herein designated GAM RNA, on one or more GAM337591 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337591 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337591 RNA, herein designated GAM RNA, of GAM337591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337591 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337591 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337591 RNA correlate with, and may be deduced from, the identity of the GAM337591 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337592 6932 GTGTTGAGAT Fig. 8 further provides a conceptual description of another novel bioinformatically

CCTTTCACAG detected oligonucleotides of the present invention, referred to here as Genomic Address

TTGTGGTTAC Messenger 337592 (GAM337592) oligonucleotides modulates expression of respective target

AATTACGTTC genes whose function and utility is known in the art.

ACAAGCTACA GAM337592 is a novel bioinformatically detectable regulatory, non protein
CCTGCCATGA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337592 was detected
GAGAATACTT is described with additional reference to Figs. 9-15.

GGCAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337592 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337592 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337592 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337592 precursor RNA is designated SEQ ID:6932, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6932 is located from position 143693599 to position 143693673 relative to chromosome 7 on the `+` strand.

GAM337592 precursor RNA folds onto itself, forming GAM337592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337592 precursor RNA, designated SEQ ID NO: 6932, and a schematic representation of a predicted secondary folding of GAM337592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337592 folded precursor RNA yielding a GAM337592 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337592 RNA, hereby incorporated herein.

GAM337592 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337592 target RNA, herein designated GAM TARGET RNA.

GAM337592 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the

nucleotide sequence of GAM337592 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337592 RNA, herein designated GAM RNA, to target binding sites on GAM337592 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337592 target RNA into GAM337592 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337592 target genes. The mRNA of each one of this plurality of GAM337592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337592 RNA, herein designated GAM RNA, and which when bound by GAM337592 RNA causes inhibition of translation of the GAM337592 target mRNA into a corresponding GAM337592 target protein.

The mechanism of the translational inhibition exerted by GAM337592 RNA, herein designated GAM RNA, on one or more GAM337592 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337592 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337592 RNA, herein designated GAM RNA, of GAM337592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337592 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337592 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337592 RNA correlate with, and may be deduced from, the identity of the GAM337592 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337593 5935 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337593 (GAM337593) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337593 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337593 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337593 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337593 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337593 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337593 precursor RNA is designated SEQ ID:5935, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5935 is located from position 144215955 to position 144216036 relative to chromosome X on the `-` strand.

GAM337593 precursor RNA folds onto itself, forming GAM337593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337593 precursor RNA, designated SEQ ID NO: 5935, and a schematic representation of a predicted secondary folding of GAM337593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337593 folded precursor RNA yielding a GAM337593 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337593 RNA, hereby incorporated herein.

GAM337593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337593 target RNA, herein designated GAM TARGET RNA.

GAM337593 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337593 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337593 RNA, herein designated GAM RNA, to target binding sites on GAM337593 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337593 target RNA into GAM337593 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337593 target genes. The mRNA of each one of this plurality of GAM337593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337593 RNA, herein designated GAM RNA, and which when bound by GAM337593 RNA causes inhibition of translation of the GAM337593 target mRNA into a corresponding GAM337593 target protein.

The mechanism of the translational inhibition exerted by GAM337593 RNA, herein designated GAM RNA, on one or more GAM337593 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337593 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337593 RNA, herein designated GAM RNA, of GAM337593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337593 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337593 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337593 RNA correlate with, and may be deduced from, the identity of the GAM337593 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337594 5936 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337594 (GAM337594) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337594 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337594 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337594 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337594 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337594 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337594 precursor RNA is designated SEQ ID:5936, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5936 is located from position 145082321 to position 145082402 relative to chromosome 6 on the `-` strand.

GAM337594 precursor RNA folds onto itself, forming GAM337594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337594 precursor RNA, designated SEQ ID NO: 5936, and a schematic representation of a predicted secondary folding of GAM337594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337594 folded precursor RNA yielding a GAM337594 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337594 RNA, hereby incorporated herein.

GAM337594 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337594 target RNA, herein designated GAM TARGET RNA.

GAM337594 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337594 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337594 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337594 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337594 RNA, herein designated GAM RNA, to target binding sites on GAM337594 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337594 target RNA into GAM337594 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337594 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337594 target genes. The mRNA of each one of this plurality of GAM337594 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337594 RNA, herein designated GAM RNA, and which when bound by GAM337594 RNA causes inhibition of translation of the GAM337594 target mRNA into a corresponding GAM337594 target protein.

The mechanism of the translational inhibition exerted by GAM337594 RNA, herein designated GAM RNA, on one or more GAM337594 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337594 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337594 RNA, herein designated GAM RNA, of GAM337594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337594 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337594 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337594 RNA correlate with, and may be deduced from, the identity of the GAM337594 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337595 5937 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337595 (GAM337595) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337595 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337595 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337595 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337595 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337595 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337595 precursor RNA is designated SEQ ID:5937, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5937 is located from position 146634571 to position 146634652 relative to chromosome 4 on the `+` strand.

GAM337595 precursor RNA folds onto itself, forming GAM337595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337595 precursor RNA, designated SEQ ID NO: 5937, and a schematic representation of a predicted secondary folding of GAM337595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337595 folded precursor RNA yielding a GAM337595 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337595 RNA, hereby incorporated herein.

GAM337595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337595 target RNA, herein designated GAM TARGET RNA.

GAM337595 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337595 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337595 RNA, herein designated GAM RNA, to target binding sites on GAM337595 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337595 target RNA into GAM337595 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337595 target genes. The mRNA of each one of this plurality of GAM337595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337595 RNA, herein designated GAM RNA, and which when bound by GAM337595 RNA causes inhibition of translation of the GAM337595 target mRNA into a corresponding GAM337595 target protein.

The mechanism of the translational inhibition exerted by GAM337595 RNA, herein designated GAM RNA, on one or more GAM337595 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337595 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337595 RNA, herein designated GAM RNA, of GAM337595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth
in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337595 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337595 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337595 RNA correlate with, and may be deduced from, the identity of the GAM337595 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337597 7108 TGAGGCAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically
GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address
AACCCAGGAG Messenger 337597 (GAM337597) oligonucleotides modulates expression of respective target
GCAGAGGTTG genes whose function and utility is known in the art.

AAGTGAGCCG GAM337597 is a novel bioinformatically detectable regulatory, non protein
AGATCGTGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337597 was detected
ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAAGAGCGA encoded by the human genome.

AACTCCGTCT GAM337597 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
CA GAM337597 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337597 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337597 precursor RNA is designated SEQ ID:7108, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7108 is located from position 148136535 to position 148136636 relative to chromosome 7 on the `-` strand.

GAM337597 precursor RNA folds onto itself, forming GAM337597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337597 precursor RNA, designated SEQ ID NO: 7108, and a schematic representation of a predicted secondary folding of GAM337597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337597 folded precursor RNA yielding a GAM337597 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337597 RNA, hereby incorporated herein. Expression of GAM337597 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337597 target RNA, herein designated GAM TARGET RNA.

GAM337597 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337597 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337597 RNA, herein designated GAM RNA, to target binding sites on GAM337597 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337597 target RNA into GAM337597 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337597 target genes. The mRNA of each one of this plurality of GAM337597 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337597 RNA,

herein designated GAM RNA, and which when bound by GAM337597 RNA causes inhibition of translation of the GAM337597 target mRNA into a corresponding GAM337597 target protein.

The mechanism of the translational inhibition exerted by GAM337597 RNA, herein designated GAM RNA, on one or more GAM337597 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337597 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337597 RNA, herein designated GAM RNA, of GAM337597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337597 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337597 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337597 RNA correlate with, and may be deduced from, the identity of the GAM337597 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337598 6370 GAGGCAAGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCCAGGAGG Messenger 337598 (GAM337598) oligonucleotides modulates expression of respective target

CAGAGGTTGA genes whose function and utility is known in the art.

AGTGAGCCGA GAM337598 is a novel bioinformatically detectable regulatory, non protein

GATCGTGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337598 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAAGAGCGAA encoded by the human genome.

ACTCCGTCTC GAM337598 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337598 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337598 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337598 precursor RNA is designated SEQ ID:6370, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6370 is located from position 148136536 to position 148136635 relative to chromosome 7 on the `-` strand.

GAM337598 precursor RNA folds onto itself, forming GAM337598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337598 precursor RNA, designated SEQ ID NO: 6370, and a schematic representation of a predicted secondary folding of GAM337598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337598 folded precursor RNA yielding a GAM337598 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337598 RNA, hereby incorporated herein. Expression of GAM337598 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337598 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337598 target RNA, herein designated GAM TARGET RNA.

GAM337598 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337598 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337598 RNA, herein designated GAM RNA, to target binding sites on GAM337598 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337598 target RNA into GAM337598 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337598 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337598 target genes. The mRNA of each one of this plurality of GAM337598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337598 RNA, herein designated GAM RNA, and which when bound by GAM337598 RNA causes inhibition of translation of the GAM337598 target mRNA into a corresponding GAM337598 target protein.

The mechanism of the translational inhibition exerted by GAM337598 RNA, herein designated GAM RNA, on one or more GAM337598 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337598 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337598 RNA, herein designated GAM RNA, of GAM337598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337598 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337598 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337598 RNA correlate with, and may be deduced from, the identity of the GAM337598 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337599 6963 TACTTGTGCA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGTTTGTTAA detected oligonucleotides of the present invention, referred to here as Genomic Address

ATGGGTTTAT Messenger 337599 (GAM337599) oligonucleotides modulates expression of respective target

TGTGTAATGC genes whose function and utility is known in the art.

TGAGATTTGG GAM337599 is a novel bioinformatically detectable regulatory, non protein

GCTTCTAATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337599 was detected

ATCCCATTGC is described with additional reference to Figs. 9-15.

CCAAGTAGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AACATAGTAC encoded by the human genome.

CTAATAGAAT GAM337599 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CAATAGGTA GAM337599 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337599 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337599 precursor RNA is designated SEQ ID:6963, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6963 is located from position 148237793 to position 148237901 relative to chromosome X on the `+` strand.

GAM337599 precursor RNA folds onto itself, forming GAM337599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337599 precursor RNA, designated SEQ ID NO: 6963, and a schematic representation of a predicted secondary folding of GAM337599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337599 folded precursor RNA yielding a GAM337599 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337599 RNA, hereby incorporated herein.

GAM337599 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337599 target RNA, herein designated GAM TARGET RNA.

GAM337599 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337599 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337599 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337599 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337599 RNA, herein designated GAM RNA, to target binding sites on GAM337599 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337599 target RNA into GAM337599 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337599 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337599 target genes. The mRNA of each one of this plurality of GAM337599 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337599 RNA, herein designated GAM RNA, and which when bound by GAM337599 RNA causes inhibition of translation of the GAM337599 target mRNA into a corresponding GAM337599 target protein.

The mechanism of the translational inhibition exerted by GAM337599 RNA, herein designated GAM RNA, on one or more GAM337599 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337599 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337599 RNA, herein designated GAM RNA, of GAM337599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337599 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337599 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337599 RNA correlate with, and may be deduced from, the identity of the GAM337599 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337601 6480 GCAAAGCACT Fig. 8 further provides a conceptual description of another novel bioinformatically

TACTTCTTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

CAGATGAGAC Messenger 337601 (GAM337601) oligonucleotides modulates expression of respective target

TGAGACATAG genes whose function and utility is known in the art.

TTACAAAGTC GAM337601 is a novel bioinformatically detectable regulatory, non protein

TCAGTTTCCT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337601 was detected

CTGCAAACAG is described with additional reference to Figs. 9-15.

TTGTAAGTGC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

TTAGC encoded by the human genome.

GAM337601 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337601 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337601 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337601 precursor RNA is designated SEQ ID:6480, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6480 is located from position 148876208 to position 148876292 relative to chromosome X on the `+` strand.

GAM337601 precursor RNA folds onto itself, forming GAM337601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337601 precursor RNA, designated SEQ ID NO: 6480, and a schematic representation of a predicted secondary folding of GAM337601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337601 folded precursor RNA yielding a GAM337601 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337601 RNA, hereby incorporated herein.

GAM337601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337601 target RNA, herein designated GAM TARGET RNA.

GAM337601 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337601 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337601 RNA, herein designated GAM RNA, to target binding sites on GAM337601 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337601 target RNA into GAM337601 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337601 target genes. The mRNA of each one of this plurality of GAM337601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337601 RNA, herein designated GAM RNA, and which when bound by GAM337601 RNA causes inhibition of translation of the GAM337601 target mRNA into a corresponding GAM337601 target protein.

The mechanism of the translational inhibition exerted by GAM337601 RNA, herein designated GAM RNA, on one or more GAM337601 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337601 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337601 RNA, herein designated GAM RNA, of GAM337601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337601 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337601 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337601 RNA correlate with, and may be deduced from, the identity of the GAM337601 target gene

inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337602 5665 AAGCACTTAC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTCTTTGCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
ATGAGACTGA Messenger 337602 (GAM337602) oligonucleotides modulates expression of respective target
GACATAGTTA genes whose function and utility is known in the art.

CAAAGTCTCA GAM337602 is a novel bioinformatically detectable regulatory, non protein
GTTTCCTCTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337602 was detected
CAAACAGTTG is described with additional reference to Figs. 9-15.

TAAGTGCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
encoded by the human genome.

GAM337602 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337602 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes
GAM337602 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337602 precursor RNA is designated SEQ ID:5665, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5665 is located from position 148876211 to position 148876289 relative to chromosome X on the `+` strand.

GAM337602 precursor RNA folds onto itself, forming GAM337602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337602 precursor RNA, designated SEQ ID NO: 5665, and a schematic representation of a predicted secondary folding of GAM337602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337602 folded precursor RNA yielding a GAM337602 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337602 RNA, hereby incorporated herein.

GAM337602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337602 target RNA, herein designated GAM TARGET RNA.

GAM337602 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337602 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337602 RNA, herein designated GAM RNA, to target binding sites on GAM337602 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337602 target RNA into GAM337602 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337602 target genes. The mRNA of each one of this plurality of GAM337602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337602 RNA, herein designated GAM RNA, and which when bound by GAM337602 RNA causes inhibition of translation of the GAM337602 target mRNA into a corresponding GAM337602 target protein.

The mechanism of the translational inhibition exerted by GAM337602 RNA, herein designated GAM RNA, on one or more GAM337602 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337602 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337602 RNA, herein designated GAM RNA, of GAM337602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING

SITE-II and BINDING SITE-III of Fig. 8, found on GAM337602 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337602 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337602 RNA correlate with, and may be deduced from, the identity of the GAM337602 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337605 7330 TTGGAGTTAG Fig. 8 further provides a conceptual description of another novel bioinformatically
GATCCCCAGG detected oligonucleotides of the present invention, referred to here as Genomic Address
TTCTAGTCCT Messenger 337605 (GAM337605) oligonucleotides modulates expression of respective target
GAGTCTGGAC genes whose function and utility is known in the art.

TCTGGGTAAG GAM337605 is a novel bioinformatically detectable regulatory, non protein
TGACTCAGCG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337605 was detected
ATTCTGAACC is described with additional reference to Figs. 9-15.

TTGTTTCCTT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ATCTTTGA encoded by the human genome.

GAM337605 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337605 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337605 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337605 precursor RNA is designated SEQ ID:7330, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7330 is located from position 150253092 to position 150253179 relative to chromosome 7 on the `-` strand.

GAM337605 precursor RNA folds onto itself, forming GAM337605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337605 precursor RNA, designated SEQ ID NO: 7330, and a schematic representation of a predicted secondary folding of GAM337605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337605 folded precursor

RNA yielding a GAM337605 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337605 RNA, hereby incorporated herein.

GAM337605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337605 target RNA, herein designated GAM TARGET RNA.

GAM337605 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337605 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337605 RNA, herein designated GAM RNA, to target binding sites on GAM337605 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337605 target RNA into GAM337605 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337605 target genes. The mRNA of each one of this plurality of GAM337605 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337605 RNA, herein designated GAM RNA, and which when bound by GAM337605 RNA causes inhibition of translation of the GAM337605 target mRNA into a corresponding GAM337605 target protein.

The mechanism of the translational inhibition exerted by GAM337605 RNA, herein designated GAM RNA, on one or more GAM337605 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337605 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337605 RNA, herein designated GAM RNA, of GAM337605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337605 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337605 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337605 RNA correlate with, and may be deduced from, the identity of the GAM337605 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337606 5978 ATTACTAGGT TTAAATAAGA ACAGATGCTT GCTTTGGTTC AAGTTAGGCA TGCCTCTGAT GCATTTCTTA ATACCAAGGC AAATCTCTGA GGGCTTAGAC TTAGTAGT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337606 (GAM337606) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337606 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337606 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337606 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337606 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337606 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337606 precursor RNA is designated SEQ ID:5978, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5978 is located from position 150584218 to position 150584325 relative to chromosome 7 on the `+` strand.

GAM337606 precursor RNA folds onto itself, forming GAM337606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337606 precursor RNA, designated SEQ ID NO: 5978, and a schematic representation of a predicted secondary folding of GAM337606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337606 folded precursor RNA yielding a GAM337606 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337606 RNA, hereby incorporated herein.

GAM337606 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337606 target RNA, herein designated GAM TARGET RNA.

GAM337606 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337606 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337606 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337606 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337606 RNA, herein designated GAM RNA, to target binding sites on GAM337606 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337606 target RNA into GAM337606 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337606 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337606 target genes. The mRNA of each one of this plurality of GAM337606 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337606 RNA, herein designated GAM RNA, and which when bound by GAM337606 RNA causes inhibition of translation of the GAM337606 target mRNA into a corresponding GAM337606 target protein.

The mechanism of the translational inhibition exerted by GAM337606 RNA, herein designated GAM RNA, on one or more GAM337606 target genes, herein collectively designated

GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337606 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337606 RNA, herein designated GAM RNA, of GAM337606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337606 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337606 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337606 RNA correlate with, and may be deduced from, the identity of the GAM337606 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337607 7148 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCTGGGAG Messenger 337607 (GAM337607) oligonucleotides modulates expression of respective target

GTGGAGGTTG genes whose function and utility is known in the art.

TGGTGAGCCG GAM337607 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337607 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AGAGCAAAAC encoded by the human genome.

TCTGTCTCA GAM337607 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337607 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337607 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337607 precursor RNA is designated SEQ ID:7148, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7148 is located from position 151095622 to position 151095720

relative to chromosome 1 on the `+` strand.

GAM337607 precursor RNA folds onto itself, forming GAM337607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337607 precursor RNA, designated SEQ ID NO: 7148, and a schematic representation of a predicted secondary folding of GAM337607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337607 folded precursor RNA yielding a GAM337607 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337607 RNA, hereby incorporated herein. Expression of GAM337607 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337607 target RNA, herein designated GAM TARGET RNA.

GAM337607 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337607 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337607 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337607 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337607 RNA, herein designated GAM RNA, to target binding sites on GAM337607 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337607 target RNA into GAM337607 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337607 target genes. The mRNA of each one of this plurality of GAM337607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337607 RNA, herein designated GAM RNA, and which when bound by GAM337607 RNA causes inhibition of translation of the GAM337607 target mRNA into a corresponding GAM337607 target protein.

The mechanism of the translational inhibition exerted by GAM337607 RNA, herein designated GAM RNA, on one or more GAM337607 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337607 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337607 RNA, herein designated GAM RNA, of GAM337607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337607 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337607 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337607 RNA correlate with, and may be deduced from, the identity of the GAM337607 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337608 6402 GAGGCAGGAG Fig. 8 further provides a conceptual description of another novel bioinformatically

AATCGCTTGA detected oligonucleotides of the present invention, referred to here as Genomic Address

ACCTGGGAGG Messenger 337608 (GAM337608) oligonucleotides modulates expression of respective target

TGGAGGTTGT genes whose function and utility is known in the art.

GGTGAGCCGA GAM337608 is a novel bioinformatically detectable regulatory, non protein

GATCGCGCCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337608 was detected

TTGCACTCCA is described with additional reference to Figs. 9-15.

GCCTGGGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCAAAACT encoded by the human genome.

CTGTCTC GAM337608 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337608 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337608 precursor RNA is designated SEQ ID:6402, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6402 is located from position 151095623 to position 151095719 relative to chromosome 1 on the `+` strand.

GAM337608 precursor RNA folds onto itself, forming GAM337608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337608 precursor RNA, designated SEQ ID NO: 6402, and a schematic representation of a predicted secondary folding of GAM337608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337608 folded precursor RNA yielding a GAM337608 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337608 RNA, hereby incorporated herein. Expression of GAM337608 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337608 target RNA, herein designated GAM TARGET RNA.

GAM337608 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337608 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be

present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337608 RNA, herein designated GAM RNA, to target binding sites on GAM337608 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337608 target RNA into GAM337608 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337608 target genes. The mRNA of each one of this plurality of GAM337608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337608 RNA, herein designated GAM RNA, and which when bound by GAM337608 RNA causes inhibition of translation of the GAM337608 target mRNA into a corresponding GAM337608 target protein.

The mechanism of the translational inhibition exerted by GAM337608 RNA, herein designated GAM RNA, on one or more GAM337608 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337608 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337608 RNA, herein designated GAM RNA, of GAM337608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337608 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337608 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337608 RNA correlate with, and may be deduced from, the identity of the GAM337608 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337613 5938 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337613 (GAM337613) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337613 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337613 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337613 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337613 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337613 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337613 precursor RNA is designated SEQ ID:5938, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5938 is located from position 152750152 to position 152750233 relative to chromosome 5 on the `-` strand.

GAM337613 precursor RNA folds onto itself, forming GAM337613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337613 precursor RNA, designated SEQ ID NO: 5938, and a schematic representation of a predicted secondary folding of GAM337613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337613 folded precursor RNA yielding a GAM337613 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337613 RNA, hereby incorporated herein.

GAM337613 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337613 target RNA, herein designated GAM TARGET RNA.

GAM337613 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337613 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337613 target RNA, herein

designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337613 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337613 RNA, herein designated GAM RNA, to target binding sites on GAM337613 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337613 target RNA into GAM337613 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337613 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337613 target genes. The mRNA of each one of this plurality of GAM337613 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337613 RNA, herein designated GAM RNA, and which when bound by GAM337613 RNA causes inhibition of translation of the GAM337613 target mRNA into a corresponding GAM337613 target protein.

The mechanism of the translational inhibition exerted by GAM337613 RNA, herein designated GAM RNA, on one or more GAM337613 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337613 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337613 RNA, herein designated GAM RNA, of GAM337613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337613 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337613 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337613 RNA correlate with, and may be deduced from, the identity of the GAM337613 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337614 6851 GGTGGTGAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GGGGCCTGGG detected oligonucleotides of the present invention, referred to here as Genomic Address

GCGTGGTGTG Messenger 337614 (GAM337614) oligonucleotides modulates expression of respective target

GAGGGTCGAG genes whose function and utility is known in the art.

TTCTTTGTCG GAM337614 is a novel bioinformatically detectable regulatory, non protein

TCCCACAGTC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337614 was detected

ACCCCCAGGA is described with additional reference to Figs. 9-15.

CCACCTTGCG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

AAGCC encoded by the human genome.

GAM337614 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337614 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337614 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337614 precursor RNA is designated SEQ ID:6851, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6851 is located from position 155774514 to position 155774598 relative to chromosome 7 on the `-` strand.

GAM337614 precursor RNA folds onto itself, forming GAM337614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337614 precursor RNA, designated SEQ ID NO: 6851, and a schematic representation of a predicted secondary folding of GAM337614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337614 folded precursor RNA yielding a GAM337614 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337614 RNA, hereby incorporated herein.

GAM337614 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM337614 target RNA, herein designated GAM TARGET RNA.

GAM337614 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337614 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337614 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337614 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337614 RNA, herein designated GAM RNA, to target binding sites on GAM337614 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337614 target RNA into GAM337614 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337614 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337614 target genes. The mRNA of each one of this plurality of GAM337614 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337614 RNA, herein designated GAM RNA, and which when bound by GAM337614 RNA causes inhibition of translation of the GAM337614 target mRNA into a corresponding GAM337614 target protein.

The mechanism of the translational inhibition exerted by GAM337614 RNA, herein designated GAM RNA, on one or more GAM337614 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337614 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337614 RNA, herein designated GAM RNA, of GAM337614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337614 target RNA, herein designated

GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337614 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337614 RNA correlate with, and may be deduced from, the identity of the GAM337614 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337615 7298 TTCCAAGTGA Fig. 8 further provides a conceptual description of another novel bioinformatically
AAATAGACTT detected oligonucleotides of the present invention, referred to here as Genomic Address
TCTGGAGGAG Messenger 337615 (GAM337615) oligonucleotides modulates expression of respective target
CAGAAAGGAC genes whose function and utility is known in the art.

AGCTCTTGGT GAM337615 is a novel bioinformatically detectable regulatory, non protein
ATCTTGCTGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337615 was detected
CCTGAGAACT is described with additional reference to Figs. 9-15.

GCTCCAGTTA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AATATATTTG encoded by the human genome.

TATTTAGAGG GAM337615 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
AA GAM337615 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337615 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337615 precursor RNA is designated SEQ ID:7298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7298 is located from position 156346946 to position 156347047 relative to chromosome 7 on the `+` strand.

GAM337615 precursor RNA folds onto itself, forming GAM337615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337615 precursor RNA, designated SEQ ID NO: 7298, and a schematic representation of a predicted secondary folding of GAM337615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337615 folded precursor

RNA yielding a GAM337615 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337615 RNA, hereby incorporated herein.

GAM337615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337615 target RNA, herein designated GAM TARGET RNA.

GAM337615 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337615 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337615 RNA, herein designated GAM RNA, to target binding sites on GAM337615 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337615 target RNA into GAM337615 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337615 target genes. The mRNA of each one of this plurality of GAM337615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337615 RNA, herein designated GAM RNA, and which when bound by GAM337615 RNA causes inhibition of translation of the GAM337615 target mRNA into a corresponding GAM337615 target protein.

The mechanism of the translational inhibition exerted by GAM337615 RNA, herein designated GAM RNA, on one or more GAM337615 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337615 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337615 RNA, herein designated GAM RNA, of GAM337615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337615 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337615 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337615 RNA correlate with, and may be deduced from, the identity of the GAM337615 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337616 6904 GTGCATTTCT Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTTCTAGTT detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTCACGGAA Messenger 337616 (GAM337616) oligonucleotides modulates expression of respective target

CTGACCAGGC genes whose function and utility is known in the art.

AATTCAGTCA GAM337616 is a novel bioinformatically detectable regulatory, non protein

GTAGCTGTCA coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337616 was detected

AAACTGGAGT is described with additional reference to Figs. 9-15.

CCAGAACAGG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CAC encoded by the human genome.

GAM337616 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337616 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337616 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337616 precursor RNA is designated SEQ ID:6904, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6904 is located from position 156956195 to position 156956277 relative to chromosome 7 on the `+` strand.

GAM337616 precursor RNA folds onto itself, forming GAM337616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337616 precursor RNA, designated SEQ ID NO: 6904, and a schematic representation of a predicted secondary folding of GAM337616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337616 folded precursor RNA yielding a GAM337616 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337616 RNA, hereby incorporated herein.

GAM337616 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337616 target RNA, herein designated GAM TARGET RNA.

GAM337616 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337616 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337616 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337616 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337616 RNA, herein designated GAM RNA, to target binding sites on GAM337616 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337616 target RNA into GAM337616 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337616 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337616 target genes. The mRNA of each one of this plurality of GAM337616 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337616 RNA, herein designated GAM RNA, and which when bound by GAM337616 RNA causes inhibition of translation of the GAM337616 target mRNA into a corresponding GAM337616 target protein.

The mechanism of the translational inhibition exerted by GAM337616 RNA, herein designated GAM RNA, on one or more GAM337616 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational

inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337616 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337616 RNA, herein designated GAM RNA, of GAM337616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337616 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337616 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337616 RNA correlate with, and may be deduced from, the identity of the GAM337616 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337617 7317 TTGCTTGAAC Fig. 8 further provides a conceptual description of another novel bioinformatically

CCGGGAGGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGTTGCAG Messenger 337617 (GAM337617) oligonucleotides modulates expression of respective target

TGAGCTGAGA genes whose function and utility is known in the art.

TGGTGCCACT GAM337617 is a novel bioinformatically detectable regulatory, non protein

GCACTCCAGC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337617 was detected

CTGGGCAACA is described with additional reference to Figs. 9-15.

GAGCAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337617 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337617 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337617 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337617 precursor RNA is designated SEQ ID:7317, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7317 is located from position 157286075 to position 157286150 relative to chromosome 1 on the `-` strand.

GAM337617 precursor RNA folds onto itself, forming GAM337617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337617 precursor RNA, designated SEQ ID NO: 7317, and a schematic representation of a predicted secondary folding of GAM337617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337617 folded precursor RNA yielding a GAM337617 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337617 RNA, hereby incorporated herein. Expression of GAM337617 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337617 target RNA, herein designated GAM TARGET RNA.

GAM337617 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337617 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337617 RNA, herein designated GAM RNA, to target binding sites on GAM337617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337617 target RNA into GAM337617 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337617 target gene, herein designated GAM TARGET GENE,

in fact represents a plurality of GAM337617 target genes. The mRNA of each one of this plurality of GAM337617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337617 RNA, herein designated GAM RNA, and which when bound by GAM337617 RNA causes inhibition of translation of the GAM337617 target mRNA into a corresponding GAM337617 target protein.

The mechanism of the translational inhibition exerted by GAM337617 RNA, herein designated GAM RNA, on one or more GAM337617 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337617 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337617 RNA, herein designated GAM RNA, of GAM337617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337617 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337617 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337617 RNA correlate with, and may be deduced from, the identity of the GAM337617 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337619 5939 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address

CAACATGCAG Messenger 337619 (GAM337619) oligonucleotides modulates expression of respective target

GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337619 is a novel bioinformatically detectable regulatory, non protein

TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337619 was detected

TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

CT encoded by the human genome.

GAM337619 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337619 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337619 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337619 precursor RNA is designated SEQ ID:5939, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5939 is located from position 158225419 to position 158225500 relative to chromosome 2 on the `+` strand.

GAM337619 precursor RNA folds onto itself, forming GAM337619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337619 precursor RNA, designated SEQ ID NO: 5939, and a schematic representation of a predicted secondary folding of GAM337619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337619 folded precursor RNA yielding a GAM337619 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337619 RNA, hereby incorporated herein.

GAM337619 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337619 target RNA, herein designated GAM TARGET RNA.

GAM337619 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337619 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337619 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337619 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337619 RNA, herein designated GAM RNA, to target

binding sites on GAM337619 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337619 target RNA into GAM337619 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337619 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337619 target genes. The mRNA of each one of this plurality of GAM337619 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337619 RNA, herein designated GAM RNA, and which when bound by GAM337619 RNA causes inhibition of translation of the GAM337619 target mRNA into a corresponding GAM337619 target protein.

The mechanism of the translational inhibition exerted by GAM337619 RNA, herein designated GAM RNA, on one or more GAM337619 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337619 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337619 RNA, herein designated GAM RNA, of GAM337619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337619 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337619 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337619 RNA correlate with, and may be deduced from, the identity of the GAM337619 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337620 6039 CATGAAATTT Fig. 8 further provides a conceptual description of another novel bioinformatically

AGTGTGATTA detected oligonucleotides of the present invention, referred to here as Genomic Address

TTTTTTCTAC Messenger 337620 (GAM337620) oligonucleotides modulates expression of respective target

TTTTTAATCA genes whose function and utility is known in the art.

TCATTATTTT GAM337620 is a novel bioinformatically detectable regulatory, non protein

GAAGTTTATG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337620 was detected

is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337620 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337620 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes GAM337620 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337620 precursor RNA is designated SEQ ID:6039, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6039 is located from position 159014706 to position 159014766 relative to chromosome 4 on the `+` strand.

GAM337620 precursor RNA folds onto itself, forming GAM337620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337620 precursor RNA, designated SEQ ID NO: 6039, and a schematic representation of a predicted secondary folding of GAM337620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337620 folded precursor RNA yielding a GAM337620 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337620 RNA, hereby incorporated herein. Expression of GAM337620 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337620 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337620 target RNA, herein designated GAM TARGET RNA.

GAM337620 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337620 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337620 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337620 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337620 RNA, herein designated GAM RNA, to target binding sites on GAM337620 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337620 target RNA into GAM337620 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337620 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337620 target genes. The mRNA of each one of this plurality of GAM337620 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337620 RNA, herein designated GAM RNA, and which when bound by GAM337620 RNA causes inhibition of translation of the GAM337620 target mRNA into a corresponding GAM337620 target protein.

The mechanism of the translational inhibition exerted by GAM337620 RNA, herein designated GAM RNA, on one or more GAM337620 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337620 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337620 RNA, herein designated GAM RNA, of GAM337620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337620 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337620 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337620 RNA correlate with, and may be deduced from, the identity of the GAM337620 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337621 5940 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically

TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337621 (GAM337621) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337621 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337621 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337621 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337621 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337621 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337621 precursor RNA is designated SEQ ID:5940, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5940 is located from position 162284736 to position 162284817 relative to chromosome 1 on the `-` strand.

GAM337621 precursor RNA folds onto itself, forming GAM337621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337621 precursor RNA, designated SEQ ID NO: 5940, and a schematic representation of a predicted secondary folding of GAM337621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337621 folded precursor RNA yielding a GAM337621 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337621 RNA, hereby incorporated herein.

GAM337621 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337621 target RNA, herein designated GAM TARGET RNA.

GAM337621 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337621 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337621 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337621 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337621 RNA, herein designated GAM RNA, to target binding sites on GAM337621 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337621 target RNA into GAM337621 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337621 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337621 target genes. The mRNA of each one of this plurality of GAM337621 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337621 RNA, herein designated GAM RNA, and which when bound by GAM337621 RNA causes inhibition of translation of the GAM337621 target mRNA into a corresponding GAM337621 target protein.

The mechanism of the translational inhibition exerted by GAM337621 RNA, herein designated GAM RNA, on one or more GAM337621 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337621 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337621 RNA, herein designated GAM RNA, of GAM337621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337621 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337621 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337621

RNA correlate with, and may be deduced from, the identity of the GAM337621 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337622 5941 AGTTTTAGGG TACATGTGCA CAACATGCAG GTTTGTTACA TATGTATACA TGTGCCATGT TGGTGTGCTG CACCCATTAA CT

Fig. 8 further provides a conceptual description of another novel bioinformatically detected oligonucleotides of the present invention, referred to here as Genomic Address Messenger 337622 (GAM337622) oligonucleotides modulates expression of respective target genes whose function and utility is known in the art.

GAM337622 is a novel bioinformatically detectable regulatory, non protein coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337622 was detected is described with additional reference to Figs. 9-15.

GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene encoded by the human genome.

GAM337622 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337622 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337622 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337622 precursor RNA is designated SEQ ID:5941, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5941 is located from position 164286556 to position 164286637 relative to chromosome 6 on the `+` strand.

GAM337622 precursor RNA folds onto itself, forming GAM337622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337622 precursor RNA, designated SEQ ID NO: 5941, and a schematic representation of a predicted secondary folding of GAM337622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337622 folded precursor RNA yielding a GAM337622 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337622 RNA, hereby incorporated herein.

GAM337622 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337622 target RNA, herein designated GAM TARGET RNA.

GAM337622 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337622 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337622 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337622 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337622 RNA, herein designated GAM RNA, to target binding sites on GAM337622 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337622 target RNA into GAM337622 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337622 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337622 target genes. The mRNA of each one of this plurality of GAM337622 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337622 RNA, herein designated GAM RNA, and which when bound by GAM337622 RNA causes inhibition of translation of the GAM337622 target mRNA into a corresponding GAM337622 target protein.

The mechanism of the translational inhibition exerted by GAM337622 RNA, herein designated GAM RNA, on one or more GAM337622 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337622 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337622 RNA, herein designated GAM RNA, of GAM337622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337622 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337622 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337622 RNA correlate with, and may be deduced from, the identity of the GAM337622 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337623 5942 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337623 (GAM337623) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337623 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337623 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337623 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337623 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337623 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337623 precursor RNA is designated SEQ ID:5942, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5942 is located from position 165593729 to position 165593810 relative to chromosome 3 on the `+` strand.

GAM337623 precursor RNA folds onto itself, forming GAM337623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337623 precursor RNA, designated SEQ ID NO: 5942, and a schematic representation of a predicted secondary folding of GAM337623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337623 folded precursor RNA yielding a GAM337623 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337623 RNA, hereby incorporated herein.

GAM337623 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337623 target RNA, herein designated GAM TARGET RNA.

GAM337623 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337623 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337623 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337623 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337623 RNA, herein designated GAM RNA, to target binding sites on GAM337623 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337623 target RNA into GAM337623 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337623 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337623 target genes. The mRNA of each one of this plurality of GAM337623 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337623 RNA, herein designated GAM RNA, and which when bound by GAM337623 RNA causes inhibition of translation of the GAM337623 target mRNA into a corresponding GAM337623 target protein.

The mechanism of the translational inhibition exerted by GAM337623 RNA, herein designated GAM RNA, on one or more GAM337623 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337623 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337623 RNA, herein designated GAM RNA, of GAM337623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337623 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337623 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337623 RNA correlate with, and may be deduced from, the identity of the GAM337623 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337624 6275 CTTTTCCACC Fig. 8 further provides a conceptual description of another novel bioinformatically

ATCTAAGAGA detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGGAAGTTC Messenger 337624 (GAM337624) oligonucleotides modulates expression of respective target

AGAGCCTTAG genes whose function and utility is known in the art.

CTTCAACACC GAM337624 is a novel bioinformatically detectable regulatory, non protein

ACAATTTCTT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337624 was detected

AACTGGAAAA is described with additional reference to Figs. 9-15.

G GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

encoded by the human genome.

GAM337624 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337624 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337624 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337624 precursor RNA is designated SEQ ID:6275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6275 is located from position 168691834 to position 168691904 relative to chromosome 1 on the `-` strand.

GAM337624 precursor RNA folds onto itself, forming GAM337624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of

the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337624 precursor RNA, designated SEQ ID NO: 6275, and a schematic representation of a predicted secondary folding of GAM337624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337624 folded precursor RNA yielding a GAM337624 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337624 RNA, hereby incorporated herein. Expression of GAM337624 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337624 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337624 target RNA, herein designated GAM TARGET RNA.

GAM337624 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337624 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337624 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337624 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337624 RNA, herein designated GAM RNA, to target binding sites on GAM337624 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337624 target RNA into GAM337624 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337624 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337624 target genes. The mRNA of each one of this plurality of GAM337624 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337624 RNA, herein designated GAM RNA, and which when bound by GAM337624 RNA causes inhibition of translation of the GAM337624 target mRNA into a corresponding GAM337624 target protein.

The mechanism of the translational inhibition exerted by GAM337624 RNA, herein designated GAM RNA, on one or more GAM337624 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337624 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337624 RNA, herein designated GAM RNA, of GAM337624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337624 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337624 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337624 RNA correlate with, and may be deduced from, the identity of the GAM337624 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337625 7149 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATCGCTTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AAGCCGTGAG Messenger 337625 (GAM337625) oligonucleotides modulates expression of respective target

GTGGAGGTTT genes whose function and utility is known in the art.

TGGTGAGCTG GAM337625 is a novel bioinformatically detectable regulatory, non protein

AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337625 was detected

ATTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAAGAGCGA encoded by the human genome.

AACTCTGTCT GAM337625 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

CA GAM337625 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337625 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337625 precursor RNA is designated SEQ

ID:7149, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7149 is located from position 171453855 to position 171453956 relative to chromosome 1 on the `+` strand.

GAM337625 precursor RNA folds onto itself, forming GAM337625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337625 precursor RNA, designated SEQ ID NO: 7149, and a schematic representation of a predicted secondary folding of GAM337625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337625 folded precursor RNA yielding a GAM337625 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337625 RNA, hereby incorporated herein. Expression of GAM337625 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337625 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337625 target RNA, herein designated GAM TARGET RNA.

GAM337625 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337625 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337625 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337625 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337625 RNA, herein designated GAM RNA, to target binding sites on GAM337625 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337625 target RNA

into GAM337625 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337625 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337625 target genes. The mRNA of each one of this plurality of GAM337625 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337625 RNA, herein designated GAM RNA, and which when bound by GAM337625 RNA causes inhibition of translation of the GAM337625 target mRNA into a corresponding GAM337625 target protein.

The mechanism of the translational inhibition exerted by GAM337625 RNA, herein designated GAM RNA, on one or more GAM337625 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337625 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337625 RNA, herein designated GAM RNA, of GAM337625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337625 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337625 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337625 RNA correlate with, and may be deduced from, the identity of the GAM337625 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337626 6716 GGAGTATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGAACCTGC detected oligonucleotides of the present invention, referred to here as Genomic Address

GAGGCGGAGG Messenger 337626 (GAM337626) oligonucleotides modulates expression of respective target

TTGCAGTGAG genes whose function and utility is known in the art.

CCGGGATCGC GAM337626 is a novel bioinformatically detectable regulatory, non protein

ACCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337626 was detected

TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGACTCC encoded by the human genome.

GAM337626 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337626 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337626 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337626 precursor RNA is designated SEQ ID:6716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6716 is located from position 176442690 to position 176442777 relative to chromosome 1 on the `-` strand.

GAM337626 precursor RNA folds onto itself, forming GAM337626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337626 precursor RNA, designated SEQ ID NO: 6716, and a schematic representation of a predicted secondary folding of GAM337626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337626 folded precursor RNA yielding a GAM337626 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337626 RNA, hereby incorporated herein. Expression of GAM337626 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337626 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337626 target RNA, herein designated GAM TARGET RNA.

GAM337626 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337626 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337626 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337626 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in

Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337626 RNA, herein designated GAM RNA, to target binding sites on GAM337626 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337626 target RNA into GAM337626 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337626 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337626 target genes. The mRNA of each one of this plurality of GAM337626 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337626 RNA, herein designated GAM RNA, and which when bound by GAM337626 RNA causes inhibition of translation of the GAM337626 target mRNA into a corresponding GAM337626 target protein.

The mechanism of the translational inhibition exerted by GAM337626 RNA, herein designated GAM RNA, on one or more GAM337626 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337626 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337626 RNA, herein designated GAM RNA, of GAM337626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337626 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337626 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337626 RNA correlate with, and may be deduced from, the identity of the GAM337626 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337627 7159 TGAGGCAGGA Fig. 8 further provides a conceptual description of another novel bioinformatically

GAATGGCGTG detected oligonucleotides of the present invention, referred to here as Genomic Address

AACCCGGGAG Messenger 337627 (GAM337627) oligonucleotides modulates expression of respective target
GCGGAGCTTG genes whose function and utility is known in the art.

CAGTGAGCCG GAM337627 is a novel bioinformatically detectable regulatory, non protein
AGATCGCGCC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337627 was detected
ACTGCACTCC is described with additional reference to Figs. 9-15.

AGCCTGGGCA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
ACAGAGTGAG encoded by the human genome.

ACTCCGTCTC GAM337627 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a
A GAM337627 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337627 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337627 precursor RNA is designated SEQ ID:7159, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:7159 is located from position 177506687 to position 177506787 relative to chromosome 1 on the `+` strand.

GAM337627 precursor RNA folds onto itself, forming GAM337627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337627 precursor RNA, designated SEQ ID NO: 7159, and a schematic representation of a predicted secondary folding of GAM337627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337627 folded precursor RNA yielding a GAM337627 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337627 RNA, hereby incorporated herein. Expression of GAM337627 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337627 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337627 target RNA, herein designated GAM TARGET RNA.

GAM337627 target RNA comprises three regions, as is typical of mRNA of a protein coding

gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337627 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337627 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337627 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337627 RNA, herein designated GAM RNA, to target binding sites on GAM337627 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337627 target RNA into GAM337627 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337627 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337627 target genes. The mRNA of each one of this plurality of GAM337627 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337627 RNA, herein designated GAM RNA, and which when bound by GAM337627 RNA causes inhibition of translation of the GAM337627 target mRNA into a corresponding GAM337627 target protein.

The mechanism of the translational inhibition exerted by GAM337627 RNA, herein designated GAM RNA, on one or more GAM337627 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337627 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337627 RNA, herein designated GAM RNA, of GAM337627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337627 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337627 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337627 RNA correlate with, and may be deduced from, the identity of the GAM337627 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337628 5943 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337628 (GAM337628) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337628 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337628 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337628 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337628 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337628 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337628 precursor RNA is designated SEQ ID:5943, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5943 is located from position 182133354 to position 182133435 relative to chromosome 1 on the `-` strand.

GAM337628 precursor RNA folds onto itself, forming GAM337628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337628 precursor RNA, designated SEQ ID NO: 5943, and a schematic representation of a predicted secondary folding of GAM337628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337628 folded precursor RNA yielding a GAM337628 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins.

Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337628 RNA, hereby incorporated herein.

GAM337628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337628 target RNA, herein designated GAM TARGET RNA.

GAM337628 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337628 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337628 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337628 RNA, herein designated GAM RNA, to target binding sites on GAM337628 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337628 target RNA into GAM337628 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337628 target genes. The mRNA of each one of this plurality of GAM337628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337628 RNA, herein designated GAM RNA, and which when bound by GAM337628 RNA causes inhibition of translation of the GAM337628 target mRNA into a corresponding GAM337628 target protein.

The mechanism of the translational inhibition exerted by GAM337628 RNA, herein designated GAM RNA, on one or more GAM337628 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337628 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337628 RNA, herein designated GAM RNA, of GAM337628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set

forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337628 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337628 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337628 RNA correlate with, and may be deduced from, the identity of the GAM337628 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337629 5944 AGTTTTAGGG Fig. 8 further provides a conceptual description of another novel bioinformatically
TACATGTGCA detected oligonucleotides of the present invention, referred to here as Genomic Address
CAACATGCAG Messenger 337629 (GAM337629) oligonucleotides modulates expression of respective target
GTTTGTTACA genes whose function and utility is known in the art.

TATGTATACA GAM337629 is a novel bioinformatically detectable regulatory, non protein
TGTGCCATGT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337629 was detected
TGGTGTGCTG is described with additional reference to Figs. 9-15.

CACCCATTAA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
CT encoded by the human genome.

GAM337629 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337629 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337629 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337629 precursor RNA is designated SEQ ID:5944, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5944 is located from position 186079835 to position 186079916 relative to chromosome 4 on the `+` strand.

GAM337629 precursor RNA folds onto itself, forming GAM337629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337629 precursor RNA, designated SEQ ID NO: 5944, and a schematic representation of a predicted secondary folding of GAM337629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4

incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337629 folded precursor RNA yielding a GAM337629 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337629 RNA, hereby incorporated herein.

GAM337629 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337629 target RNA, herein designated GAM TARGET RNA.

GAM337629 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337629 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337629 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337629 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337629 RNA, herein designated GAM RNA, to target binding sites on GAM337629 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337629 target RNA into GAM337629 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337629 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337629 target genes. The mRNA of each one of this plurality of GAM337629 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337629 RNA, herein designated GAM RNA, and which when bound by GAM337629 RNA causes inhibition of translation of the GAM337629 target mRNA into a corresponding GAM337629 target protein.

The mechanism of the translational inhibition exerted by GAM337629 RNA, herein designated GAM RNA, on one or more GAM337629 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337629 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic

representation of a predicted secondary folding of GAM337629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337629 RNA, herein designated GAM RNA, of GAM337629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337629 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337629 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337629 RNA correlate with, and may be deduced from, the identity of the GAM337629 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337630 5767 AGGCAGAAGA Fig. 8 further provides a conceptual description of another novel bioinformatically

ATTGCTGGAA detected oligonucleotides of the present invention, referred to here as Genomic Address

TCTAGGAGGC Messenger 337630 (GAM337630) oligonucleotides modulates expression of respective target

GGAGGTTGCA genes whose function and utility is known in the art.

GTGAGCCAAG GAM337630 is a novel bioinformatically detectable regulatory, non protein

ATCGCGCCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337630 was detected

TGCACTCCAG is described with additional reference to Figs. 9-15.

CCTGGGCAAC GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

ACAGCGAGAC encoded by the human genome.

TCTGTCT GAM337630 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337630 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337630 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337630 precursor RNA is designated SEQ ID:5767, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5767 is located from position 199201991 to position 199202087 relative to chromosome 1 on the `+` strand.

GAM337630 precursor RNA folds onto itself, forming GAM337630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337630 precursor RNA, designated SEQ ID NO: 5767, and a schematic representation of a predicted secondary folding of GAM337630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337630 folded precursor RNA yielding a GAM337630 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337630 RNA, hereby incorporated herein. Expression of GAM337630 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337630 target RNA, herein designated GAM TARGET RNA.

GAM337630 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337630 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337630 RNA, herein designated GAM RNA, to target binding sites on GAM337630 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337630 target RNA into GAM337630 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337630 target genes. The mRNA of each one of this plurality of GAM337630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337630 RNA,

herein designated GAM RNA, and which when bound by GAM337630 RNA causes inhibition of translation of the GAM337630 target mRNA into a corresponding GAM337630 target protein.

The mechanism of the translational inhibition exerted by GAM337630 RNA, herein designated GAM RNA, on one or more GAM337630 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337630 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337630 RNA, herein designated GAM RNA, of GAM337630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337630 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337630 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337630 RNA correlate with, and may be deduced from, the identity of the GAM337630 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337631 6629 GGAGAATCGC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCAG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGCAGAGG Messenger 337631 (GAM337631) oligonucleotides modulates expression of respective target
TTGCAGTGAG genes whose function and utility is known in the art.

CCAAGATCAT GAM337631 is a novel bioinformatically detectable regulatory, non protein
GCCACTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337631 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAGAGT GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
GAGACTCC encoded by the human genome.

GAM337631 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337631 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337631 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337631 precursor RNA is designated SEQ ID:6629, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6629 is located from position 208756916 to position 208757003 relative to chromosome 1 on the `+` strand.

GAM337631 precursor RNA folds onto itself, forming GAM337631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337631 precursor RNA, designated SEQ ID NO: 6629, and a schematic representation of a predicted secondary folding of GAM337631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337631 folded precursor RNA yielding a GAM337631 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337631 RNA, hereby incorporated herein. Expression of GAM337631 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337631 target RNA, herein designated GAM TARGET RNA.

GAM337631 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337631 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337631 RNA, herein designated GAM RNA, to target binding sites on GAM337631 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337631 target RNA into GAM337631 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337631 target genes. The mRNA of each one of this plurality of GAM337631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337631 RNA, herein designated GAM RNA, and which when bound by GAM337631 RNA causes inhibition of translation of the GAM337631 target mRNA into a corresponding GAM337631 target protein.

The mechanism of the translational inhibition exerted by GAM337631 RNA, herein designated GAM RNA, on one or more GAM337631 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337631 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337631 RNA, herein designated GAM RNA, of GAM337631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337631 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337631 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337631 RNA correlate with, and may be deduced from, the identity of the GAM337631 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337632 5730 AGAGGGAGAA Fig. 8 further provides a conceptual description of another novel bioinformatically

TTGCTTGAGC detected oligonucleotides of the present invention, referred to here as Genomic Address

CCAGGATTTC Messenger 337632 (GAM337632) oligonucleotides modulates expression of respective target

GAGGCTGCAG genes whose function and utility is known in the art.

TGAGCTATGA GAM337632 is a novel bioinformatically detectable regulatory, non protein

TCACACCACT coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337632 was detected

GCACTCCAGC is described with additional reference to Figs. 9-15.

CTGGGCAACA GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene

GAGCAAGACT encoded by the human genome.

CTGTCT GAM337632 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337632 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337632 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337632 precursor RNA is designated SEQ ID:5730, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:5730 is located from position 222613184 to position 222613279 relative to chromosome 2 on the `+` strand.

GAM337632 precursor RNA folds onto itself, forming GAM337632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337632 precursor RNA, designated SEQ ID NO: 5730, and a schematic representation of a predicted secondary folding of GAM337632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337632 folded precursor RNA yielding a GAM337632 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337632 RNA, hereby incorporated herein. Expression of GAM337632 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337632 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337632 target RNA, herein designated GAM TARGET RNA.

GAM337632 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337632 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337632 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337632 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows

three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337632 RNA, herein designated GAM RNA, to target binding sites on GAM337632 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337632 target RNA into GAM337632 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337632 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337632 target genes. The mRNA of each one of this plurality of GAM337632 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337632 RNA, herein designated GAM RNA, and which when bound by GAM337632 RNA causes inhibition of translation of the GAM337632 target mRNA into a corresponding GAM337632 target protein.

The mechanism of the translational inhibition exerted by GAM337632 RNA, herein designated GAM RNA, on one or more GAM337632 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337632 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337632 RNA, herein designated GAM RNA, of GAM337632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337632 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337632 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337632 RNA correlate with, and may be deduced from, the identity of the GAM337632 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337633 6445 GAGGGAGAAT Fig. 8 further provides a conceptual description of another novel bioinformatically

TGCTTGAGCC detected oligonucleotides of the present invention, referred to here as Genomic Address
CAGGATTTCG Messenger 337633 (GAM337633) oligonucleotides modulates expression of respective target
AGGCTGCAGT genes whose function and utility is known in the art.

GAGCTATGAT GAM337633 is a novel bioinformatically detectable regulatory, non protein
CACACCACTG coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337633 was detected
CACTCCAGCC is described with additional reference to Figs. 9-15.

TGGGCAACAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
AGCAAGACTC encoded by the human genome.

TGTC GAM337633 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a

GAM337633 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337633 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337633 precursor RNA is designated SEQ ID:6445, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6445 is located from position 222613185 to position 222613278 relative to chromosome 2 on the `+` strand.

GAM337633 precursor RNA folds onto itself, forming GAM337633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337633 precursor RNA, designated SEQ ID NO: 6445, and a schematic representation of a predicted secondary folding of GAM337633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337633 folded precursor RNA yielding a GAM337633 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337633 RNA, hereby incorporated herein. Expression of GAM337633 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337633 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337633 target RNA, herein designated GAM TARGET RNA.

GAM337633 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337633 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337633 RNA, herein designated GAM RNA, to target binding sites on GAM337633 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337633 target RNA into GAM337633 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337633 target genes. The mRNA of each one of this plurality of GAM337633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337633 RNA, herein designated GAM RNA, and which when bound by GAM337633 RNA causes inhibition of translation of the GAM337633 target mRNA into a corresponding GAM337633 target protein.

The mechanism of the translational inhibition exerted by GAM337633 RNA, herein designated GAM RNA, on one or more GAM337633 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337633 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337633 RNA, herein designated GAM RNA, of GAM337633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337633 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337633 RNA, herein designated GAM RNA, are set forth in Tables

6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337633 RNA correlate with, and may be deduced from, the identity of the GAM337633 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM337634 6667 GGAGAATCTC Fig. 8 further provides a conceptual description of another novel bioinformatically
TTGAACCCGG detected oligonucleotides of the present invention, referred to here as Genomic Address
GAGGTGGAGG Messenger 337634 (GAM337634) oligonucleotides modulates expression of respective target
TTGGGGTGAG genes whose function and utility is known in the art.

CCGAGACCGC GAM337634 is a novel bioinformatically detectable regulatory, non protein
GCCATTGCAC coding, micro RNA (miRNA)-like oligonucleotide. The method by which GAM337634 was detected
TCCAGCCTGG is described with additional reference to Figs. 9-15.

GCAACAAGAG GAM PRECURSOR DNA is encoded by the human genome. GAM TARGET GENE is a humen gene
TGAGACTCC encoded by the human genome.

GAM337634 precursor DNA, herein designated GAM PRECURSOR DNA, encodes a GAM337634 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes

GAM337634 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337634 precursor RNA is designated SEQ ID:6667, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:6667 is located from position 231956115 to position 231956203 relative to chromosome 1 on the `+` strand.

GAM337634 precursor RNA folds onto itself, forming GAM337634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is a fully or partially complementary sequence of the nucleotide sequence of the second half thereof.

Nucleotide sequence of GAM337634 precursor RNA, designated SEQ ID NO: 6667, and a schematic representation of a predicted secondary folding of GAM337634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4 incorporated herein.

An enzyme complex designated DICER COMPLEX, `dices` the GAM337634 folded precursor RNA yielding a GAM337634 RNA, herein designated GAM RNA, in the form of a single stranded ~22nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product to yield a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer RNase III together with other necessary proteins. Table 5 provides a nucleotide sequence that is highly likely to be identical or highly similar to the nucleotide sequence of GAM337634 RNA, hereby incorporated herein. Expression of GAM337634 RNA was experimentally validated in HeLa cells using the methods described with reference to Figs.22 to 24.

GAM337634 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337634 target RNA, herein designated GAM TARGET RNA.

GAM337634 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

GAM337634 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337634 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM337634 RNA is a partial or fully complementary sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 8 shows target binding sites only in the 3`UTR region, these target binding sites may be located instead in the 5`UTR region or in both 3`UTR and 5`UTR regions

The complementary binding of GAM337634 RNA, herein designated GAM RNA, to target binding sites on GAM337634 target RNA, herein designated GAM TARGET RNA, such as BINDING

SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337634 target RNA into GAM337634 target protein, herein designated GAM TARGET PROTEIN,, which is shown surrounded by a broken line.

It is appreciated that GAM337634 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337634 target genes. The mRNA of each one of this plurality of GAM337634 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337634 RNA, herein designated GAM RNA, and which when bound by GAM337634 RNA causes inhibition of translation of the GAM337634 target mRNA into a corresponding GAM337634 target protein.

The mechanism of the translational inhibition exerted by GAM337634 RNA, herein designated GAM RNA, on one or more GAM337634 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted byknown miRNA genes.

Nucleotide sequence of GAM337634 precursor RNA, herein designated GAM PRECURSOR RNA, , their respective genomic sources and chromosomal locations and a schematic representation of a predicted secondary folding of GAM337634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth in Tables 3 and 4, incorporated herein.

Nucleotide sequences of a `diced` GAM337634 RNA, herein designated GAM RNA, of GAM337634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, are set forth

in Table 5, incorporated herein

Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on GAM337634 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM337634 RNA, herein designated GAM RNA, are set forth in Tables 6 and 7, incorporated herein.

It is appreciated that specific functions, and accordingly utilities, of GAM337634 RNA correlate with, and may be deduced from, the identity of the GAM337634 target gene inhibited thereby, whose functions are set forth in Table 8, incorporated herein.

GAM NAME	PRECUR SEQ-ID	ORGANISM AND	CHR	STR	CHR-START OFFSET	CHR-END OFFSET	SOURCE REF-ID
GAM25	10361	hsa	X	-	52222126	52222224	
GAM31	10712	hsa	12	-	57935139	57935222	
GAM44	10225	hsa	11	+	48222380	48222439	THC1430784
GAM55	9654	hsa	16	+	69071144	69071235	THC1550782
GAM66	9890	hsa	10	-	82042982	82043055	THC1596213
GAM83	9594	hsa	11	+	48222373	48222451	THC1430784
GAM99	10072	hsa	10	+	102246140	102246248	THC1481711
GAM106	11185	hsa	20	-	13445760	13445858	THC1578040
GAM112	9976	hsa	X	+	47490562	47490653	
GAM144	10844	hsa	22	-	29007729	29007806	THC1576207
GAM175	11029	hsa	X	+	94175190	94175299	THC1505396
GAM189	10243	hsa	4	+	95450005	95450076	
GAM193	10490	hsa	7	-	150223538	150223636	THC1461697
GAM205	10955	hsa	19	+	34136693	34136794	THC1489754
GAM206	9626	hsa	8	+	63676328	63676430	THC1555962
GAM240	11204	hsa	11	-	73803662	73803768	THC1514987
GAM259	9934	hsa	9	+	97689223	97689314	THC1497034
GAM269	10396	hsa	10	+	75439944	75440030	
GAM270	9919	hsa	12	+	46553863	46553949	THC1472192
GAM281	10402	hsa	12	-	51464300	51464397	THC1476894
GAM282	10716	hsa	9	+	117492532	117492617	THC1528843
GAM291	11179	hsa	X	+	9780990	9781067	
GAM317	10674	hsa	19	+	4462631	4462733	THC1503708
GAM329	10797	hsa	9	+	37420113	37420180	
GAM330	10273	hsa	7	-	102423230	102423315	THC1430517
GAM335	9932	hsa	22	+	22176932	22177032	THC1525711
GAM347	9752	hsa	19	-	37269373	37269456	THC1459051
GAM354	10673	hsa	19	+	50818302	50818390	
GAM361	11098	hsa	X	+	94524959	94525060	
GAM367	11120	hsa	10	+	121833627	121833742	THC1534183
GAM388	9776	hsa	1	-	16098435	16098516	THC1432163
GAM401	9669	hsa	10	+	14110787	14110879	
GAM408	10542	hsa	14	-	62113790	62113884	THC1542346
GAM426	10058	hsa	17	-	6961619	6961701	THC1532849
GAM492	11209	hsa	17	-	43642880	43642990	THC1425133
GAM495	10024	hsa					
GAM507	10728	hsa	15	+	40608766	40608865	THC1464659
GAM519	9641	hsa	18	-	32800605	32800693	THC1560312
GAM520	10809	hsa	17	+	43020516	43020604	THC1534497
GAM550	10897	hsa	15	-	28205837	28205958	
GAM569	10404	hsa	19	+	50818294	50818397	
GAM572	9658	hsa	10	-	14718325	14718418	THC1456344
GAM584	10146	hsa	11	+	67800165	67800260	THC1588098
GAM588	9928	hsa	11	-	45420375	45420453	THC1541093
GAM593	9723	hsa	15	+	43562097	43562226	
GAM604	10098	hsa	17	-	39106109	39106181	THC1442048
GAM640	10481	hsa	2	-	74052253	74052365	THC1549049

GAM667	10851	hsa	7	+	44371974	44372104	
GAM674	9938	hsa	17	+	43395844	43395930	THC1521438
GAM689	10321	hsa	5	-	69076605	69076701	
GAM744	9749	hsa					
GAM750	9628	hsa	20	-	46615364	46615467	THC1599270
GAM760	10991	hsa	10	+	15036029	15036118	THC1446951
GAM772	11168	hsa	17	+	26891775	26891870	THC1436688
GAM779	10042	hsa	10	+	131264455	131264575	THC1409862
GAM785	10027	hsa	17	+	30319064	30319171	THC1539612
GAM801	10252	hsa	12	+	53583235	53583337	THC1464135
GAM807	11034	hsa	15	-	53974897	53974997	THC1542535
GAM821	10085	hsa	19	+	50818309	50818384	
GAM828	9655	hsa	Y	-	14758025	14758108	THC1555358
GAM834	10448	hsa	14	+	90514756	90514845	THC1432704
GAM840	10568	hsa	7	+	100281294	100281382	THC1486985
GAM842	10178	hsa	17	-	1319182	1319274	THC1537468
GAM846	10989	hsa	9	+	127720318	127720391	THC1424524
GAM869	10519	hsa	20	-	43962141	43962221	THC1463637
GAM892	11175	hsa	10	+	101743922	101744004	THC1541391
GAM933	9643	hsa	14	+	86637069	86637139	THC1526006
GAM965	11190	hsa	12	+	46553864	46553948	THC1472192
GAM973	9616	hsa	7	-	150223532	150223640	THC1461697
GAM999	9667	hsa	11	+	93949150	93949235	
GAM1017	10611	hsa	20	+	18499225	18499309	
GAM1032	10472	hsa	8	-	141427052	141427182	
GAM1033	10394	hsa	X	-	126882804	126882896	THC1559611
GAM1087	9741	hsa	10	-	105533378	105533457	THC1524354
GAM1088	10043	hsa	7	-	82179625	82179720	THC1555889
GAM1089	10834	hsa	12	-	114030793	114030873	THC1563805
GAM1099	10919	hsa	21	+	46973081	46973189	THC1440523
GAM1144	10118	hsa	13	+	26088289	26088404	THC1419952
GAM1163	10865	hsa	9	+	92946370	92946462	THC1486696
GAM1191	11151	hsa	13	+	24390494	24390598	
GAM1193	10309	hsa	7	-	138504313	138504410	
GAM1197	9685	hsa	19	+	62494484	62494596	THC1581606
GAM1216	11241	hsa	16	+	69762458	69762538	
GAM1217	9644	hsa	9	+	88520253	88520356	
GAM1221	11031	hsa	10	+	26323250	26323341	THC1586339
GAM1234	11221	hsa	7	-	138312903	138312981	THC1407182
GAM1238	10560	hsa	20	-	56600621	56600711	THC1430578
GAM1293	10868	hsa	12	-	56453734	56453830	THC1439723
GAM1294	10179	hsa	16	-	74684805	74684878	THC1560089
GAM1295	11006	hsa	15	+	40608762	40608868	THC1464659
GAM1300	11148	hsa	16	+	82918189	82918283	
GAM1310	10701	hsa	14	+	51215356	51215446	
GAM1332	10431	hsa	14	+	93614973	93615063	THC1518532
GAM1338	10613	hsa	11	+	62757693	62757780	THC1439776
GAM1361	9954	hsa	X	+	40576956	40577066	
GAM1363	9672	hsa	7	+	54861174	54861256	THC1506114
GAM1372	10468	hsa	7	+	71938248	71938338	THC1481651

GAM1423	10304	hsa	9	+	97689214	97689322	THC1497034
GAM1431	10261	hsa	14	-	62113797	62113875	THC1542346
GAM1440	10231	hsa	11	-	45420363	45420458	THC1541093
GAM1443	10137	hsa	10	+	79169031	79169146	
GAM1447	10818	hsa	X	+	84120401	84120475	THC1585180
GAM1456	10902	hsa	10	+	27561775	27561847	
GAM1461	11213	hsa	16	+	11377024	11377118	THC1576092
GAM1469	10816	hsa	14	-	51978690	51978799	THC1499663
GAM1479	10721	hsa	22	-	44721810	44721887	THC1562390
GAM1484	11202	hsa	10	-	63061687	63061792	THC1535408
GAM1490	10307	hsa	12	+	132157864	132157951	
GAM1500	10450	hsa	11	+	111417608	111417699	
GAM1502	9980	hsa	13	-	37916875	37916940	
GAM1523	10010	hsa	10	-	102859224	102859309	THC1426270
GAM1543	10622	hsa	16	-	28383578	28383665	THC1588979
GAM1550	11229	hsa	9	+	35798284	35798384	THC1590719
GAM1602	10237	hsa	19	-	33016836	33016966	THC1595133
GAM1607	10917	hsa	21	+	25868151	25868239	THC1591841
GAM1617	9897	hsa	16	+	48119610	48119709	
GAM1650	11198	hsa	X	+	108489391	108489499	THC1441934
GAM1653	10791	hsa	17	+	38591310	38591381	
GAM1698	10870	hsa	16	+	30012807	30012915	
GAM1735	10829	hsa	8	+	16961669	16961761	
GAM1748	10998	hsa	19	-	17342458	17342534	THC1450994
GAM1770	10790	hsa	17	+	38591310	38591380	
GAM1782	10126	hsa	X	+	136594090	136594178	THC1478628
GAM1820	10211	hsa	14	+	79670256	79670329	
GAM1835	10904	hsa	9	+	115193597	115193726	THC1442512
GAM1860	11134	hsa	11	+	92812997	92813076	THC1457396
GAM1863	11240	hsa	X	+	65182629	65182729	THC1408667
GAM1864	10017	hsa	1	-	89090896	89090997	THC1465567
GAM1887	10077	hsa	20	-	46615376	46615449	THC1599270
GAM1896	10004	hsa	20	+	21174682	21174776	THC1424734
GAM1914	10416	hsa	10	-	93938738	93938848	THC1548235
GAM1937	9624	hsa	9	+	35798279	35798392	THC1590719
GAM1942	10777	hsa	7	+	133099401	133099514	
GAM1961	10694	hsa	12	+	111433254	111433332	THC1587276
GAM1975	9905	hsa	X	-	55606620	55606695	THC1498867
GAM1976	10517	hsa	21	+	35292418	35292494	
GAM1997	10825	hsa	4	+	79802871	79802957	THC1410841
GAM2010	9634	hsa	15	+	22660388	22660481	THC1453894
GAM2014	10682	hsa	17	-	76816688	76816817	THC1469417
GAM2022	10258	hsa	10	+	47568406	47568502	THC1596797
GAM2027	10467	hsa	17	-	3662454	3662549	THC1430335
GAM2033	10236	hsa	1	+	52243579	52243654	THC1566321
GAM2051	9948	hsa	11	+	27725973	27726056	
GAM2058	10513	hsa	15	-	89111973	89112050	THC1440062
GAM2062	11181	hsa	13	+	97732458	97732539	THC1486208
GAM2098	10197	hsa	15	+	64216383	64216457	
GAM2171	10110	hsa	8	+	54026270	54026338	

GAM2221	9920	hsa	20	+	13327337	13327414	
GAM2223	11022	hsa	20	-	50175599	50175687	THC1449211
GAM2233	9755	hsa	6	-	167487173	167487264	THC1555864
GAM2251	11172	hsa	7	+	17124868	17124962	THC1481584
GAM2260	10524	hsa	10	+	29926532	29926658	
GAM2262	9724	hsa	20	+	42901138	42901220	
GAM2263	9619	hsa	22	-	40238503	40238607	THC1454581
GAM2270	10841	hsa	X	-	19237261	19237358	X
GAM2272	9891	hsa	9	-	62131109	62131209	THC1581432
GAM2290	9630	hsa	X	+	148621116	148621208	THC1489192
GAM2300	9665	hsa	22	-	22354493	22354605	THC1524612
GAM2306	11288	hsa	9	+	78004552	78004643	
GAM2309	10021	hsa	9	+	124008737	124008820	THC1531218
GAM2350	9592	hsa	11	+	47322081	47322157	THC1583940
GAM2384	10962	hsa	7	+	35442640	35442723	THC1476644
GAM2391	10853	hsa	22	-	22354497	22354600	THC1524612
GAM2393	9775	hsa	3	+	99981233	99981339	THC1456561
GAM2398	9611	hsa	11	-	63185944	63186032	THC1481765
GAM2424	10997	hsa				BE300452	
GAM2440	11256	hsa	14	+	29072015	29072090	
GAM2514	11159	hsa	1	+	93198982	93199071	THC1442456
GAM2519	9913	hsa	10	+	80675207	80675297	
GAM2543	11152	hsa	21	+	25868146	25868248	
GAM2565	10306	hsa	22	-	17811037	17811137	THC1413987
GAM2591	10044	hsa	14	-	104342178	104342279	THC1523079
GAM2608	10221	hsa	X	-	131249037	131249167	X
GAM2618	11220	hsa	19	+	10351230	10351307	
GAM2624	9903	hsa	X	-	128731509	128731586	THC1408939
GAM2628	10846	hsa	17	-	15653139	15653240	THC1504686
GAM2631	11155	hsa	8	+	8927224	8927320	THC1574137
GAM2640	11205	hsa	10	-	13483969	13484042	THC1446810
GAM2672	10457	hsa	13	+	97817966	97818053	
GAM2732	10785	hsa	7	-	49257580	49257709	THC1524958
GAM2762	10200	hsa	13	-	110144402	110144531	THC1427725
GAM2770	10537	hsa	16	-	69984108	69984208	THC1566227
GAM2780	10174	hsa	11	+	101905422	101905503	THC1434204
GAM2799	9754	hsa	17	+	67595564	67595647	
GAM2807	9926	hsa	14	-	79828330	79828454	
GAM2808	10475	hsa	15	-	53974898	53975004	THC1542535
GAM2817	10420	hsa	16	-	15101514	15101592	THC1503496
GAM2839	10129	hsa	5	+	21329921	21330005	THC1414413
GAM2846	10104	hsa	7	+	143268257	143268368	THC1460148
GAM2868	10046	hsa	17	+	78873561	78873655	THC1479162
GAM2887	10789	hsa	11	-	69517026	69517123	THC1565280
GAM2908	10680	hsa	19	+	51977188	51977290	THC1551777
GAM2911	10165	hsa	19	+	50818311	50818382	
GAM2920	10706	hsa	17	-	1319193	1319269	THC1537468
GAM2927	10001	hsa	10	-	12168404	12168496	THC1533857
GAM2931	10668	hsa	8	+	97874565	97874649	
GAM2950	10005	hsa	5	-	170095979	170096085	THC1595210

GAM3004	10037	hsa	17	-	79931895	79931983	THC1562045
GAM3028	9743	hsa	18	+	1293547	1293665	
GAM3057	10217	hsa	19	+	8202273	8202402	THC1540352
GAM3061	10250	hsa	9	+	94124802	94124909	
GAM3064	10671	hsa	16	+	69459978	69460083	THC1413273
GAM3065	10649	hsa	11	+	120332544	120332655	THC1561193
GAM3077	9975	hsa	7	+	127843803	127843891	THC1482310
GAM3081	10054	hsa	19	+	23059753	23059842	THC1486336
GAM3089	11035	hsa	19	+	39513226	39513338	
GAM3091	10253	hsa	9	+	96671073	96671162	THC1583417
GAM3123	10050	hsa	17	+	63390513	63390591	THC1538938
GAM3126	11212	hsa	17	+	43395837	43395937	THC1521438
GAM3132	9697	hsa	15	-	53974892	53975005	THC1542535
GAM3138	9652	hsa	15	+	33981295	33981406	
GAM3140	9763	hsa	17	+	38591279	38591401	
GAM3143	10699	hsa	15	+	81003842	81003937	THC1438390
GAM3157	11285	hsa	14	-	21733645	21733720	THC1518042
GAM3163	11019	hsa	9	-	28262669	28262778	THC1420983
GAM3174	9656	hsa	13	+	42623627	42623725	THC1562314
GAM3183	9906	hsa	17	+	36044102	36044188	THC1514025
GAM3190	10415	hsa	4	+	95449990	95450087	
GAM3195	10884	hsa	11	+	68013720	68013814	
GAM3211	10984	hsa	19	+	55666192	55666299	THC1551612
GAM3227	10618	hsa				AA654979	
GAM3236	10435	hsa	15	+	48954882	48954962	
GAM3263	10041	hsa	7	-	127750640	127750740	THC1429789
GAM3266	10068	hsa	20	+	3852982	3853067	THC1510126
GAM3271	10413	hsa	10	-	93938749	93938835	THC1548235
GAM3293	9998	hsa	11	-	72746540	72746636	THC1557011
GAM3298	11281	hsa	X	-	131248823	131248915	X
GAM3311	10726	hsa	18	+	47179504	47179580	THC1457365
GAM3330	10049	hsa	20	-	62164417	62164528	THC1502484
GAM3350	10894	hsa	8	+	9289824	9289923	THC1572440
GAM3368	10953	hsa	16	-	72291796	72291909	THC1586053
GAM3414	9917	hsa	7	+	50214299	50214399	
GAM3422	10760	hsa	11	-	122969346	122969432	THC1481240
GAM3426	9899	hsa	7	+	98551385	98551453	
GAM3431	10749	hsa	12	+	6952114	6952199	
GAM3452	9648	hsa	9	-	124136937	124137028	THC1456154
GAM3461	9941	hsa	9	+	88520252	88520357	
GAM3463	10743	hsa	7	+	131571664	131571754	THC1586887
GAM3479	10822	hsa	16	+	69762451	69762553	
GAM3486	10003	hsa	20	+	59248137	59248211	THC1542580
GAM3513	10229	hsa	11	+	130044291	130044389	THC1415145
GAM3535	10223	hsa	13	+	22420611	22420710	THC1508870
GAM3593	9770	hsa	3	+	190505666	190505747	THC1542980
GAM3595	9681	hsa	14	+	79670251	79670336	
GAM3605	10089	hsa	8	+	30275106	30275196	THC1564243
GAM3630	10831	hsa	11	-	78654898	78654985	THC1472355
GAM3640	10803	hsa	11	-	47669037	47669118	THC1553582

GAM3666	10476	hsa	1	+	143019237	143019346	THC1455892
GAM3691	10139	hsa	11	+	8085889	8085960	THC1538463
GAM3747	9676	hsa	10	-	117953553	117953667	THC1561414
GAM3768	10892	hsa	X	+	47243042	47243137	
GAM3781	10427	hsa	19	-	23264656	23264729	THC1525505
GAM3788	9951	hsa	12	-	50069896	50069970	THC1556506
GAM3810	10439	hsa	11	-	119579263	119579351	THC1452347
GAM3890	11222	hsa	8	+	92752551	92752652	
GAM3892	10488	hsa	12	-	34242096	34242169	THC1547385
GAM3946	10833	hsa	11	+	44652554	44652629	THC1586614
GAM3978	10752	hsa	12	+	118768041	118768121	
GAM3990	9758	hsa	19	+	44650568	44650651	
GAM4008	10952	hsa	14	+	86637061	86637147	THC1526006
GAM4011	9765	hsa	22	+	45149119	45149212	THC1541347
GAM4020	9615	hsa	11	-	62871608	62871701	THC1452346
GAM4027	11191	hsa	17	-	6197075	6197180	THC1482663
GAM4064	10022	hsa	7	-	1197566	1197640	THC1476990
GAM4074	10140	hsa	7	+	69300375	69300459	
GAM4085	9711	hsa	11	+	71416467	71416564	
GAM4130	10199	hsa	X	+	77528890	77528958	
GAM4136	9668	hsa	19	-	58315712	58315841	THC1588241
GAM4142	10081	hsa	X	-	145175426	145175506	THC1445449
GAM4147	11207	hsa	14	-	79828332	79828452	
GAM4152	10154	hsa	22	+	25256625	25256741	
GAM4188	9909	hsa	11	+	113971971	113972049	
GAM4189	9666	hsa	19	-	32944216	32944301	THC1493174
GAM4199	10173	hsa	22	-	35997845	35997924	THC1472943
GAM4205	10494	hsa	13	-	110102091	110102175	THC1562945
GAM4238	10112	hsa	9	-	42216969	42217067	THC1595205
GAM4243	9595	hsa	15	+	62347057	62347119	THC1535339
GAM4298	10843	hsa	12	-	111675686	111675769	THC1441053
GAM4315	9960	hsa	16	+	75288703	75288810	
GAM4364	9623	hsa	X	+	98918395	98918498	THC1454247
GAM4376	10325	hsa	18	+	182465	182565	THC1549027
GAM4377	10976	hsa	20	-	49418894	49419004	THC1566325
GAM4382	9983	hsa	10	+	98489976	98490054	
GAM4398	11199	hsa	16	+	50452834	50452936	THC1449412
GAM4408	9746	hsa	8	-	138777302	138777407	THC1595183
GAM4423	10486	hsa	17	+	40086542	40086631	THC1488043
GAM4426	11283	hsa	1	-	77432988	77433078	THC1456099
GAM4429	10859	hsa	12	-	55937832	55937908	THC1500843
GAM4432	9931	hsa	9	+	27028798	27028895	THC1504877
GAM4446	10969	hsa	X	-	117986909	117986983	THC1555513
GAM4448	9953	hsa	10	+	33327986	33328081	THC1463380
GAM4459	10240	hsa	7	+	18267651	18267780	
GAM4516	10651	hsa	12	+	50034558	50034663	THC1428232
GAM4538	10975	hsa	15	-	53161338	53161430	THC1501655
GAM4544	10926	hsa	9	+	100974291	100974366	THC1553853
GAM4557	11230	hsa	9	+	88520248	88520362	
GAM4561	9992	hsa	1	+	158626687	158626806	THC1510400

GAM4571	9771	hsa	19	+	54394158	54394243	THC1427370
GAM4633	11142	hsa	X	-	71710862	71710951	THC1437961
GAM4650	10553	hsa	17	+	66913128	66913215	
GAM4656	10921	hsa	5	+	142589577	142589675	THC1539180
GAM4671	10032	hsa	10	-	840148	840239	THC1472112
GAM4685	11293	hsa	17	+	26788414	26788525	
GAM4690	10888	hsa	20	+	42013351	42013450	
GAM4707	10352	hsa	X	+	94524960	94525059	
GAM4709	10157	hsa	9	+	97691104	97691181	THC1534017
GAM4733	9593	hsa	13	+	99149260	99149327	THC1586272
GAM4738	9729	hsa	21	+	25868152	25868238	
GAM4769	10176	hsa	8	+	128497043	128497147	THC1416609
GAM4796	10896	hsa	19	+	37551256	37551383	THC1471744
GAM4800	10690	hsa	15	-	90601712	90601792	THC1585438
GAM4803	11165	hsa	7	-	128048648	128048743	THC1452742
GAM4814	10992	hsa	10	+	51241197	51241274	THC1564358
GAM4821	10930	hsa	20	+	52745273	52745386	THC1410801
GAM4844	11226	hsa	16	-	15101510	15101596	THC1503496
GAM4895	10116	hsa	11	-	119323982	119324097	THC1589309
GAM4904	10792	hsa	9	-	118036640	118036725	THC1585612
GAM4913	9599	hsa	18	+	52918008	52918100	
GAM4932	11218	hsa	9	-	116757833	116757940	THC1429106
GAM4946	10922	hsa	9	-	129644	129766	THC1592088
GAM4969	10491	hsa	20	-	43463077	43463178	THC1501266
GAM4971	10965	hsa	15	+	37937921	37938008	THC1443612
GAM4975	9993	hsa	8	+	142992769	142992862	THC1536309
GAM4986	9981	hsa	9	-	43025631	43025760	THC1581432
GAM5000	10518	hsa	12	-	116259939	116260015	THC1507051
GAM5008	10156	hsa	19	+	54394162	54394238	THC1427370
GAM5011	10837	hsa	15	+	45580563	45580638	THC1482318
GAM5035	10820	hsa	9	+	71813551	71813660	THC1549688
GAM5048	10510	hsa	12	+	118768043	118768119	
GAM5058	10645	hsa	12	+	122025582	122025669	THC1529894
GAM5082	10778	hsa	8	+	101882283	101882351	
GAM5085	10724	hsa	9	-	43025636	43025764	THC1581432
GAM5090	10160	hsa	16	+	58268693	58268792	THC1554616
GAM5127	10734	hsa	13	+	43743986	43744090	THC1558776
GAM5142	9751	hsa	20	+	4104693	4104774	THC1502117
GAM5209	10525	hsa	11	-	72669608	72669737	THC1457464
GAM5217	9631	hsa	7	-	22848134	22848223	THC1519376
GAM5222	9898	hsa	17	+	34060088	34060194	THC1412192
GAM5254	11132	hsa	X	+	107483900	107484000	
GAM5266	10941	hsa	6	+	28924785	28924860	
GAM5270	10016	hsa	10	+	99045264	99045350	
GAM5272	10727	hsa	12	-	93734228	93734316	THC1504618
GAM5278	10980	hsa	16	+	58433646	58433739	
GAM5292	11143	hsa	11	-	96304363	96304450	THC1549749
GAM5324	10951	hsa	19	-	51118141	51118216	THC1448850
GAM5329	11139	hsa	7	+	133099409	133099504	
GAM5340	9709	hsa	8	+	65014377	65014480	THC1540166

GAM5342	9601	hsa	19	-	9563450	9563548	THC1551467
GAM5354	11223	hsa	11	-	68147756	68147845	THC1577776
GAM5370	9902	hsa	11	-	26652582	26652656	THC1411839
GAM5371	9757	hsa	19	-	17214638	17214719	THC1471364
GAM5374	9987	hsa	19	+	37551253	37551383	THC1471744
GAM5385	9977	hsa	3	+	35621432	35621507	
GAM5415	10133	hsa	18	+	41537048	41537144	THC1528226
GAM5422	10860	hsa	X	+	47243046	47243133	
GAM5444	10242	hsa	9	+	127094099	127094175	
GAM5454	10545	hsa	X	+	101393105	101393197	THC1409470
GAM5486	10210	hsa	11	-	71909012	71909130	
GAM5498	9766	hsa	16	+	3674783	3674841	
GAM5512	9703	hsa	19	+	54100819	54100904	
GAM5514	10801	hsa	22	+	25442199	25442285	THC1597098
GAM5526	10393	hsa	14	-	79906276	79906371	THC1592424
GAM5560	11007	hsa	11	+	86570029	86570141	
GAM5597	9764	hsa	17	-	42550378	42550491	THC1599964
GAM5615	10117	hsa	12	-	51339544	51339646	THC1518024
GAM5617	10703	hsa	X	-	47865219	47865324	THC1507537
GAM5623	9692	hsa	11	+	113971966	113972053	
GAM5640	9747	hsa	19	-	16837776	16837864	THC1504884
GAM5653	10648	hsa	8	+	77350810	77350897	
GAM5654	9597	hsa	16	+	21698933	21699004	
GAM5657	10736	hsa	12	+	1344537	1344626	
GAM5673	9761	hsa	X	-	7772009	7772132	THC1569880
GAM5691	10719	hsa	19	+	54100823	54100899	
GAM5697	9911	hsa	16	+	31719324	31719406	THC1425734
GAM5703	10256	hsa	19	-	32944217	32944300	THC1493174
GAM5728	10119	hsa	10	+	79169049	79169129	
GAM5744	10924	hsa	18	+	901080	901209	THC1440500
GAM5749	9769	hsa	16	-	18721900	18721984	THC1544080
GAM5764	10531	hsa	9	-	62131098	62131225	THC1581432
GAM5798	10000	hsa	X	+	52222704	52222792	
GAM5800	11225	hsa	22	+	35297121	35297239	
GAM5806	11215	hsa	16	+	23608784	23608886	THC1418882
GAM5809	11252	hsa	10	+	114373899	114373992	THC1448987
GAM5814	9664	hsa	20	+	58108888	58108966	THC1515190
GAM5823	10909	hsa	X	-	7772036	7772111	THC1569880
GAM5826	10710	hsa	16	+	492716	492803	THC1479316
GAM5836	9774	hsa	2	+	232531653	232531737	THC1429623
GAM5859	10392	hsa	8	+	120684537	120684620	
GAM5868	9982	hsa	12	-	56320934	56321064	THC1416629
GAM5872	10886	hsa	7	+	78069309	78069439	
GAM5874	10189	hsa	21	+	31954910	31954992	THC1562547
GAM5884	10741	hsa	14	+	65430589	65430697	
GAM5886	10717	hsa	10	+	101743923	101744003	THC1541391
GAM5910	11032	hsa	22	-	24156183	24156291	THC1550693
GAM5916	10182	hsa	20	+	3852983	3853066	THC1510126
GAM5958	9620	hsa	15	-	90601847	90601948	THC1585438
GAM5963	9617	hsa	X	-	126883041	126883119	THC1559611

GAM5971	9950	hsa	9	-	10754212	10754308	THC1420615
GAM5973	11167	hsa	22	+	42645831	42645952	
GAM5990	11186	hsa	6	+	30850318	30850400	
GAM5998	10074	hsa	16	+	30012813	30012908	
GAM6014	10685	hsa	9	+	21850242	21850306	THC1506353
GAM6024	10230	hsa	9	-	116757829	116757944	THC1429106
GAM6051	9651	hsa	14	-	62941952	62942035	THC1548739
GAM6055	10862	hsa	19	+	43546131	43546204	THC1565950
GAM6083	9939	hsa	11	-	69517032	69517115	THC1565280
GAM6102	11170	hsa	7	+	43773501	43773597	THC1502537
GAM6121	10148	hsa	18	+	182463	182567	THC1549027
GAM6161	11182	hsa	15	-	28205840	28205952	
GAM6172	10977	hsa	13	-	73791102	73791195	THC1564754
GAM6234	11250	hsa	10	+	80342962	80343085	THC1435926
GAM6250	11290	hsa	20	+	36468581	36468697	THC1549599
GAM6265	11294	hsa	9	+	78004551	78004658	
GAM6271	10422	hsa	7	+	133099410	133099503	
GAM6296	10979	hsa	17	-	40099114	40099186	THC1585293
GAM6306	11208	hsa	12	-	56453736	56453829	THC1439723
GAM6329	10848	hsa	11	-	26729102	26729184	THC1470567
GAM6361	10433	hsa	17	-	77134484	77134572	THC1480218
GAM6366	9678	hsa	14	+	102138768	102138891	
GAM6388	10201	hsa	8	+	9805117	9805208	
GAM6414	10893	hsa	10	+	98886813	98886898	THC1477135
GAM6417	10520	hsa	9	-	116757828	116757945	THC1429106
GAM6431	10700	hsa	19	+	12904884	12904956	THC1445246
GAM6440	10971	hsa	7	+	104082529	104082634	
GAM6459	9612	hsa	6	+	30850314	30850404	
GAM6466	9733	hsa	17	+	78873540	78873668	THC1479162
GAM6467	10124	hsa	13	+	23774919	23775049	
GAM6506	10811	hsa	17	+	29270291	29270364	THC1527322
GAM6509	10051	hsa	21	+	16592351	16592462	THC1520849
GAM6531	11009	hsa	8	+	54026269	54026339	
GAM6541	10012	hsa	13	+	99881835	99881928	
GAM6564	10670	hsa	17	+	78873542	78873672	THC1479162
GAM6567	10424	hsa	11	+	88200970	88201046	
GAM6618	10920	hsa	7	-	140693627	140693722	THC1433860
GAM6638	10161	hsa	3	-	51855487	51855582	THC1491817
GAM6674	9689	hsa	16	-	4506790	4506860	THC1597694
GAM6700	9606	hsa	1	+	156731865	156731959	THC1411123
GAM6773	10819	hsa	1	+	203719518	203719616	
GAM6774	10155	hsa	5	+	175687263	175687360	THC1576455
GAM6799	10936	hsa	12	-	56320939	56321062	THC1416629
GAM6807	10082	hsa	10	+	121833616	121833746	THC1534183
GAM6811	10193	hsa	13	-	110102077	110102190	THC1562945
GAM6818	10771	hsa	7	-	122713355	122713419	THC1456310
GAM6836	10334	hsa	7	-	71860457	71860555	THC1516956
GAM6840	10967	hsa	19	+	40508403	40508488	THC1410381
GAM6842	10938	hsa	18	-	22646286	22646415	THC1587491
GAM6858	9933	hsa	X	+	118137371	118137458	THC1589537

GAM6978	9973	hsa	7	-	140693634	140693712	THC1433860
GAM6982	9985	hsa	22	-	44721785	44721914	THC1562390
GAM6994	11149	hsa	19	+	44650573	44650646	
GAM6996	10970	hsa	17	-	6197081	6197176	THC1482663
GAM7017	10244	hsa	9	-	43025637	43025753	THC1581432
GAM7022	10767	hsa	X	-	47741101	47741215	THC1416555
GAM7067	10053	hsa	19	+	42704752	42704859	THC1564785
GAM7078	10852	hsa	17	-	38614091	38614177	THC1513966
GAM7080	10009	hsa	1	-	1047334	1047441	
GAM7095	10960	hsa	7	+	104082522	104082644	
GAM7102	10939	hsa	1	+	152542921	152542996	
GAM7124	9762	hsa	16	+	75288695	75288819	
GAM7135	11161	hsa	X	-	47741108	47741208	THC1416555
GAM7140	10443	hsa	16	+	69762447	69762557	
GAM7146	9924	hsa	13	+	35139835	35139920	
GAM7162	9773	hsa	20	+	53192373	53192473	THC1579830
GAM7166	10492	hsa	10	-	109789635	109789705	THC1458161
GAM7169	9622	hsa	16	+	50572112	50572240	THC1553866
GAM7199	10669	hsa	13	-	48078880	48078943	THC1599986
GAM7201	9649	hsa	17	+	27583817	27583894	
GAM7212	10691	hsa	21	-	45164402	45164486	THC1562047
GAM7241	9910	hsa	12	-	46762982	46763077	THC1530062
GAM7250	9971	hsa	7	-	82179628	82179717	THC1555889
GAM7255	10218	hsa	15	+	33981298	33981403	
GAM7257	10808	hsa	6	-	159922811	159922884	THC1453470
GAM7260	10138	hsa	X	+	61858740	61858831	THC1520561
GAM7264	10497	hsa	11	-	78654885	78654988	THC1472355
GAM7272	10040	hsa	20	+	44585164	44585243	THC1485240
GAM7302	10059	hsa	15	-	53161341	53161428	THC1501655
GAM7320	10130	hsa	5	-	69298330	69298411	THC1414413
GAM7331	10397	hsa	20	+	61512957	61513055	THC1457355
GAM7345	10245	hsa	9	-	62131103	62131215	THC1581432
GAM7349	10185	hsa	12	-	43372332	43372433	THC1564824
GAM7350	10828	hsa	1	+	83600201	83600312	THC1413248
GAM7363	9686	hsa	9	+	97689215	97689321	THC1497034
GAM7366	10635	hsa	12	+	49033585	49033673	
GAM7369	11010	hsa	13	+	26088279	26088405	THC1419952
GAM7371	10718	hsa	7	-	127634676	127634751	THC1471217
GAM7374	10056	hsa	20	-	36127247	36127336	THC1530397
GAM7400	10658	hsa	13	+	92806795	92806880	
GAM7415	10006	hsa	16	+	69762453	69762552	
GAM7440	10107	hsa	21	-	42307485	42307562	THC1502578
GAM7446	9680	hsa	19	+	45848125	45848210	THC1523801
GAM7449	11162	hsa	7	+	26847818	26847898	
GAM7464	10499	hsa	8	-	37872487	37872595	THC1446607
GAM7473	10168	hsa	19	-	3484360	3484468	
GAM7477	9962	hsa	7	+	72048231	72048360	THC1461329
GAM7520	10937	hsa	17	+	42534098	42534177	THC1467464
GAM7530	10502	hsa	7	-	3260144	3260217	
GAM7542	10697	hsa	12	+	129239735	129239827	THC1466501

GAM7546	10064	hsa	17	+	60900963	60901037	THC1551816
GAM7553	9603	hsa	7	-	26917372	26917455	
GAM7559	11219	hsa	12	+	49747946	49748037	THC1494932
GAM7591	11291	hsa	2	-	136686979	136687030	
GAM7592	9988	hsa	21	+	22819631	22819716	THC1466992
GAM7601	9925	hsa	11	+	92812990	92813082	THC1457396
GAM7636	10163	hsa	9	+	88520255	88520353	
GAM7654	10171	hsa	10	-	102859212	102859317	THC1426270
GAM7663	10023	hsa	11	+	68334837	68334946	
GAM7700	9895	hsa	8	+	101882286	101882348	
GAM7707	10136	hsa	9	+	68168613	68168714	THC1445488
GAM7729	11171	hsa	22	-	37886140	37886212	THC1421992
GAM7776	10338	hsa	X	+	120997504	120997603	THC1453918
GAM7777	9688	hsa	11	-	96304357	96304457	THC1549749
GAM7784	10812	hsa	13	+	107796034	107796141	THC1462983
GAM7817	10084	hsa	14	+	101053737	101053810	
GAM7837	11248	hsa	12	+	29387505	29387634	THC1496165
GAM7845	9677	hsa	11	+	68013714	68013820	
GAM7854	11177	hsa	19	-	52841049	52841155	THC1466094
GAM7865	10071	hsa	10	+	102246140	102246247	
GAM7884	10879	hsa	12	+	102447082	102447156	
GAM7889	10195	hsa	20	-	50175600	50175686	THC1449211
GAM7898	11292	hsa	11	+	47657707	47657795	THC1551035
GAM7902	11246	hsa	10	+	29022047	29022132	THC1551030
GAM7911	10241	hsa	8	+	25092986	25093099	THC1518415
GAM7915	9767	hsa	4	-	14497507	14497582	THC1479780
GAM7933	10714	hsa	7	-	3260143	3260218	
GAM7954	10654	hsa	19	+	43546115	43546217	THC1565950
GAM7966	10015	hsa	14	-	67546633	67546732	THC1566842
GAM7980	9944	hsa	15	+	55163316	55163417	THC1506760
GAM8013	10484	hsa	21	+	36439313	36439388	THC1440331
GAM8026	11200	hsa	19	-	58074215	58074327	THC1495667
GAM8031	10474	hsa	12	+	26287592	26287680	THC1546633
GAM8047	9650	hsa	X	+	136594089	136594179	THC1478628
GAM8100	10927	hsa	18	-	10904327	10904425	THC1429003
GAM8109	10255	hsa	15	+	48231664	48231745	THC1589068
GAM8145	10534	hsa	10	+	90807704	90807788	THC1510482
GAM8164	10756	hsa	17	-	76816710	76816797	THC1469417
GAM8206	10265	hsa	11	+	107994686	107994771	
GAM8276	9662	hsa	19	-	61627070	61627153	THC1409031
GAM8285	9996	hsa	1	+	158626692	158626797	THC1510400
GAM8288	11188	hsa	18	+	54931946	54932023	THC1578650
GAM8311	10567	hsa	15	+	96904480	96904567	THC1513521
GAM8339	10047	hsa	X	+	107487845	107487922	
GAM8349	10804	hsa	X	+	136594068	136594192	THC1478628
GAM8362	10477	hsa	15	+	43562099	43562221	
GAM8380	11178	hsa	3	-	23784450	23784553	THC1462671
GAM8386	10715	hsa	19	+	18386080	18386138	THC1520594
GAM8396	10963	hsa	9	-	113370917	113371017	THC1490929
GAM8439	11244	hsa	X	+	77528891	77528957	

GAM8447	11197	hsa	15	+	26678132	26678230	THC1453010
GAM8452	10018	hsa	1	+	10844836	10844919	
GAM8473	10257	hsa	16	+	3585727	3585790	
GAM8489	10498	hsa	15	+	49193542	49193626	THC1577110
GAM8506	11282	hsa	14	+	80296015	80296094	THC1473700
GAM8531	11133	hsa	12	+	80266794	80266861	THC1449666
GAM8539	10907	hsa	11	+	88200943	88201072	
GAM8542	10858	hsa	16	-	25177054	25177119	THC1540035
GAM8563	9636	hsa	8	-	81283739	81283810	THC1550510
GAM8598	11295	hsa	21	+	31954902	31955007	
GAM8601	10899	hsa	9	+	114561400	114561477	
GAM8631	10973	hsa	17	+	30319063	30319172	THC1539612
GAM8636	10398	hsa	14	+	93614982	93615066	THC1518532
GAM8647	10913	hsa	16	-	30002913	30003001	THC1439119
GAM8665	11079	hsa	11	+	10301954	10302053	
GAM8678	10842	hsa	19	+	62449343	62449421	THC1568419
GAM8693	9740	hsa	10	-	105533389	105533457	THC1524354
GAM336121	9627	hsa					
GAM336122	9713	hsa					THC1591730
GAM336123	9714	hsa					
GAM336124	9716	hsa					
GAM336125	9918	hsa					
GAM336126	10095	hsa					
GAM336127	10105	hsa					
GAM336128	10147	hsa					
GAM336129	10149	hsa					
GAM336130	10167	hsa					
GAM336131	10203	hsa					
GAM336132	10206	hsa					
GAM336133	10208	hsa					
GAM336134	10249	hsa					
GAM336135	10254	hsa					
GAM336136	10266	hsa					
GAM336137	10267	hsa					
GAM336138	10270	hsa					
GAM336139	10276	hsa					
GAM336140	10285	hsa					
GAM336141	10290	hsa					
GAM336142	10291	hsa					THC1438462
GAM336143	10302	hsa					THC1577759
GAM336144	10312	hsa					
GAM336145	10313	hsa					
GAM336146	10318	hsa					
GAM336147	10319	hsa					
GAM336148	10320	hsa					
GAM336149	10326	hsa					THC1599200
GAM336150	10331	hsa					
GAM336151	10332	hsa					
GAM336152	10333	hsa					
GAM336153	10336	hsa					

GAM336154	10337	hsa	
GAM336155	10339	hsa	THC1597055
GAM336156	10343	hsa	
GAM336157	10346	hsa	
GAM336158	10353	hsa	
GAM336159	10354	hsa	
GAM336160	10358	hsa	THC1544476
GAM336161	10362	hsa	
GAM336162	10364	hsa	
GAM336163	10367	hsa	
GAM336164	10369	hsa	
GAM336165	10371	hsa	THC1466766
GAM336166	10376	hsa	
GAM336167	10378	hsa	
GAM336168	10383	hsa	
GAM336169	10444	hsa	
GAM336170	10464	hsa	
GAM336171	10466	hsa	
GAM336172	10479	hsa	
GAM336173	10503	hsa	
GAM336174	10505	hsa	
GAM336175	10508	hsa	
GAM336176	10530	hsa	
GAM336177	10533	hsa	
GAM336178	10547	hsa	
GAM336179	10557	hsa	
GAM336180	10570	hsa	
GAM336181	10571	hsa	
GAM336182	10573	hsa	
GAM336183	10576	hsa	THC1477598
GAM336184	10584	hsa	
GAM336185	10601	hsa	
GAM336186	10608	hsa	THC1505172
GAM336187	10615	hsa	
GAM336188	10616	hsa	
GAM336189	10619	hsa	
GAM336190	10621	hsa	THC1529728
GAM336191	10628	hsa	
GAM336192	10630	hsa	
GAM336193	10631	hsa	
GAM336194	10636	hsa	
GAM336195	10638	hsa	
GAM336196	10641	hsa	
GAM336197	10656	hsa	THC1523983
GAM336198	10657	hsa	THC1577759
GAM336199	10663	hsa	THC1504611
GAM336200	10676	hsa	
GAM336201	10679	hsa	
GAM336202	10681	hsa	THC1590122
GAM336203	10755	hsa	THC1455312

GAM336204	10838	hsa					
GAM336205	10942	hsa					
GAM336206	10943	hsa					
GAM336207	10948	hsa					
GAM336208	10968	hsa					THC1455312
GAM336209	10996	hsa					
GAM336210	11040	hsa					
GAM336211	11045	hsa					THC1438462
GAM336212	11046	hsa					
GAM336213	11048	hsa					THC1443841
GAM336214	11055	hsa					
GAM336215	11058	hsa					
GAM336216	11069	hsa					
GAM336217	11072	hsa					
GAM336218	11073	hsa					
GAM336219	11081	hsa					
GAM336220	11089	hsa					
GAM336221	11090	hsa					
GAM336222	11097	hsa					
GAM336223	11099	hsa					
GAM336224	11106	hsa					
GAM336225	11107	hsa					
GAM336226	11109	hsa					
GAM336227	11112	hsa					
GAM336228	11113	hsa					
GAM336229	11114	hsa					
GAM336230	11118	hsa					
GAM336231	11119	hsa					
GAM336232	11121	hsa					
GAM336233	11157	hsa					
GAM336234	11158	hsa					THC1443841
GAM336235	11160	hsa					THC1437587
GAM336236	11184	hsa					
GAM336237	11254	hsa					
GAM336238	11259	hsa					
GAM336239	11261	hsa					
GAM336240	11267	hsa					
GAM336241	11268	hsa					
GAM336242	11270	hsa					
GAM336243	11271	hsa					
GAM336244	11274	hsa					
GAM336245	10781	hsa	16	+	253589	253668	THC1574872
GAM336246	9748	hsa	12	-	265415	265505	
GAM336247	10587	hsa	16	+	377662	377749	
GAM336251	10995	hsa	19	+	851357	851432	
GAM336252	10145	hsa	17	+	960158	960264	
GAM336255	10866	hsa	17	+	1228075	1228159	
GAM336256	10867	hsa	17	+	1228075	1228161	
GAM336257	10441	hsa	19	+	1312908	1312995	
GAM336259	10493	hsa	8	+	1889566	1889651	

GAM336260	10408	hsa	X	+	1984914	1985013	
GAM336261	10705	hsa	10	+	2004805	2004903	
GAM336264	10915	hsa	20	+	2764962	2765033	
GAM336267	10238	hsa	19	+	2999427	2999516	
GAM336270	9940	hsa	10	+	3269951	3270046	
GAM336271	9721	hsa	12	+	3307949	3308029	
GAM336272	11194	hsa	12	+	3477981	3478093	
GAM336275	11273	hsa	12	-	3861125	3861212	
GAM336279	11012	hsa	17	+	4367585	4367684	
GAM336281	9777	hsa	6	+	4437001	4437082	THC1432163
GAM336282	9957	hsa	17	+	4444093	4444183	
GAM336283	10409	hsa	17	+	4444095	4444180	
GAM336284	9778	hsa	6	+	4649605	4649686	THC1432163
GAM336285	9779	hsa	18	-	4756826	4756907	THC1432163
GAM336289	11021	hsa	11	+	5537268	5537354	
GAM336290	10190	hsa	11	+	5537269	5537353	
GAM336291	10094	hsa	11	-	5605037	5605141	
GAM336292	9780	hsa	6	+	5676458	5676539	THC1432163
GAM336293	10768	hsa	17	+	5710623	5710717	
GAM336294	10806	hsa	7	-	5786960	5787033	THC1539594
GAM336297	11049	hsa	10	+	6079591	6079694	
GAM336298	10299	hsa	10	+	6079592	6079693	
GAM336299	10787	hsa	9	+	6225060	6225155	
GAM336300	10940	hsa	9	+	6225073	6225145	
GAM336303	9722	hsa	17	+	6623046	6623142	THC1486168
GAM336304	10294	hsa	12	-	6644614	6644719	THC1429005
GAM336306	9730	hsa	19	+	6790508	6790610	
GAM336307	10405	hsa	19	+	6790516	6790607	
GAM336308	9690	hsa	17	-	6865733	6865789	
GAM336309	10826	hsa	12	+	6882641	6882714	
GAM336311	10359	hsa	19	+	7027442	7027538	
GAM336313	10610	hsa	19	+	7192320	7192401	
GAM336315	11043	hsa	5	+	7755711	7755812	
GAM336316	10287	hsa	5	+	7755712	7755811	
GAM336317	10591	hsa	5	+	7755718	7755806	
GAM336318	10204	hsa	17	-	7839733	7839801	
GAM336320	11105	hsa	17	+	8370724	8370824	
GAM336321	10620	hsa	17	+	8370731	8370818	
GAM336322	9781	hsa	11	-	8383107	8383188	THC1432163
GAM336323	9660	hsa	19	+	8427810	8427893	THC1529920
GAM336324	10198	hsa	19	-	8553447	8553552	THC1569262
GAM336325	10684	hsa	8	+	8562574	8562668	
GAM336326	9683	hsa	11	+	8745924	8746036	THC1422230
GAM336329	10880	hsa	17	-	9095043	9095136	
GAM336330	9782	hsa	10	+	9107249	9107330	THC1432163
GAM336331	10172	hsa	11	-	9202641	9202751	THC1509380
GAM336332	10166	hsa	11	+	9215763	9215833	
GAM336334	11108	hsa	11	+	9504192	9504293	
GAM336335	10366	hsa	11	+	9504193	9504292	
GAM336336	11084	hsa	2	-	9554905	9555006	THC1537102

GAM336337	10578	hsa	2	-	9554911	9554999	THC1537102
GAM336338	10872	hsa	18	+	9584579	9584691	
GAM336339	10370	hsa	18	+	9731276	9731375	THC1544485
GAM336340	10351	hsa	3	+	9732603	9732700	
GAM336341	9663	hsa	3	+	9793682	9793765	
GAM336342	11255	hsa	3	+	9793686	9793761	
GAM336343	10480	hsa	3	+	9793688	9793759	
GAM336344	10748	hsa	11	+	9881789	9881884	
GAM336347	9671	hsa	19	+	10064670	10064749	
GAM336348	9783	hsa	4	-	10077912	10077993	THC1432163
GAM336349	11033	hsa	7	-	10202193	10202274	
GAM336350	10348	hsa	19	+	10212232	10212331	
GAM336352	9784	hsa	8	-	10343377	10343458	THC1432163
GAM336353	10355	hsa	16	+	10535996	10536094	
GAM336354	11042	hsa	19	+	10593137	10593237	
GAM336357	10988	hsa	17	-	10669795	10669870	THC1569888
GAM336359	11030	hsa	8	-	10822733	10822833	
GAM336360	9632	hsa	8	-	10822748	10822821	
GAM336361	10629	hsa	2	+	10939875	10939962	
GAM336362	10061	hsa	X	-	10975636	10975715	
GAM336363	9687	hsa	16	+	11000648	11000730	
GAM336364	11272	hsa	12	-	11034593	11034668	
GAM336365	9965	hsa	12	-	11079910	11080020	
GAM336368	10187	hsa	11	+	11301473	11301581	
GAM336369	10164	hsa	19	+	11451765	11451866	
GAM336372	10216	hsa	10	-	11647684	11647758	
GAM336373	11088	hsa	1	-	11686899	11687000	
GAM336374	10341	hsa	1	-	11686900	11686999	
GAM336375	9914	hsa	19	+	11850038	11850168	
GAM336376	10177	hsa	16	-	11968201	11968285	
GAM336377	11214	hsa	16	-	11968215	11968272	
GAM336378	9785	hsa	17	+	12026100	12026181	THC1432163
GAM336380	10175	hsa	16	+	12103390	12103473	
GAM336381	10419	hsa	16	+	12103394	12103469	
GAM336382	10562	hsa	16	-	12118809	12118896	
GAM336384	11286	hsa	20	-	12348835	12348933	
GAM336385	10423	hsa	20	-	12348840	12348928	
GAM336386	9625	hsa	16	+	12401666	12401757	
GAM336387	11269	hsa	X	+	12619567	12619645	
GAM336388	10883	hsa	10	+	12778141	12778254	THC1449659
GAM336389	10708	hsa	10	+	12778156	12778235	THC1449659
GAM336390	11057	hsa	19	-	12791804	12791904	
GAM336391	10239	hsa	19	-	12791805	12791897	
GAM336392	10125	hsa	19	-	12791819	12791890	
GAM336393	11024	hsa	17	+	12833782	12833874	THC1466980
GAM336394	10159	hsa	8	+	12908963	12909065	
GAM336395	10836	hsa	8	+	12908972	12909059	
GAM336397	10465	hsa	16	+	13120513	13120614	
GAM336399	9989	hsa	18	+	13641031	13641147	
GAM336400	9786	hsa	3	+	13789635	13789716	THC1432163

GAM336403	10212	hsa	Y	+	14113783	14113853	
GAM336404	10786	hsa	22	-	14534146	14534255	
GAM336405	11189	hsa	18	+	14872165	14872228	
GAM336406	11216	hsa	17	+	14912408	14912493	
GAM336407	10733	hsa	10	-	15010865	15010956	THC1457141
GAM336408	10793	hsa	10	-	15010865	15010959	THC1457141
GAM336409	10543	hsa	10	-	15010870	15010952	THC1457141
GAM336412	10062	hsa	9	-	15155243	15155347	
GAM336413	10328	hsa	16	+	15476401	15476499	
GAM336414	9699	hsa	7	-	15591278	15591386	
GAM336420	9787	hsa	10	+	16256343	16256424	THC1432163
GAM336422	10278	hsa	3	+	16344259	16344345	
GAM336424	10406	hsa	16	+	16592675	16592767	
GAM336426	9788	hsa	3	-	16815249	16815330	THC1432163
GAM336428	10876	hsa	22	+	16882174	16882253	
GAM336429	10536	hsa	17	+	17033275	17033360	
GAM336430	10695	hsa	7	+	17062054	17062167	
GAM336431	10109	hsa	7	+	17062060	17062156	
GAM336432	10463	hsa	7	+	17062066	17062151	THC1579034
GAM336433	10093	hsa	7	+	17062067	17062150	THC1579034
GAM336434	10262	hsa	20	+	17392534	17392608	
GAM336435	10914	hsa	10	-	17533127	17533225	
GAM336439	11280	hsa	11	+	18148992	18149071	
GAM336440	10773	hsa	11	+	18148996	18149069	
GAM336441	10675	hsa	Y	+	18229150	18229239	
GAM336442	10485	hsa	9	+	18307900	18307989	
GAM336445	10103	hsa	22	+	18488728	18488800	THC1431185
GAM336447	9657	hsa	17	-	18512666	18512795	
GAM336448	10407	hsa	16	-	18720857	18720949	
GAM336450	10122	hsa	10	+	18853144	18853257	
GAM336451	10451	hsa	18	+	18960647	18960760	
GAM336452	10757	hsa	18	+	18960660	18960750	
GAM336453	11140	hsa	15	-	19104724	19104809	
GAM336454	11070	hsa	1	+	19125660	19125759	THC1500671
GAM336455	10421	hsa	17	+	19182411	19182470	
GAM336456	10459	hsa	13	+	19183141	19183217	
GAM336458	10555	hsa	12	+	19294864	19294956	
GAM336460	9646	hsa	16	+	19464207	19464315	THC1457170
GAM336461	10458	hsa	18	+	19661582	19661668	THC1541259
GAM336462	10799	hsa	13	+	19699736	19699855	
GAM336465	10550	hsa	20	+	19884809	19884896	
GAM336468	10910	hsa	8	+	19896011	19896086	
GAM336469	9737	hsa	20	+	20036295	20036382	
GAM336470	9738	hsa	20	+	20036295	20036385	
GAM336472	9959	hsa	15	+	20299247	20299338	
GAM336474	9979	hsa	Y	-	20354510	20354577	
GAM336475	10617	hsa	15	+	20384897	20384984	
GAM336476	10847	hsa	17	-	20417307	20417408	THC1504686
GAM336477	10855	hsa	16	+	20421189	20421285	THC1552118
GAM336478	11137	hsa	16	+	20421197	20421282	THC1552118

GAM336479	10856	hsa	16	-	20480066	20480162	THC1552118
GAM336480	11138	hsa	16	-	20480069	20480154	THC1552118
GAM336483	11276	hsa	8	+	20641538	20641624	
GAM336484	9682	hsa	12	+	20790820	20790916	
GAM336486	9744	hsa	18	-	21001411	21001516	THC1531401
GAM336487	9621	hsa	5	-	21104974	21105023	
GAM336488	9694	hsa	22	-	21165273	21165366	
GAM336489	9789	hsa	12	+	21185062	21185143	THC1432163
GAM336490	10579	hsa	5	-	21350021	21350108	
GAM336491	10507	hsa	21	+	21374719	21374791	
GAM336492	10538	hsa	16	-	21380738	21380838	
GAM336493	10686	hsa	14	-	21401896	21401977	
GAM336494	10974	hsa	21	+	21775643	21775725	
GAM336495	10539	hsa	16	-	21813001	21813101	
GAM336496	9790	hsa	18	-	21821931	21822012	THC1432163
GAM336497	11289	hsa	8	+	21935927	21936033	
GAM336498	9955	hsa	8	+	21935946	21936015	
GAM336499	10861	hsa	10	+	21981294	21981405	
GAM336502	9995	hsa	22	-	22350120	22350199	
GAM336503	9994	hsa	13	-	22360083	22360172	
GAM336504	10445	hsa	13	-	22376839	22376946	
GAM336505	10526	hsa	14	+	22426100	22426188	
GAM336506	10540	hsa	16	+	22435583	22435683	
GAM336507	10891	hsa	10	-	22440215	22440311	THC1586362
GAM336508	10890	hsa	10	-	22440222	22440311	THC1586362
GAM336509	11266	hsa	22	+	22444388	22444458	
GAM336510	10541	hsa	16	+	22480967	22481067	
GAM336511	9791	hsa	5	+	22524532	22524613	THC1432163
GAM336512	10932	hsa	18	+	22572448	22572552	
GAM336513	9921	hsa	15	+	22650373	22650445	
GAM336514	10277	hsa	15	+	22660392	22660478	
GAM336516	9700	hsa	22	+	22796154	22796241	
GAM336518	10449	hsa	15	+	22950966	22951048	THC1441640
GAM336519	9792	hsa	18	-	23259601	23259682	THC1432163
GAM336520	10500	hsa	19	-	23264637	23264744	
GAM336522	9735	hsa	X	+	23295481	23295586	THC1553039
GAM336523	9793	hsa	12	-	23320241	23320322	THC1432163
GAM336524	10079	hsa	16	-	23523635	23523731	THC1533234
GAM336526	10929	hsa	X	-	23528432	23528525	THC1529129
GAM336527	9930	hsa	X	-	23528447	23528517	THC1529129
GAM336528	10114	hsa	22	+	24199772	24199865	
GAM336529	10070	hsa	22	+	24199774	24199862	
GAM336532	10310	hsa	15	-	24278760	24278860	THC1473420
GAM336533	10839	hsa	15	-	24278769	24278851	THC1473420
GAM336534	10643	hsa	13	-	24437886	24437973	
GAM336535	10535	hsa	13	+	24538340	24538420	
GAM336536	9794	hsa	11	+	24634603	24634684	THC1432163
GAM336537	9772	hsa	16	+	24755757	24755839	THC1428340
GAM336538	10887	hsa	16	+	24755758	24755838	THC1428340
GAM336539	10850	hsa	10	+	24906581	24906683	THC1540601

GAM336540	9705	hsa	10	+	24922097	24922182	
GAM336541	10127	hsa	14	-	25258227	25258300	AA676592
GAM336545	10597	hsa	2	+	25807898	25807988	
GAM336546	9795	hsa	11	+	25943926	25944007	THC1432163
GAM336548	10925	hsa	12	+	26121979	26122055	THC1502105
GAM336549	9796	hsa	14	+	26362757	26362838	THC1432163
GAM336550	9633	hsa	12	+	26370649	26370725	
GAM336551	10696	hsa	7	+	26442598	26442683	
GAM336552	9653	hsa	9	+	26468156	26468242	
GAM336553	10931	hsa	X	-	26541313	26541418	
GAM336556	9997	hsa	17	+	26895579	26895689	
GAM336557	9797	hsa	18	+	26976985	26977066	THC1432163
GAM336558	10580	hsa	6	+	26978328	26978415	
GAM336559	9640	hsa	Y	+	27187756	27187828	
GAM336560	11234	hsa	8	+	27457170	27457279	
GAM336561	10482	hsa	11	+	27480931	27481041	
GAM336563	9704	hsa	12	+	27711245	27711331	
GAM336564	10546	hsa	6	+	27748402	27748493	
GAM336565	9942	hsa	10	+	27947083	27947172	
GAM336567	10911	hsa	17	+	28064331	28064435	
GAM336568	10215	hsa	17	+	28064340	28064429	
GAM336569	11287	hsa	17	+	28064341	28064427	
GAM336570	10522	hsa	22	+	28404293	28404393	THC1518713
GAM336571	10501	hsa	15	-	28441207	28441337	
GAM336572	10410	hsa	8	-	28604728	28604829	
GAM336573	10623	hsa	16	+	28680032	28680119	THC1588979
GAM336574	11253	hsa	8	+	28740486	28740597	
GAM336575	10624	hsa	16	+	28794191	28794278	THC1588979
GAM336578	11111	hsa	17	-	28958697	28958796	
GAM336579	10372	hsa	17	-	28958698	28958795	
GAM336580	10566	hsa	10	+	28986610	28986698	
GAM336581	10496	hsa	8	-	29024288	29024372	THC1457456
GAM336582	10625	hsa	16	+	29073962	29074049	THC1588979
GAM336583	10770	hsa	17	+	29086596	29086707	
GAM336584	10873	hsa	17	+	29086598	29086705	
GAM336585	11284	hsa	15	+	29098204	29098280	
GAM336586	10637	hsa	17	+	29424019	29424104	
GAM336587	10662	hsa	7	+	29435833	29435937	
GAM336588	10412	hsa	7	+	29435834	29435936	
GAM336589	10762	hsa	22	+	29509893	29509970	THC1542768
GAM336590	10028	hsa	12	-	29554384	29554493	
GAM336591	9798	hsa	18	+	29889968	29890049	THC1432163
GAM336592	10722	hsa	22	+	30010422	30010511	
GAM336593	10898	hsa	15	+	30068447	30068568	
GAM336594	11183	hsa	15	+	30068453	30068565	
GAM336595	10732	hsa	8	+	30119301	30119414	THC1577621
GAM336596	10135	hsa	8	+	30119306	30119399	THC1577621
GAM336597	10092	hsa	7	-	30195269	30195380	THC1409997
GAM336598	9799	hsa	11	+	30200618	30200699	THC1432163
GAM336599	11095	hsa	16	+	30643328	30643429	

GAM336600	10349	hsa	16	+	30643329	30643428	
GAM336601	9969	hsa	13	+	30673441	30673570	
GAM336602	11116	hsa	10	+	30748368	30748468	
GAM336605	11147	hsa	8	+	31058191	31058297	
GAM336606	10677	hsa	1	+	31418591	31418686	
GAM336607	11100	hsa	6	+	31554609	31554709	
GAM336608	10356	hsa	6	+	31554610	31554708	
GAM336609	10414	hsa	10	-	31572572	31572664	THC1528632
GAM336610	10150	hsa	6	+	31820024	31820126	
GAM336611	10783	hsa	18	+	32058440	32058540	
GAM336614	9800	hsa	10	+	32152882	32152963	THC1432163
GAM336615	9968	hsa	7	-	32235142	32235239	THC1495052
GAM336617	10292	hsa	9	+	32403384	32403481	THC1540659
GAM336618	10180	hsa	21	+	32615342	32615449	
GAM336619	10901	hsa	21	+	32615357	32615436	
GAM336620	9607	hsa	21	+	32615358	32615435	
GAM336621	10667	hsa	7	+	32661984	32662086	
GAM336622	10489	hsa	12	-	32800023	32800121	THC1580990
GAM336626	9801	hsa	3	+	33075772	33075853	THC1432163
GAM336628	9679	hsa	17	+	33138955	33139063	
GAM336629	10446	hsa	17	+	33138970	33139049	
GAM336630	11110	hsa	9	+	33338251	33338351	THC1456106
GAM336631	10644	hsa	9	+	33338258	33338345	THC1456106
GAM336632	10008	hsa	17	-	33407353	33407429	
GAM336633	11263	hsa	20	+	33688439	33688514	
GAM336634	10263	hsa	10	+	33692940	33693053	
GAM336637	10814	hsa	11	+	33804195	33804279	
GAM336638	9802	hsa	13	+	33909250	33909331	THC1432163
GAM336639	10453	hsa	11	-	33928191	33928297	THC1577473
GAM336640	10802	hsa	21	-	33934627	33934699	
GAM336642	10794	hsa	21	+	34257285	34257378	THC1483407
GAM336643	10795	hsa	21	+	34257285	34257379	THC1483407
GAM336646	10516	hsa	17	+	34615664	34615762	
GAM336651	10102	hsa	7	+	34790992	34791065	THC1534750
GAM336652	9732	hsa	21	-	34813290	34813387	THC1475522
GAM336653	10400	hsa	19	-	34876504	34876602	THC1455164
GAM336656	9803	hsa	3	+	35023682	35023763	THC1432163
GAM336657	11203	hsa	11	+	35289635	35289735	
GAM336658	10720	hsa	17	-	35608725	35608830	
GAM336659	10280	hsa	22	-	35681759	35681843	
GAM336660	9804	hsa	X	-	35708263	35708344	THC1432163
GAM336661	10382	hsa	20	+	35736486	35736584	THC1407133
GAM336662	10698	hsa	20	+	35736488	35736582	THC1407133
GAM336663	10634	hsa	20	+	35736492	35736579	THC1407133
GAM336664	11265	hsa	20	+	35736498	35736573	THC1407133
GAM336665	10456	hsa	17	+	35840280	35840355	
GAM336669	9805	hsa	2	+	36383567	36383648	THC1432163
GAM336670	9598	hsa	10	-	36386596	36386703	
GAM336671	9693	hsa	10	-	36386600	36386699	
GAM336672	10115	hsa	10	-	36386609	36386690	

GAM336673	11036	hsa	21	-	36425183	36425281	
GAM336674	10073	hsa	22	+	36639912	36640014	
GAM336675	10284	hsa	9	+	36669197	36669295	
GAM336676	11174	hsa	22	+	36951386	36951467	
GAM336677	10934	hsa	17	+	36970296	36970396	
GAM336681	9661	hsa	9	+	37422585	37422668	
GAM336683	11101	hsa	21	-	37445099	37445199	
GAM336685	11026	hsa	20	+	37606073	37606186	
GAM336686	11087	hsa	3	+	37624000	37624101	
GAM336689	10191	hsa	7	+	37948104	37948211	THC1454222
GAM336690	11037	hsa	7	-	37983831	37983930	
GAM336691	10871	hsa	20	+	38081171	38081249	
GAM336697	10950	hsa	8	+	38541864	38541939	
GAM336699	10052	hsa	15	+	38679676	38679764	
GAM336701	10881	hsa	22	+	38828150	38828261	
GAM336702	9806	hsa	6	+	38853404	38853485	THC1432163
GAM336703	10303	hsa	21	-	39141230	39141318	
GAM336704	10642	hsa	1	+	39394031	39394118	THC1444871
GAM336705	10279	hsa	1	+	39394032	39394117	THC1444871
GAM336706	10317	hsa	X	+	39568547	39568628	
GAM336707	10455	hsa	22	+	39605027	39605122	THC1562223
GAM336709	10298	hsa	22	+	39769473	39769571	
GAM336710	10169	hsa	15	-	39771457	39771552	
GAM336713	10029	hsa	19	-	39876405	39876499	
GAM336715	10271	hsa	X	+	39935490	39935576	
GAM336716	10551	hsa	4	+	40002861	40002949	
GAM336717	10945	hsa	4	+	40002867	40002943	
GAM336718	9698	hsa	22	+	40074931	40075020	
GAM336719	10600	hsa	22	-	40082689	40082777	
GAM336720	9745	hsa	17	+	40086888	40086975	THC1488043
GAM336722	9807	hsa	8	+	40227896	40227977	THC1432163
GAM336723	10264	hsa	19	+	40285217	40285302	
GAM336727	10863	hsa	22	+	40420544	40420641	THC1489438
GAM336728	9753	hsa	19	+	40578117	40578229	
GAM336729	10650	hsa	15	+	40608767	40608864	
GAM336730	10417	hsa	11	-	40623807	40623936	
GAM336731	11278	hsa	17	-	40762540	40762621	THC1510028
GAM336732	11180	hsa	17	-	40762541	40762620	THC1510028
GAM336734	10432	hsa	8	-	40925498	40925573	
GAM336736	9808	hsa	4	+	41122390	41122471	THC1432163
GAM336738	11076	hsa	17	+	41382416	41382517	THC1510611
GAM336739	10170	hsa	20	+	41425604	41425676	
GAM336740	9904	hsa	17	-	41446302	41446381	
GAM336743	10083	hsa	19	-	41560746	41560831	
GAM336744	10903	hsa	19	-	41616369	41616498	
GAM336745	9701	hsa	19	-	41616372	41616496	
GAM336746	10269	hsa	8	+	41616885	41616975	
GAM336747	10506	hsa	8	+	41616892	41616964	
GAM336749	10810	hsa	19	+	41749003	41749113	
GAM336750	11102	hsa	6	-	41757315	41757415	

GAM336751	9706	hsa	8	+	41765141	41765226	
GAM336752	9915	hsa	7	-	41880845	41880957	THC1602167
GAM336755	11083	hsa	17	-	42527933	42528034	THC1572973
GAM336756	10577	hsa	17	-	42527939	42528027	THC1572973
GAM336757	10134	hsa	8	+	42675594	42675671	
GAM336760	11258	hsa	6	-	42757406	42757482	
GAM336761	9638	hsa	21	+	42800191	42800271	
GAM336762	11227	hsa	19	-	42860934	42861021	
GAM336763	10653	hsa	22	-	42899850	42899946	THC1597091
GAM336764	10314	hsa	20	+	42908008	42908094	
GAM336765	11206	hsa	20	+	42908013	42908088	
GAM336767	10725	hsa	13	+	43301518	43301601	
GAM336768	10379	hsa	17	-	43393809	43393905	
GAM336770	10933	hsa	13	+	43586567	43586675	
GAM336771	10827	hsa	13	+	43586571	43586670	
GAM336772	10569	hsa	5	-	43590234	43590321	
GAM336773	10807	hsa	7	+	43594076	43594152	
GAM336775	10857	hsa	10	+	43900231	43900331	
GAM336776	10923	hsa	17	+	44128391	44128493	
GAM336777	9809	hsa	12	+	44151668	44151749	THC1432163
GAM336778	10958	hsa	10	+	44172084	44172167	
GAM336780	9613	hsa	18	+	44287793	44287892	
GAM336781	9695	hsa	21	+	44376402	44376496	
GAM336782	10766	hsa	21	+	44376407	44376492	
GAM336783	10232	hsa	X	-	44431916	44432022	
GAM336784	10966	hsa	X	-	44431925	44432017	
GAM336785	11210	hsa	17	+	44596378	44596488	THC1425133
GAM336786	9810	hsa	10	+	44812786	44812867	THC1432163
GAM336787	9708	hsa	22	+	44900341	44900433	THC1553978
GAM336788	10779	hsa	20	+	44989605	44989690	
GAM336789	10380	hsa	21	+	45081110	45081210	
GAM336790	10075	hsa	17	+	45349110	45349210	
GAM336792	9720	hsa	19	-	45455573	45455684	THC1519988
GAM336793	11193	hsa	19	-	45455579	45455678	THC1519988
GAM336794	11196	hsa	10	+	45732059	45732138	
GAM336795	11018	hsa	22	+	45867956	45868051	
GAM336796	9922	hsa	18	+	45983536	45983630	
GAM336797	11242	hsa	19	+	46014999	46015128	
GAM336798	11092	hsa	17	+	46038899	46039000	THC1452989
GAM336799	10345	hsa	17	+	46038900	46038999	
GAM336800	9947	hsa	13	+	46120406	46120503	THC1592477
GAM336801	9811	hsa	19	-	46150469	46150550	THC1432163
GAM336804	10711	hsa	11	+	46229800	46229904	
GAM336806	9812	hsa	16	-	46270121	46270202	THC1432163
GAM336807	10162	hsa	17	-	46314585	46314665	
GAM336809	9614	hsa	14	+	46540199	46540291	
GAM336810	9742	hsa	11	-	46654581	46654674	
GAM336811	10800	hsa	11	-	46654582	46654673	
GAM336812	10461	hsa	21	+	46926845	46926945	
GAM336814	10436	hsa	20	+	47053946	47054014	

GAM336815	11063	hsa	10	-	47056630	47056730	
GAM336816	10153	hsa	16	+	47073422	47073512	
GAM336817	10428	hsa	16	+	47073424	47073510	
GAM336818	10035	hsa	16	+	47279033	47279105	
GAM336819	9590	hsa	17	+	47313354	47313455	THC1423222
GAM336820	11054	hsa	15	+	47490707	47490809	
GAM336821	11064	hsa	10	+	47538323	47538423	
GAM336822	10045	hsa	10	+	47560720	47560814	THC1596798
GAM336823	9736	hsa	X	-	47606004	47606083	THC1553812
GAM336824	10592	hsa	19	-	47747389	47747476	
GAM336825	10268	hsa	X	-	47783494	47783585	THC1466914
GAM336826	10504	hsa	X	-	47783507	47783578	THC1466914
GAM336827	11249	hsa	17	+	47935242	47935317	
GAM336828	11014	hsa	17	+	47935243	47935316	
GAM336829	11008	hsa	19	+	47956679	47956775	
GAM336830	10030	hsa	17	+	47994779	47994859	
GAM336832	9927	hsa	17	-	48134831	48134904	THC1542103
GAM336833	10300	hsa	16	-	48164886	48165016	
GAM336834	10514	hsa	16	-	48164907	48164998	
GAM336835	11065	hsa	10	+	48175291	48175391	
GAM336836	11028	hsa	19	+	48190562	48190640	
GAM336837	10259	hsa	10	+	48206347	48206443	THC1596797
GAM336838	10442	hsa	19	-	48246637	48246721	
GAM336840	10640	hsa	17	+	48506039	48506126	
GAM336841	11086	hsa	4	+	48685091	48685193	
GAM336842	10864	hsa	14	+	48783661	48783753	
GAM336844	9970	hsa	22	+	48973458	48973551	THC1511796
GAM336845	9728	hsa	22	+	48973459	48973550	THC1511796
GAM336846	10746	hsa	12	-	49032571	49032658	THC1486982
GAM336847	9813	hsa	6	+	49043749	49043830	THC1432163
GAM336848	10918	hsa	12	-	49044659	49044768	
GAM336849	10745	hsa	12	-	49044673	49044765	
GAM336852	11066	hsa	10	-	49108311	49108411	
GAM336853	9943	hsa	20	+	49118815	49118914	
GAM336854	10272	hsa	19	+	49184841	49184926	THC1521345
GAM336855	10430	hsa	14	-	49197664	49197776	THC1563278
GAM336857	11020	hsa	17	-	49351290	49351391	
GAM336860	9814	hsa	X	+	49440469	49440550	THC1432163
GAM336861	10091	hsa	20	+	49549736	49549821	
GAM336862	10788	hsa	20	+	49549738	49549816	
GAM336863	9659	hsa	17	-	49602636	49602719	
GAM336864	10702	hsa	18	-	49753165	49753265	
GAM336866	10815	hsa	20	+	50086828	50086917	
GAM336867	10754	hsa	16	+	50178453	50178558	
GAM336868	10585	hsa	12	+	50244509	50244596	
GAM336869	10947	hsa	19	-	50257437	50257513	
GAM336870	10575	hsa	12	+	50356669	50356756	
GAM336871	11173	hsa	12	+	50415753	50415840	
GAM336872	10798	hsa	12	+	50638127	50638202	
GAM336873	11279	hsa	8	+	50704929	50705016	

GAM336874	10713	hsa	10	-	50706273	50706364	
GAM336875	10483	hsa	10	-	50833625	50833732	
GAM336876	9929	hsa	12	+	50911119	50911224	
GAM336877	9900	hsa	12	+	50911122	50911218	
GAM336878	10916	hsa	13	+	51269225	51269326	
GAM336879	10993	hsa	10	-	51538284	51538361	THC1564358
GAM336880	10327	hsa	10	-	51698913	51699010	THC1569688
GAM336882	10832	hsa	19	+	51927028	51927129	
GAM336883	9958	hsa	12	+	51938752	51938835	
GAM336886	10316	hsa	20	+	52749150	52749248	
GAM336887	10374	hsa	19	+	52879973	52880069	
GAM336888	10395	hsa	10	+	53047643	53047723	
GAM336889	9916	hsa	14	+	53301337	53301429	
GAM336892	11038	hsa	12	-	53823632	53823726	THC1462250
GAM336893	10817	hsa	12	-	53823634	53823720	THC1462250
GAM336894	9635	hsa	8	-	53863297	53863388	
GAM336895	10672	hsa	8	-	53863302	53863382	
GAM336896	9691	hsa	15	-	54032470	54032561	
GAM336897	10462	hsa	12	-	54122958	54123027	
GAM336898	10598	hsa	12	-	54260659	54260747	
GAM336901	9815	hsa	16	+	55006289	55006370	THC1432163
GAM336903	11047	hsa	20	+	55618701	55618802	
GAM336906	11077	hsa	12	-	56423119	56423220	THC1487590
GAM336907	10558	hsa	12	-	56423125	56423213	THC1487590
GAM336908	9816	hsa	2	-	56590496	56590577	THC1432163
GAM336909	10660	hsa	12	+	56700933	56700988	
GAM336911	10875	hsa	16	+	56703572	56703669	
GAM336913	9642	hsa	12	-	56716065	56716146	THC1509286
GAM336914	10055	hsa	12	-	56716066	56716145	THC1509286
GAM336916	10247	hsa	19	-	56865886	56865996	
GAM336917	10078	hsa	15	+	56876889	56876994	
GAM336918	10515	hsa	15	+	56876894	56877002	
GAM336919	9817	hsa	5	+	56896949	56897030	THC1432163
GAM336920	11192	hsa	16	+	56913348	56913430	
GAM336921	11050	hsa	17	+	57181803	57181903	
GAM336922	10544	hsa	17	+	57181813	57181895	
GAM336923	10403	hsa	4	+	57192272	57192372	
GAM336924	9818	hsa	8	+	57442342	57442423	THC1432163
GAM336925	10729	hsa	12	+	57533860	57533947	
GAM336926	10213	hsa	12	+	57533866	57533943	
GAM336927	11245	hsa	20	+	57662274	57662379	
GAM336931	10594	hsa	19	+	57796024	57796113	
GAM336932	10120	hsa	14	+	58065317	58065427	
GAM336933	10235	hsa	17	+	58083077	58083172	THC1437587
GAM336934	11115	hsa	17	+	58103929	58104030	
GAM336937	9901	hsa	17	+	58596055	58596160	
GAM336938	10687	hsa	17	+	58596062	58596151	
GAM336939	10830	hsa	12	+	58665635	58665764	
GAM336941	9819	hsa	4	-	59119812	59119893	THC1432163
GAM336942	11187	hsa	11	+	59207699	59207789	

GAM336945	10181	hsa	18	+	59990343	59990451	
GAM336946	9768	hsa	20	+	60087508	60087603	
GAM336947	10990	hsa	15	+	60363185	60363260	
GAM336950	9820	hsa	17	-	60746489	60746570	THC1432163
GAM336951	10111	hsa	11	+	60952390	60952496	
GAM336956	11131	hsa	19	+	61750038	61750123	
GAM336957	9605	hsa	11	-	61814814	61814909	
GAM336958	10228	hsa	11	-	61985320	61985401	THC1422166
GAM336959	9821	hsa	X	+	62004748	62004829	THC1432163
GAM336961	9893	hsa	9	-	62131101	62131209	
GAM336962	10905	hsa	20	-	62164421	62164526	
GAM336963	11231	hsa	8	-	62264330	62264422	THC1526730
GAM336964	9822	hsa	5	+	62270288	62270369	THC1432163
GAM336965	10222	hsa	14	+	62330677	62330788	THC1552175
GAM336966	10983	hsa	14	+	62330682	62330781	THC1552175
GAM336967	11228	hsa	11	+	62410126	62410220	
GAM336968	10113	hsa	9	+	62447485	62447583	THC1595205
GAM336969	9823	hsa	12	-	62677320	62677401	THC1432163
GAM336970	9727	hsa	12	+	62689480	62689571	
GAM336971	10709	hsa	12	+	62689481	62689570	
GAM336972	9824	hsa	13	-	62708765	62708846	THC1432163
GAM336974	11135	hsa	11	-	62725558	62725650	THC1408122
GAM336975	11123	hsa	11	+	62729661	62729762	
GAM336976	10067	hsa	11	+	62755250	62755324	
GAM336978	10532	hsa	9	-	62875338	62875465	THC1581432
GAM336979	9894	hsa	9	-	62875341	62875449	
GAM336980	10246	hsa	9	-	62875343	62875455	THC1581432
GAM336981	9892	hsa	9	-	62875349	62875449	THC1581432
GAM336983	10878	hsa	11	+	62901709	62901784	
GAM336984	9990	hsa	14	+	62916210	62916302	
GAM336989	9949	hsa	19	-	63216696	63216771	
GAM336990	10214	hsa	7	+	63236493	63236580	
GAM336991	9825	hsa	11	+	63263870	63263951	THC1432163
GAM336992	11211	hsa	17	-	63315058	63315168	THC1425133
GAM336995	10572	hsa	19	+	63490699	63490787	
GAM336996	10994	hsa	19	+	63490705	63490781	
GAM336997	9718	hsa	20	+	63567534	63567605	
GAM337000	9647	hsa	12	+	63919661	63919772	
GAM337001	10060	hsa	17	+	63948506	63948574	
GAM337003	10207	hsa	7	-	64886976	64887044	
GAM337004	10090	hsa	17	+	65016569	65016664	
GAM337007	11075	hsa	5	+	65030778	65030878	
GAM337008	10108	hsa	9	+	65050472	65050577	
GAM337009	9826	hsa	8	+	65068010	65068091	THC1432163
GAM337010	9827	hsa	X	+	65112308	65112389	THC1432163
GAM337011	10426	hsa	X	+	65182638	65182721	
GAM337013	9828	hsa	15	+	65319486	65319567	THC1432163
GAM337015	10368	hsa	3	-	65550880	65550979	
GAM337016	9935	hsa	9	+	65582433	65582528	
GAM337017	11146	hsa	9	+	65582733	65582809	

GAM337018	9829	hsa	1	-	65709159	65709240	THC1432163
GAM337019	9830	hsa	5	+	65710652	65710733	THC1432163
GAM337022	11296	hsa	12	+	65754862	65754974	
GAM337023	10495	hsa	7	+	65815377	65815468	
GAM337024	10987	hsa	7	+	65815381	65815459	
GAM337025	11169	hsa	11	+	65938364	65938458	THC1461556
GAM337027	11130	hsa	7	-	66122717	66122817	
GAM337028	10401	hsa	7	-	66122718	66122816	
GAM337029	10928	hsa	14	-	66268768	66268871	
GAM337030	11176	hsa	14	-	66268779	66268869	
GAM337031	9710	hsa	16	+	66387514	66387607	
GAM337032	11277	hsa	12	+	66457769	66457885	
GAM337033	10565	hsa	12	+	66457785	66457872	
GAM337035	10194	hsa	12	+	66813729	66813813	
GAM337036	10769	hsa	16	+	66902019	66902108	THC1432572
GAM337037	10730	hsa	9	+	66974964	66975068	
GAM337038	10652	hsa	9	+	66974965	66975067	
GAM337039	10297	hsa	9	+	66974966	66975066	
GAM337041	11257	hsa	17	-	67244014	67244089	
GAM337042	10689	hsa	16	+	67268904	67268981	
GAM337043	10823	hsa	11	-	67274771	67274844	
GAM337045	9831	hsa	18	-	67383500	67383581	THC1432163
GAM337046	10219	hsa	8	-	67560293	67560365	
GAM337047	10889	hsa	12	+	67697723	67697833	
GAM337051	10296	hsa	9	+	68096932	68097039	THC1547991
GAM337052	9670	hsa	9	+	68096933	68097038	THC1547991
GAM337053	10688	hsa	12	-	68550580	68550687	
GAM337055	11238	hsa	12	-	68796420	68796543	
GAM337056	9972	hsa	12	-	68796422	68796541	
GAM337057	9937	hsa	12	-	68796444	68796515	
GAM337058	10982	hsa	12	-	68796449	68796510	
GAM337059	9961	hsa	12	+	68875043	68875152	
GAM337060	11059	hsa	5	-	69076604	69076702	
GAM337061	10076	hsa	9	+	69104781	69104892	
GAM337062	10581	hsa	5	+	69278504	69278591	
GAM337063	10131	hsa	5	+	69410140	69410221	THC1414413
GAM337064	10582	hsa	5	-	69429920	69430007	
GAM337066	11236	hsa	11	-	69498130	69498220	
GAM337068	10224	hsa	16	+	69692764	69692835	
GAM337069	11060	hsa	5	+	69818313	69818411	
GAM337070	10322	hsa	5	+	69818314	69818410	
GAM337071	9725	hsa	10	+	69991881	69991958	
GAM337074	11044	hsa	16	+	70140212	70140312	
GAM337075	10288	hsa	16	+	70140213	70140311	
GAM337076	10596	hsa	16	+	70140219	70140306	
GAM337077	10132	hsa	5	+	70161182	70161263	THC1414413
GAM337078	10583	hsa	5	-	70180992	70181079	
GAM337079	11052	hsa	15	-	70204344	70204443	
GAM337080	10659	hsa	8	+	70205172	70205252	
GAM337081	11061	hsa	5	+	70361144	70361242	

GAM337082	10323	hsa	5	+	70361145	70361241	
GAM337083	10737	hsa	10	+	70411479	70411570	THC1598106
GAM337084	9707	hsa	10	+	70411482	70411567	THC1598106
GAM337087	10437	hsa	7	+	70589904	70589996	
GAM337088	9750	hsa	12	-	70649160	70649247	THC1456820
GAM337089	11154	hsa	12	-	70649166	70649237	THC1456820
GAM337091	11103	hsa	9	+	70793499	70793599	
GAM337092	9832	hsa	14	+	70852306	70852387	THC1432163
GAM337093	10759	hsa	14	+	71022428	71022515	
GAM337094	9833	hsa	15	+	71135679	71135760	THC1432163
GAM337095	10511	hsa	17	+	71404046	71404134	
GAM337096	10329	hsa	7	+	71522779	71522877	
GAM337097	10473	hsa	17	+	71688944	71689047	
GAM337098	11027	hsa	X	-	71710852	71710981	
GAM337099	9834	hsa	13	+	71711305	71711386	THC1432163
GAM337100	10512	hsa	16	+	71825337	71825440	
GAM337101	10805	hsa	12	+	71906731	71906814	
GAM337105	10747	hsa	11	-	71960660	71960764	THC1421005
GAM337106	9966	hsa	14	+	72006752	72006831	
GAM337108	9967	hsa	14	+	72038936	72039015	
GAM337109	10751	hsa	7	-	72098256	72098348	
GAM337110	9835	hsa	13	-	72187619	72187700	THC1432163
GAM337111	10301	hsa	7	+	72274763	72274860	
GAM337112	10548	hsa	7	+	72274769	72274855	
GAM337113	10248	hsa	7	+	72274772	72274855	
GAM337115	9726	hsa	17	+	72530482	72530568	
GAM337118	10184	hsa	18	-	72678382	72678477	THC1458230
GAM337119	10784	hsa	7	-	73042551	73042656	
GAM337126	10305	hsa	11	+	73205614	73205689	
GAM337127	11091	hsa	7	+	73215042	73215141	
GAM337128	10344	hsa	7	+	73215043	73215140	
GAM337129	10357	hsa	3	-	73257733	73257831	THC1552388
GAM337130	10554	hsa	15	+	73327088	73327176	
GAM337131	11117	hsa	17	+	73549131	73549240	
GAM337133	9963	hsa	7	+	73601903	73602032	THC1461329
GAM337135	10469	hsa	7	+	73747698	73747788	THC1481651
GAM337136	10935	hsa	7	+	73803663	73803769	
GAM337138	10293	hsa	9	-	73912141	73912249	THC1595134
GAM337140	9964	hsa	7	-	73970646	73970775	THC1461329
GAM337143	10470	hsa	7	-	74080872	74080962	THC1481651
GAM337144	10014	hsa	18	+	74099672	74099745	
GAM337145	11217	hsa	16	+	74141948	74142029	
GAM337146	11041	hsa	2	+	74273377	74273475	THC1594763
GAM337147	10281	hsa	2	+	74273378	74273474	THC1594763
GAM337148	11004	hsa	2	+	74273390	74273463	THC1594763
GAM337149	9600	hsa	8	+	74455579	74455655	
GAM337150	10471	hsa	7	-	74495125	74495215	THC1481651
GAM337151	10335	hsa	7	+	74600951	74601049	THC1516956
GAM337152	10429	hsa	8	-	74682720	74682801	
GAM337153	10384	hsa	7	-	74726081	74726185	

GAM337154	11078	hsa	10	+	74733011	74733111	
GAM337155	10330	hsa	10	+	74733012	74733110	
GAM337156	10559	hsa	10	+	74733018	74733105	
GAM337157	10646	hsa	17	-	74841732	74841819	
GAM337158	10666	hsa	15	-	74959089	74959183	
GAM337159	9836	hsa	18	-	75061068	75061149	THC1432163
GAM337160	10283	hsa	X	-	75203402	75203500	
GAM337161	10882	hsa	14	-	75209026	75209115	
GAM337162	10614	hsa	3	-	75245669	75245756	THC1439776
GAM337166	10385	hsa	7	+	75764518	75764622	
GAM337167	10527	hsa	10	-	75774294	75774389	
GAM337168	10835	hsa	7	+	75794832	75794924	
GAM337169	10251	hsa	11	+	75944727	75944827	
GAM337170	10192	hsa	12	+	76136262	76136343	
GAM337171	10386	hsa	7	+	76283582	76283686	
GAM337172	11201	hsa	12	+	76484385	76484483	
GAM337173	9936	hsa	15	-	76490700	76490800	
GAM337174	9760	hsa	7	+	76516598	76516670	
GAM337177	10750	hsa	17	-	76741418	76741502	
GAM337179	11163	hsa	11	+	77038644	77038729	THC1577906
GAM337180	9991	hsa	16	+	77109458	77109567	
GAM337181	10011	hsa	16	+	77109464	77109561	
GAM337183	10639	hsa	1	+	77738565	77738652	
GAM337184	10821	hsa	14	+	78244320	78244429	
GAM337185	10340	hsa	16	+	78245362	78245461	THC1433804
GAM337186	10589	hsa	16	+	78245368	78245456	THC1433804
GAM337187	10391	hsa	16	+	78638936	78639029	
GAM337188	10704	hsa	7	+	78652714	78652814	
GAM337189	10275	hsa	7	+	78652725	78652810	
GAM337190	11251	hsa	11	-	78654888	78654992	
GAM337191	10780	hsa	11	-	79303486	79303580	
GAM337192	9837	hsa	6	+	79485331	79485412	THC1432163
GAM337193	10978	hsa	17	-	79931894	79931984	
GAM337194	11150	hsa	17	+	80018909	80019008	
GAM337195	10487	hsa	17	+	80018910	80019007	
GAM337196	9838	hsa	13	+	80622214	80622295	THC1432163
GAM337197	10647	hsa	17	+	81064708	81064796	
GAM337199	9731	hsa	16	+	81438779	81438890	
GAM337200	9674	hsa	8	-	81629047	81629130	THC1482911
GAM337202	10002	hsa	7	-	82178830	82178931	
GAM337203	10593	hsa	9	+	82201058	82201145	
GAM337204	9839	hsa	9	+	82464706	82464787	THC1432163
GAM337206	9840	hsa	9	-	83433939	83434020	THC1432163
GAM337207	10964	hsa	7	+	84223987	84224086	
GAM337208	10096	hsa	7	+	84223991	84224085	
GAM337209	9841	hsa	8	-	84490971	84491052	THC1432163
GAM337210	9842	hsa	5	+	84536421	84536502	THC1432163
GAM337211	9843	hsa	12	-	84648170	84648251	THC1432163
GAM337212	9844	hsa	12	+	84939391	84939472	THC1432163
GAM337213	9717	hsa	12	+	85256084	85256182	

GAM337214	10655	hsa	12	+	85256089	85256178	
GAM337215	10311	hsa	12	+	85256090	85256177	
GAM337216	9845	hsa	7	-	85369298	85369379	THC1432163
GAM337217	10036	hsa	15	+	86608510	86608588	THC1418799
GAM337218	9719	hsa	14	+	86923030	86923105	
GAM337220	10260	hsa	15	+	87035430	87035503	
GAM337221	10775	hsa	10	-	87449030	87449128	
GAM337224	9846	hsa	7	-	88198417	88198498	THC1432163
GAM337225	10141	hsa	15	+	88408163	88408240	
GAM337226	10813	hsa	9	+	88578225	88578314	
GAM337227	11067	hsa	10	+	88903075	88903175	
GAM337228	9847	hsa	3	+	88997770	88997851	THC1432163
GAM337229	11156	hsa	16	+	89060884	89060970	
GAM337230	10063	hsa	9	-	89181165	89181284	
GAM337232	10152	hsa	11	-	89243160	89243260	
GAM337233	10664	hsa	14	-	89325453	89325535	THC1449162
GAM337234	11005	hsa	14	-	89325457	89325532	THC1449162
GAM337235	10087	hsa	14	-	89325458	89325531	THC1449162
GAM337237	10360	hsa	4	+	89368234	89368331	THC1415671
GAM337238	10626	hsa	4	+	89368240	89368326	THC1415671
GAM337242	11141	hsa	7	+	89742768	89742864	
GAM337243	10885	hsa	14	+	89931751	89931839	
GAM337245	10895	hsa	11	+	90083877	90083972	
GAM337246	10900	hsa	11	+	90083887	90083965	
GAM337247	10824	hsa	11	-	90114587	90114677	
GAM337248	9848	hsa	11	+	90495199	90495280	THC1432163
GAM337250	9849	hsa	14	-	91509421	91509502	THC1432163
GAM337251	10782	hsa	10	+	91699065	91699140	
GAM337254	9702	hsa	7	-	91841622	91841706	
GAM337255	10906	hsa	14	+	92455725	92455811	THC1601591
GAM337256	9645	hsa	14	+	92455726	92455810	THC1601591
GAM337257	10196	hsa	10	+	92938874	92938983	
GAM337258	10183	hsa	10	+	92938880	92938977	
GAM337263	9850	hsa	10	-	93264106	93264187	THC1432163
GAM337264	11144	hsa	9	+	93648456	93648552	
GAM337265	11013	hsa	9	+	93648460	93648544	
GAM337266	10121	hsa	9	+	93648461	93648543	
GAM337267	10100	hsa	X	+	93666704	93666803	
GAM337269	11017	hsa	15	-	94289451	94289527	THC1525813
GAM337270	10460	hsa	10	-	94365822	94365929	THC1531347
GAM337271	11015	hsa	10	-	94365825	94365925	THC1531347
GAM337273	10086	hsa	1	+	94706874	94706945	
GAM337274	10295	hsa	15	-	94819576	94819678	THC1426889
GAM337275	10101	hsa	15	-	94819582	94819674	THC1426889
GAM337277	10066	hsa	11	-	94888202	94888309	THC1453966
GAM337278	9945	hsa	8	-	94917186	94917266	
GAM337279	9739	hsa	9	+	95196288	95196387	
GAM337281	11074	hsa	10	+	95469300	95469400	
GAM337282	10549	hsa	10	+	95469307	95469394	
GAM337283	10763	hsa	14	+	96090585	96090666	

GAM337285	11153	hsa	13	-	96668219	96668343	
GAM337286	10048	hsa	13	-	96668245	96668335	
GAM337288	10026	hsa	12	-	96681277	96681379	THC1498750
GAM337289	10025	hsa	12	-	96681278	96681379	THC1498750
GAM337290	10959	hsa	X	+	96688012	96688102	
GAM337291	10158	hsa	8	+	97011857	97011947	
GAM337292	9851	hsa	5	+	97029751	97029832	THC1432163
GAM337293	10874	hsa	15	+	97153223	97153319	
GAM337294	10869	hsa	15	+	97153225	97153317	
GAM337296	10226	hsa	13	-	97963174	97963273	THC1450795
GAM337297	10740	hsa	13	-	97963178	97963269	THC1450795
GAM337298	10692	hsa	15	+	98182570	98182651	
GAM337299	11039	hsa	7	+	98227794	98227885	
GAM337300	11260	hsa	7	+	98227800	98227875	
GAM337301	9852	hsa	1	-	98287751	98287832	THC1432163
GAM337302	9853	hsa	2	-	98298734	98298815	THC1432163
GAM337303	10633	hsa	X	+	98459191	98459277	
GAM337304	11264	hsa	X	+	98459197	98459271	
GAM337305	11233	hsa	10	+	98645765	98645836	
GAM337306	9908	hsa	10	+	98645767	98645834	
GAM337310	9854	hsa	5	+	98924324	98924405	THC1432163
GAM337311	10342	hsa	12	+	98930879	98930978	THC1552841
GAM337312	10678	hsa	12	+	98930881	98930976	
GAM337313	10595	hsa	12	+	98930885	98930973	
GAM337314	10588	hsa	15	+	98985382	98985469	
GAM337315	11195	hsa	14	+	99006060	99006135	
GAM337317	10438	hsa	12	+	99096789	99096891	
GAM337318	10440	hsa	12	+	99096793	99096891	
GAM337319	10735	hsa	12	+	99096802	99096878	
GAM337320	9602	hsa	13	+	99149261	99149326	
GAM337321	10609	hsa	7	+	99258727	99258807	
GAM337324	10590	hsa	14	+	99463318	99463406	
GAM337326	10961	hsa	11	+	99654607	99654737	
GAM337327	10774	hsa	11	+	99654622	99654724	
GAM337328	9609	hsa	11	+	99654625	99654720	
GAM337329	9604	hsa	14	+	99733672	99733752	
GAM337330	9855	hsa	6	-	100140600	100140681	THC1432163
GAM337331	11080	hsa	7	+	100281287	100281388	
GAM337333	9856	hsa	1	+	100558408	100558489	THC1432163
GAM337334	10854	hsa	14	+	100644251	100644338	
GAM337336	9857	hsa	10	+	100912899	100912980	THC1432163
GAM337337	10377	hsa	12	+	100953716	100953814	
GAM337341	10840	hsa	6	-	101077081	101077193	THC1455312
GAM337343	9596	hsa	7	+	101399275	101399382	
GAM337344	9858	hsa	13	-	101536725	101536806	THC1432163
GAM337345	10387	hsa	7	+	101538287	101538391	
GAM337346	10381	hsa	9	+	101601185	101601282	
GAM337350	10739	hsa	7	+	101642187	101642299	
GAM337351	10707	hsa	7	+	101642191	101642298	
GAM337352	10761	hsa	7	+	101642197	101642292	

GAM337353	10454	hsa	13	-	101658818	101658891	
GAM337354	10039	hsa	13	-	101658819	101658890	
GAM337355	10388	hsa	7	-	101744915	101745019	
GAM337356	10957	hsa	9	+	101746098	101746178	THC1584357
GAM337357	10389	hsa	7	-	101843971	101844075	
GAM337358	9591	hsa	14	-	101964516	101964621	
GAM337359	9896	hsa	14	-	101964525	101964613	
GAM337361	10188	hsa	10	+	103489943	103490054	THC1544958
GAM337363	9859	hsa	3	+	103632887	103632968	THC1432163
GAM337364	10099	hsa	9	+	103784499	103784597	
GAM337366	10447	hsa	7	+	104305997	104306075	
GAM337367	9999	hsa	14	-	104342178	104342288	
GAM337368	10776	hsa	14	-	104342181	104342277	
GAM337370	10723	hsa	10	+	104509126	104509226	
GAM337371	10972	hsa	12	+	104616032	104616129	
GAM337372	10033	hsa	14	-	104762497	104762573	
GAM337373	10034	hsa	14	-	104787214	104787290	
GAM337374	10742	hsa	10	+	104818818	104818907	
GAM337375	10128	hsa	8	+	104911214	104911286	
GAM337376	10308	hsa	14	+	104932380	104932478	
GAM337377	10529	hsa	10	-	105033873	105033966	THC1559539
GAM337378	10528	hsa	10	-	105033875	105033966	THC1559539
GAM337379	10985	hsa	9	-	105338344	105338451	THC1521015
GAM337380	10599	hsa	2	+	105566898	105566986	
GAM337383	10981	hsa	10	-	106366445	106366543	
GAM337384	10731	hsa	12	+	106504624	106504719	
GAM337385	11125	hsa	2	-	106622467	106622569	THC1505172
GAM337386	10603	hsa	2	-	106622476	106622562	THC1505172
GAM337387	10999	hsa	2	-	106622480	106622556	THC1505172
GAM337388	9978	hsa	8	-	106717983	106718083	
GAM337389	9912	hsa	8	-	106717988	106718079	
GAM337390	10007	hsa	9	+	106800362	106800469	
GAM337391	9673	hsa	9	+	106800378	106800455	
GAM337393	10627	hsa	11	-	107416407	107416495	THC1408193
GAM337394	9952	hsa	5	+	107752512	107752584	
GAM337395	11126	hsa	2	+	108115430	108115532	THC1505172
GAM337396	10604	hsa	2	+	108115437	108115523	THC1505172
GAM337397	11000	hsa	2	+	108115443	108115519	THC1505172
GAM337399	11124	hsa	2	+	108732269	108732371	
GAM337400	10563	hsa	2	+	108732276	108732362	
GAM337401	10564	hsa	2	+	108732276	108732363	
GAM337402	10949	hsa	2	+	108732282	108732358	
GAM337403	10956	hsa	8	+	109155677	109155783	THC1506053
GAM337405	10151	hsa	4	+	109967299	109967401	THC1458309
GAM337407	9860	hsa	5	-	110039924	110040005	THC1432163
GAM337408	11232	hsa	7	+	110149400	110149483	
GAM337409	11127	hsa	2	+	110164979	110165081	THC1505172
GAM337410	10605	hsa	2	+	110164986	110165072	THC1505172
GAM337411	11001	hsa	2	+	110164992	110165068	THC1505172
GAM337413	11056	hsa	12	+	110356261	110356361	

GAM337414	9986	hsa	10	-	110439070	110439163	
GAM337415	11128	hsa	2	-	110894746	110894848	THC1505172
GAM337416	10606	hsa	2	-	110894755	110894841	THC1505172
GAM337417	11002	hsa	2	-	110894759	110894835	THC1505172
GAM337418	10123	hsa	12	+	111066449	111066548	
GAM337419	11239	hsa	9	+	111125711	111125821	
GAM337420	10693	hsa	11	-	111321485	111321597	
GAM337421	11023	hsa	12	+	111340859	111340956	
GAM337424	10665	hsa	11	+	111702787	111702869	
GAM337425	10509	hsa	11	+	111702792	111702863	
GAM337426	9861	hsa	7	+	111728469	111728550	THC1432163
GAM337428	10289	hsa	12	+	112035396	112035491	
GAM337429	10097	hsa	9	+	112396737	112396831	
GAM337430	10845	hsa	12	-	112469045	112469165	
GAM337431	11237	hsa	12	-	112469049	112469161	
GAM337432	10954	hsa	12	-	112469050	112469160	
GAM337433	11136	hsa	12	-	112469065	112469149	
GAM337435	9862	hsa	11	+	112801451	112801532	THC1432163
GAM337437	11164	hsa	13	+	112997384	112997485	
GAM337438	11129	hsa	2	-	113030916	113031018	THC1505172
GAM337439	10607	hsa	2	-	113030925	113031011	THC1505172
GAM337440	11003	hsa	2	-	113030929	113031005	THC1505172
GAM337441	9734	hsa	11	+	113128395	113128478	THC1413356
GAM337442	10764	hsa	11	+	113128396	113128477	THC1413356
GAM337443	10772	hsa	11	+	113128397	113128476	THC1413356
GAM337445	10986	hsa	13	+	113838652	113838743	
GAM337446	10556	hsa	7	+	113861407	113861496	
GAM337447	10946	hsa	7	+	113861413	113861490	
GAM337448	10205	hsa	7	+	113861416	113861485	
GAM337449	9863	hsa	X	-	114300062	114300143	THC1432163
GAM337450	11145	hsa	12	+	114520290	114520386	
GAM337452	10753	hsa	10	-	115482747	115482828	THC1584751
GAM337453	11096	hsa	1	-	116189890	116189991	
GAM337454	10350	hsa	1	-	116189891	116189990	
GAM337456	11068	hsa	12	-	116582532	116582632	
GAM337457	10324	hsa	12	-	116582533	116582631	
GAM337458	9907	hsa	11	-	116689623	116689732	THC1572618
GAM337459	9759	hsa	11	-	116689628	116689728	THC1572618
GAM337460	10944	hsa	9	+	116939053	116939128	
GAM337461	10683	hsa	X	-	116942975	116943053	
GAM337462	10632	hsa	9	+	117189825	117189907	
GAM337463	10080	hsa	9	+	117327121	117327212	
GAM337464	10434	hsa	9	+	117327126	117327205	
GAM337465	9864	hsa	7	-	117891472	117891553	THC1432163
GAM337466	9865	hsa	8	+	118241872	118241953	THC1432163
GAM337469	10399	hsa	8	-	118785414	118785498	THC1564919
GAM337470	10142	hsa	12	-	119479486	119479613	
GAM337472	10234	hsa	12	-	120043180	120043285	
GAM337473	9866	hsa	6	+	120076221	120076302	THC1432163
GAM337476	11082	hsa	X	+	120997503	120997604	THC1453916

GAM337477	9867	hsa	9	-	121175114	121175195	THC1432163
GAM337478	9618	hsa	8	+	121180039	121180116	
GAM337479	10143	hsa	12	+	121585232	121585334	
GAM337480	9868	hsa	10	+	121875870	121875951	THC1432163
GAM337481	9589	hsa	11	+	122005663	122005744	
GAM337482	10602	hsa	4	+	122221602	122221690	
GAM337485	11016	hsa	12	+	122598663	122598741	
GAM337486	11051	hsa	8	-	122851359	122851451	
GAM337488	9637	hsa	7	+	123179192	123179304	
GAM337489	11166	hsa	11	-	123330334	123330415	
GAM337490	10282	hsa	9	+	123435499	123435595	
GAM337495	10738	hsa	12	-	123734213	123734294	
GAM337496	10552	hsa	12	-	124130227	124130314	
GAM337497	10144	hsa	9	-	124151674	124151773	THC1583612
GAM337498	10031	hsa	9	-	124608557	124608669	THC1555969
GAM337499	10452	hsa	9	-	124608566	124608670	THC1555969
GAM337500	10106	hsa	9	-	124608567	124608662	THC1555969
GAM337501	10758	hsa	9	-	124608570	124608658	THC1555969
GAM337502	9869	hsa	6	+	124663501	124663582	THC1432163
GAM337507	10020	hsa	11	+	126234545	126234646	
GAM337508	10013	hsa	11	+	126234553	126234633	
GAM337510	10363	hsa	12	+	126518661	126518759	
GAM337511	9974	hsa	10	+	126721975	126722071	
GAM337512	10523	hsa	10	+	126808650	126808746	
GAM337515	10065	hsa	7	+	127715522	127715596	THC1551816
GAM337516	10088	hsa	7	-	127763749	127763823	
GAM337518	9946	hsa	10	+	127854074	127854179	
GAM337520	10038	hsa	9	+	128242511	128242620	
GAM337521	9956	hsa	9	+	128399235	128399346	THC1599871
GAM337522	11011	hsa	9	+	128399242	128399340	THC1599871
GAM337523	11025	hsa	9	+	128399246	128399335	THC1599871
GAM337524	10744	hsa	8	+	128497045	128497145	
GAM337525	10478	hsa	8	+	128533191	128533264	
GAM337526	10233	hsa	11	+	128779961	128780046	
GAM337528	10521	hsa	12	+	129138656	129138730	THC1528702
GAM337529	9696	hsa	7	-	129198494	129198576	THC1490071
GAM337530	10057	hsa	12	+	129432365	129432458	
GAM337531	9870	hsa	2	+	129487964	129488045	THC1432163
GAM337533	9871	hsa	12	-	129681005	129681086	THC1432163
GAM337534	9872	hsa	12	+	129687004	129687085	THC1432163
GAM337541	10365	hsa	10	+	130940694	130940792	
GAM337542	10274	hsa	10	+	130940701	130940786	
GAM337543	9873	hsa	5	+	131254288	131254369	THC1432163
GAM337544	9874	hsa	9	+	131317013	131317094	THC1432163
GAM337545	10561	hsa	X	+	131445968	131446055	
GAM337547	10019	hsa	10	+	131841260	131841363	
GAM337548	11085	hsa	2	+	131845700	131845800	
GAM337549	10586	hsa	2	+	131845707	131845794	
GAM337552	11062	hsa	12	-	132503685	132503786	
GAM337553	9639	hsa	8	-	132744616	132744726	

GAM337554	10418	hsa	8	-	132744625	132744712	
GAM337555	10375	hsa	12	-	132911257	132911355	
GAM337556	10202	hsa	12	-	132911271	132911340	
GAM337558	9715	hsa	7	+	133234415	133234511	
GAM337566	9875	hsa	10	-	135316221	135316302	THC1432163
GAM337567	11224	hsa	8	-	135501500	135501599	
GAM337568	10227	hsa	8	-	135501507	135501593	
GAM337569	9756	hsa	8	-	135501511	135501590	
GAM337570	10765	hsa	7	-	137087025	137087138	THC1472957
GAM337571	9684	hsa	7	-	137087030	137087131	THC1472957
GAM337572	10069	hsa	7	-	137087038	137087121	THC1472957
GAM337573	9876	hsa	6	-	137116843	137116924	THC1432163
GAM337574	11071	hsa	7	+	137674434	137674535	
GAM337575	10286	hsa	7	+	138359964	138360063	
GAM337576	9877	hsa	6	+	138611911	138611992	THC1432163
GAM337578	9878	hsa	8	-	138845677	138845758	THC1432163
GAM337579	10373	hsa	5	-	139758518	139758616	
GAM337580	10912	hsa	7	+	140494572	140494682	
GAM337581	9608	hsa	7	+	140505904	140506013	
GAM337584	10209	hsa	8	-	141088822	141088914	
GAM337585	9629	hsa	8	-	141088826	141088910	
GAM337586	10411	hsa	8	+	141572888	141572988	
GAM337587	10186	hsa	8	+	141572899	141572976	
GAM337588	11235	hsa	1	-	142629616	142629696	THC1553567
GAM337589	9879	hsa	8	-	142638211	142638292	THC1432163
GAM337590	11122	hsa	7	+	142719208	142719308	
GAM337591	11247	hsa	7	+	143679711	143679823	
GAM337592	10877	hsa	7	+	143693599	143693673	
GAM337593	9880	hsa	X	-	144215955	144216036	THC1432163
GAM337594	9881	hsa	6	-	145082321	145082402	THC1432163
GAM337595	9882	hsa	4	+	146634571	146634652	THC1432163
GAM337597	11053	hsa	7	-	148136535	148136636	THC1490832
GAM337598	10315	hsa	7	-	148136536	148136635	THC1490832
GAM337599	10908	hsa	X	+	148237793	148237901	
GAM337601	10425	hsa	X	+	148876208	148876292	
GAM337602	9610	hsa	X	+	148876211	148876289	
GAM337605	11275	hsa	7	-	150253092	150253179	THC1523723
GAM337606	9923	hsa	7	+	150584218	150584325	
GAM337607	11093	hsa	1	+	151095622	151095720	
GAM337608	10347	hsa	1	+	151095623	151095719	
GAM337613	9883	hsa	5	-	152750152	152750233	THC1432163
GAM337614	10796	hsa	7	-	155774514	155774598	
GAM337615	11243	hsa	7	+	156346946	156347047	THC1529471
GAM337616	10849	hsa	7	+	156956195	156956277	
GAM337617	11262	hsa	1	-	157286075	157286150	
GAM337619	9884	hsa	2	+	158225419	158225500	THC1432163
GAM337620	9984	hsa	4	+	159014706	159014766	
GAM337621	9885	hsa	1	-	162284736	162284817	THC1432163
GAM337622	9886	hsa	6	+	164286556	164286637	THC1432163
GAM337623	9887	hsa	3	+	165593729	165593810	THC1432163

GAM337624	10220	hsa	1	-	168691834	168691904	
GAM337625	11094	hsa	1	+	171453855	171453956	
GAM337626	10661	hsa	1	-	176442690	176442777	
GAM337627	11104	hsa	1	+	177506687	177506787	
GAM337628	9888	hsa	1	-	182133354	182133435	THC1432163
GAM337629	9889	hsa	4	+	186079835	186079916	THC1432163
GAM337630	9712	hsa	1	+	199201991	199202087	
GAM337631	10574	hsa	1	+	208756916	208757003	
GAM337632	9675	hsa	2	+	222613184	222613279	THC1529741
GAM337633	10390	hsa	2	+	222613185	222613278	THC1529741
GAM337634	10612	hsa	1	+	231956115	231956203	

GAM NAME PRECUR PRECURSOR-SEQUENCE GAM FOLDED PRECURSOR RNA
SEQ-ID

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GAM25 10361 GAGGCAGGAGAATTGCTTGA G AA GAA-- AG GCTT A - AGAA
ACCCAGGAAGTGGAGGCTTC GAGGCAG AG TTGCTT CCCAGGA TGGAG CAGTG GC TG

AGTGAGCTGAGAACACGCCA CTCTGTC TC AACGAG GGGTCCT ACCTC GTCAC CG AC

CTGCACTCCAGTCCTGGGCA - AG ACAAC G- AC-- - C ----
ACAGAGCAAGACTCTGTCTC

GAM31 10712 GGCTGTGGCTGGATTCAAGT GG TG TT C GTTTCCATCTGTGA
AATCCAGGATAGGCTGTTTC GGCTGT C GA CAAGTAATC AGGATAGGCT
CATCTGTGAGGCCTATTCTT TCGACG G CT GTTCATTAG TCTTATCCGG
GATTACTTGTTTCTGGAGGC GA GT TT T ----------
AGCT

GAM44 10225 GAAAAGGTGGTGTCATGTTT - TG G ATGT AATCTTA
TGGGGAGAATCTTACTTCTC GAAAAG G GT TC TTTGGGGAG
AAATGGAAATTGCACTTTTT TTTTTC C TA AG AAACTCTTC
A GT A GT-- -------

GAM55 9654 ACTGGAAATCACTGCCATTT ATCAC TCC - A--------- AGTTTTG
CCAGGAGATCACCTATCCTA ACTGGAA TGCCATT AGGAGATC ACCT TCCT
GTTTTGAGGAATAGTCATTG TGATCTT ACGGTAA TCCTTTGG TGGA AGGA
AGGTGGGTTTCCTTAATGGC CTCT- T-- G GTTACTGATA -------
ATCTCTTCTAGT

GAM66 9890 AGTTTTGCACCTGAGACAGA A TCACTC TC- CCTA
TAGCCTCACTCGCCTCACCC AGTTTTGCACCTGAGACAGAT GCC GCC AC
TAGTCCTGGTGGCATTTGTC TTAAAACGTGGACTCTGTTTA CGG TGG TG
TCAGGTGCAAAATT - ------ TCC ----

GAM83 9594 AAAGGATGAAAAGGTGGTGT ----- - TG G ATGT AATCTTA
CATGTTTTGGGGAGAATCTT AAAGGAT GAAAAG G GT TC TTTGGGGAG
ACTTCTCAAATGGAAATTGC TTTCCTA TTTTTC C TA AG AAACTCTTC
ACTTTTTGCTGAATCCTTT AGTCG A GT A GT-- -------

GAM99 10072 CCTTCAAAAAGTTTGTAGCC AAAAAG G A G G TAA---- AAG - GATAACCA
TATCGGGGTGGAGAGATAAG CCTTC TTTGTA CCT TCG GGTG AGAGA GCC TAT CCA
CCAAGTATCCAGATAACCAT GGGAG AAACAT GGA AGT TCAT TCTTT CGG ATA GGT
GGCATAAGGCAGAATATTTT GGG--- - G A G TATAAGA A-- C --------
CTGTACTATGAGAGGTACAA
AGGGGAGGG

GAM106 11185 TGGGGCCTTGGTAATATAGG ------- G AAA C CAA G- TTGA
AAACCTTCTTGCCAATATAG TGGGGCCT TG TAATATAGG CCTT TTGC TATAG AATATG

GAATATGTTGACATATTAGC GTCTCGGA AC ATTATATTC GGAA AACG ATATC TTATAC
TATAGCAAAAGGCTTATATT GTAAGCC G --- - --- GA ----
AGCACCGAATGAGGCTCTG

GAM112 9976 CAGTAAACATAAGTTCCTCA ACATA C - AGA T - G TAGAAC
GGAGAGTTTGATGTGTGTCA CAGTAA AGTTC TCA GG GTT GAT GTGTGTCAGGT CT
GGTGCTTAGAACAGGGCCTG GTCATT TCGAG AGT CC CGA CTA TATATAGTCCG GA
ATATATAATCAGCCCATGAT A---- T A --- - A G ------
GAGCTATTACTG

GAM144 10844 GTGATCCACACGCTGGCCCA G ACA-- T C AG GACA GCGA
GGAGTTCGACATTTACCGCG GT ATCC CGC GGC CAGG TTC TTTACC
AGGTGGGCGGAGAGCCTGTG TA TAGG GTG CCG GTCC GAG GGGTGG
CCTGTGACGAGGGATGAT G GAGCA T T GA GC-- ----
GAM175 11029 TGAACCAGCTTCTCAGCTCT ACC - A A T TGA TG TTCA GT A TATA
ACTGTGTTTGACCCTGTGTT TGA AGC TTCTC GCTCT CTG GTT CCC TG AG T GGGGAAT

CAAGGTTAGGGGAATTATAG ACT TCG AAGAG CGGGG GAC TAA GGG GC TC G CCCTTTG

TTTCCCAGGTCTCCATCGTG --- G A A - TG- GT TACC TG A ----
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GAAGGCTTCA
GAM189 10243 GAAGTTCCAGGCTGTAGTGC GT- T CT A- A ACGT
ACTATGATGATCGTACGTAT GAA TCCAGGCTG AGTGCA ATG TG TCGT
GAACAGCCATTGCACTCCAG CTT GGGTCCGAC TCACGT TAC AC AGTA
CCTGGGCAATTC AAC C -- CG A ----
GAM193 10490 GCTGGATATTGCTAAGAATT - G AGAA AG CG AGA CCATACTA
CAGGTAGTCTCGGGATCTCC GCTGGAT ATT CTA TTCAGGT TCT GGATCTCC GTCT
AGAGTCTCCATACTAGGACA TGATCTG TAA GGT AGGTCCA AGA TCTAGAGG CAGG
GGAGATCTTCAGAACCTGGA A A AAGG -- CT A-- --------
GGAATGGAAATAGTCTAGT
GAM205 10955 TCAGGCCTGGAGCCCAGGAA AG CCC AGT TTC TGCTTCTAAC TG CTGTAC

GTCTGGTTTCGAATTTCATG TC GCCTGGAG AGGA CTGGT GAATTTCA C AGCA
CTTCTAACCTGAGCACTGTA AG CGGACTTT TCCT GATCG CTTGAGGT G TCGT
CTGCTTGGTGGAGTTCTCTG A- CCA --- TCT ---------- GT ------
CTAGTCCTACCTTTCAGGCA
GA
GAM206 9626 ACAATAGTCTAAGAGCTAAC - TCTAA TA AG TAC TA CT AAATAA
TAGTTGCACTTGTCTTTACC ACAA TAG GAGC ACT TTGCACTTGTCTT CC GAGG TGCT

CTAGAGGCTTGCTAAATAAA TGTT GTC TTCG TGG GACGTGAACGGGA GG TTTC ACGA

GCATACTTTCTGGAGGGCAA T ----- C- G- --- TC AT ------
GTGCAGGGGTCGCTTCTGTT
TGT
GAM240 11204 TGGTTTAGCTTAGGAACAGC T A - T GTA-- TTCA AC TAGCTATT
ATCTGGCACATAGTAAGTGT TGGT TAGCTTAGGA CAG CA CTGGCACATA AGTG GTGA GT

TCAGTGAACGTTAGCTATTA ATTA ATTGAGTCCT GTC GT GATCGTGTGT TCAC TACT CA

CCATCATCACTATTAATGTG C - A - AATTA ---- AC --------
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TACATTA
GAM259 9934 CAAGTTGTGACCTTCCCAGT T ---- CCA - AT A T CAAGCTT
CCTCTCTCCATTTGCAGATC CAAGTTG GACCT TC GTCC TCTCTCC TTGC GA CAG
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GAGGGGTGGACAATGAAACT - TCAA TAA T -- A - -------
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GAM269 10396 GAGGTAAGTTTGAACCCAGG AAG-- A- AG AG T GA AAGAT
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CAAGATGGCACCATTGCACT CTTCA AGAC TGGGTCC CCTC CG TACCA CGG
CCAGCCTGGGTGACAGAGTG GAGTG AG GA A- T -- -----
AGACTTC
GAM270 9919 ATGGGTAGCATGAACTAAGG CAT A A- AAAG C G TTTGG
TAGATAAAGGCTTCACGTGG ATGGGTAG GAACT AGGT GAT GCTT ACGT GTG
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TAGATTGGACCTCAGTTTTC T-- C GG GATG - G -----
TGCCCAT
GAM281 10402 GAGGTGGGAGGATTGCTTGT TG G GA C GG A CTA - CTTGATT
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CTGCACTCCAGCCTGGGCAA GT - AG C -- C AC- G -------
CAGGTAAGACTCTGTCTC
GAM282 10716 GGCTTTAGGAATCGCCTGGC A -- CTG ACCCTCTCAC T T ATAC
TCTACCCTCTCACTTCATGG GGCTTT GGAA TCGC GCTCT TTCA GGC ACAG
CTACAGATACTTGTGCCCTG CCGAAA CCTT AGTG CGAGA GAGT CCG TGTT
AGAGAGCAAGTGAATTTCCC C TA AA- ---------- C - ----
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GAM291 11179 TGGGCCAGATAGTTCTCTGT CC T TCTCTGTTGT GG TG GCATT
TGTTGGGGGATTTCTTGTGC TGGG AGA AGT TGGG ATTTCT T
ATTGTGGGAGATTTCCCATC ACCC TCT TCA ACCC TAGAGG G
TTTCCTCACTTCTACCCA A- - CTCCTTTCT- TT GT -----
GAM317 10674 GGCAGAGGAGGGCTCACTTT G ACT ---------- AAA CA GTGT
TCAAAGTTCCAAATAGGGCA GGCAGAG AGGGCTC TTTCAAAG TTCC TAGGG AAAT
AAATGTGTGTTTCCCTAGGA CTGTCTC TTCTGAG AGAGTTTT AAGG ATCCC TTTG
AGTATTTTTTAAAAACATTT G AT- TACAAAAATTTTTTATG --- -- ----
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GAM329 10797 GGTGGTGGGTGTGAGGAAGG GG G ----- CT CTTTCAC
GCTGGGCACTTTCACTGTCT GGTGGTG TGT AG GAAGGG GGGCA
TTTCCTTCATAAACTGGCAA CCATCAC ACG TC CTTCCT TCTGT
GCACTACC GA G AAATA TT -------
GAM330 10273 GAGAATTGCTTGAACCCAGG AA TG GA-- AGG GT G CGAGATCAC
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CGAGATCACGCTACTGCACT CTC A GAG TGGGTCC ACCTC ACGTCA TCG
CCAGCCTGGGTGACAGAGTG AG GT ACAG G-- -- - ---------
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GAM335 9932 CAACCCAGTAAGTGTCCCCA GTA- CC---- TC G AGGAGA TGTAAAT
GTCAATGCTTCTCTCCATAG CAACCCA AGTGT CCAG AAT CTTCTCTCCAT CC
GAGACCTGTAAATGGGCGGT GTTGGGT TCACA GGTC TTA GGAGGGGGGTG GG
GGGGGGAGGAATTTTCTGGT ATTA CACTCT TT A GCG--- -------
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G
GAM347 9752 AGTCTCACTCTGTCTCCTAG TC C TC T-- C -- C ATCT
GCTGGAGTGCAGTGGCGTGA AG TCACT TG TCC AGG TGGAG TGCAGTGG GTG
TCTCATCTCATTGCAACCTC TC AGTGA AC AGG TCC ACCTC ACGTTACT TAC
CACCTCCTGGATTCAAGTGA TT - TT TCC - CA C ----

TTCT
GAM354 10673 GGCAGAGCGCTGCCTCTCTG A G CA G - T- G TGATCTT
CAGGCCGTGTGCTTTGCTCG GGC GA CGCTGCCTCTCTG GGCC TGTG CTT GCTC GT

GTTGATCTTGCAGAGCCTAA CCG CT GTGACGGAGAGAC CCGG ACAC GAA CGAG CG

GACACAGGCCCAGAGAGGCA - A -- - A TC A -------
GTGATCGCC
GAM361 11098 TGAGGCAGGAGAATCGTTTG CA AA GAA--- AGGC - T T CCGAGAT
AACCTGGGAGGCGGAGGTTG TGAGG GGAG TCGTTT CCTGGG GGAG GT GTG TGAG

TGTTGAGCCGAGATCTCGCC ACTCT CCTC AGCGAG GGATCC CCTC CG TAC GCTC
ATTGCACTCCAGCCTAGGCA A- AA AACAAC GA-- A T C -------
ACAAGAGCGAAACTCCATCT
CA
GAM367 11120 TGAGGTAAGTATGTTATTGG AG A A GG G TG TATATAGAA A T AAA A AGATG

AAAGGTGTGATCTATATAGA TG GT AGT TGTTATT AAA G TGATC CCCTGT CA GA GG GG

ACCCTGTACATGAAAAGGAG AC CA TCA ATGATAA TTT T ACTAG GGGACG GT CT TC CC

GAGATGCCGCTATCTTGGCA GA C - AG A GT TA------- - T A-- G -----
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ATAGTAACTCACAGCA
GAM388 9776 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM401 9669 AGAGAGAGTCTCACTCTGTC A TC C TCG C-- T -- TG ATCT
GCCCAGGCTGGAGTGCAGTG AG GAGAG TCACT TG CC AGGC GGAG TGCAGTGG TG

GTGTGATCTCGGCTCACTGC TC CTCTT AGTGA AC GG TCCG TCTC ACGTCACT GC
AACCTCTGCCTTCCGGATTC - -- - TTA CCT - CA CG ----
AAGTGATTCTCCT
GAM408 10542 GGACTGAAAGAGAACTGGGA A AAA A- AG A A GTG TGTTTC
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GTGTGGTGTTTCCCAAGACA CC GAT CTCT GACCCTATC TTCT AGTC CCTAC ACC
TCCCCTGATCTTGCTATCCC A C-- AC G- - C AGA ------
AGCATCTCCTAGACC
GAM426 10058 CCTCCTGCTGAAGCTTCTGG T T- GA- T A TG GAG CAG
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CAGGAGAGTGAAGCGAGTTG GG GG TGA TCGA GACC GG T CGAAGTGAGAG
GGCCAGAGCTGAGAGTCTGG T TC GAG - - GT GAG ---
TGG
GAM492 11209 TGTCTATAGAGTATGTGGGC AGAGTA T TT- TG C- A TT T CTCTCTCT
CATTTTCTGCCCGTAAAATG TGTCTAT TG GGGCCA TTC CC GTA AATG CAAA GTTTT
TTCAAATGTTTTCTCTCTCT ACAGATG AC CTTGGT AAG GG TAT TTAC GTTT CGAAA
AAAGCTTTGTTCATTGTATC AGGG-- T TTT GT TC G TT - --------

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GGGAGTAGACA
GAM495 10024 CCCGACCACTAGCAGCCTCT C- T AGCCTCTTTC T - AA AGGCA A CATCAT
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TACAGGCAGTAGCCACCATC GG TTGGTG TCG TC GTGA CCT TACGGGTG CA CGGTG

ATGTGGCACAAAGTGGGCAT TC - AATTTACAA- T T AC AAA-- - ------
CATCCTAGTGTCTAACATTT
AAGCTGTGGTTCTGG
GAM507 10728 GGGAGACCCAGGACCCGGGA CCA C G GTAGAGG - C--- CACCA
GAGAGGTAGAGGGGAGCAGA GGGAGAC GGAC CG GAGAGAG GGAGCAGA GA AGC

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TTCTGCTCTAAGCACATTCT AA- A A ACACGAA T ATCT -----
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GAM519 9641 ACCTATTCCCTGTGGCTTAG C------- T T A -- - CCTGGCCT
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GGCCTCCTGAGTCCCACAGC TGGGTAAG GACACCGA TCC TTCG ACA CTG GTCC
TTCCTAGCCACAGTGATAAA AAAATAGT - - - CC A --------
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TCTGGTTTGAGAGACAATGA GTAGGAG CAGGG CTG TTTGAGAGA TGA AC
CACACACCCCTAAGTTCACC CATTCTC GTCCC GAT AAGCTCTCT ACT TG
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TGCTCTTAC
GAM550 10897 TAAATCTGGGCTGAGGGAAA ATC TGAG- ---- T C ---- -- - TCT TG
GCATGTCCACACCAGGTGCC TAA TGGGC GGAAA GCA GTCCA AC CAGGTGCC CAG ACA
GGT GC
CAGACATCTGGTTGGCTTTG ATT ACCCG CCTTT CGT TAGGT TG GTCCACGG GTC TGT
TTA CG
GCTGATTTGTCCTGCAGGCA --- TTGAA CACA T C TTCC AC C --- GT
CCTGCCTTGTCTGGATTTGC TTTG
ACACTTTCCAAGTTGCCCAT
TA

GAM569 10404 GAGTAAGGGGCAGAGCGCTG GTAAGG A G CA G - T- G TGATCTT
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GATC
GAM572 9658 AGAACAAGGGCTAAATTCAA GG AA AA--- - T TAC GAAAAATAA
ATCAAATTTTCCCTGTACCC AGAACAA GCT ATTCA TCAAAT TTTCCC G CCTAA
TAAGAAAAATAATTAGGCCG TCTTGTT CGG TGAGT AGTTTG AGAGGG C GGATT
GGAGATGTTTGACTAAGTGA A- A- GAATC T C --- ---------
GTAGGCATTGTTCT
GAM584 10146 CTGAGGCACCTCCACTGGCC A ACCTCCAC - - - -- GA - GGTTT
CCTTTGTGAGGCACGCTTGA CTG GGC TGGC CCCTTTG TGAGG CACG CTT CC TG

CCTGGGTTTCATGGAAAGAA GAC CCG ATCG GGGAAAC ACTCC GTGT GAA GG AC
TGTGCCCTCACCAAAGGGTG C GAACAA-- T C C AA A- T -----
CTAAACAAGGCCCCAG
GAM588 9928 CAAAGAGGTGTAGAATCTGG -- AGAAT TT T TTCAA A TCATT
GTTGGTCCTTCAAGGCAGCT CAAAGAGG TGT CTGGG GG CC GGC GC
CATTGCAGCTACTGGCCTCC GTTTCTCT ACA GACCT CC GG TCG CG
AGTGAAACAGGTCTCTTTG GG AAGT- -- - TCA-- A -----
GAM593 9723 AGGCTCACACAGCAAGTCTT --- C A CT TG AA TTAGGAATG - CCCTCC CA-
TGTCAAAGCTTAGGAATGGA AGGC TCACA AGCA GT T TCA GC GAAGTA GGTTGTC
TAGT
AGTAGGTTGTCCCCTCCTAG TCCG AGTGT TCGT CA A AGT CG TTTCGT CTAACAG ATCA

TCATGGGATCTCTCCAACTC ACG C A -- GT -- TGCA----- T ------ CTC
ACTAGACAATCTTGCTTTAC - ATCTC
GTGCTGATGAACATGCTCTG TGGG
TGAGCAGCCT ACCT
A -----
GAM604 10098 CTAGCTGCTGCCAGCCAAGC C TG G GC C A C TGC
TGCTACCAGACCAGCTCCTG CTAG TGC CCA CCAA TGCTAC AG CCAG TCC
CGGAACTGGCTGTGGCATTG GGTT ACG GGT GGTT ACGGTG TC GGTC AGG
GTGGTGGCATTGG - GT - -- - - A ---
GAM640 10481 GCTCGTTGCCCAGGCTGGAG TC TG- -- -- T AAT TCTTG CACCAC
CCACTTCCC
TGCAATGGCGTGATCTTGGC GC GT CCCAG GCT GGAG GC GGCGTGA GCT AACCT
TCACCACAACCTCCACTTCC CG CA GGGTC TGA CCTC CG CCGTACT CGA TTGGA
CAGGTTCAAGCGATTCTCAT GA TTA GA AC - ATT CTTAG AC---- ---------
GCCTTAGCCTCCCAAGTAGC
TGGGATTACAGGC
GAM667 10851 GTGCCTCATCTGTAGGTGGT TGCC TCT TGGTT A- GAAA--- - ---- A A CA
TGAGAGAATGAAAGGAGGTA G TCA GTAGG GAG GAAT GGAGGTA GCA TG GC
GGGCACT G
GCATGAGCAGGGCACTCAGC T AGT CATCC TTC TTTA CTTCTAT CGT AC CG TCCGTGA
C
TCGGAGGCAGTGCCTAGCCA TCTA TCT TTTT- GG AGTGTCA T TACA - A --
ACATTGCTTATCTTCACTGT CGGA
GAATTTGGCTTTTTTCCTAC CT
TCTTGAATCTT GG

GAM674 9938 CACAGCCAGTTTCTTTGATG ---- T ---- - ACGTA T GATCTT
ACTCAAAACGTACTTTGTGA CACAGCCA GTT CTT TGATGA CTCAAA CTT GT
TCTTGCCAAGCTTTGAGATC GTGTTGGT CGA GAA GCTACT GAGTTT GAA CG
ATCGTTACAAGCAGCATTTT TTTA C CATT A C---- C ------
GGTTGTG
GAM689 10321 GAGGCAGGAAAATCGCTTGA AAAATC GAA-- A A- GT CA- ATA
ACCCAAGGCAGAGGTTGCAG GAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG
TCAGCAGATATTGCACCACT CTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
GCACTCCAGCCTGGGCAACA CAGAA- ACAAC - AC -- CCA ---
AAGCAAGACTCTGCCTC
GAM744 9749 AGTCACTGGAAAATGCTTAC T - AA AGGCA A CATCAT
AGGCAGTAGCCACCATCATG AG CACT GGA ATGCTTAC GT GCCAC

TGGCACAAAGTGGGCATCAT TC GTGA CCT TACGGGTG CA CGGTG
CCTAGTGTCT T T AC AAA-- - ------
GAM750 9628 ACACCTCCAACCTCCCTGCC CTC-- CCCTGCCTTTGAA TTAA G T ATTTGA
TTTGAACCCTGTGTTAACAA ACAC CAACCT CCCTGTG CAATGAGAA CT GTTT
TGAGAAGCTTGTTTATTTGA TGTG GTTGGA GGGACAC GTTACTCTT GG CGGA
AGGCTGGGTTCTCATTGGCC TTAAT TG---------- CCG- G T ------
CACAGGGGTAGGTTGTAATT
GTGT
GAM760 10991 TCGCAGTCAGACGTTTGGCA C A G CAAC GGAA- AA GCTTTTCA
ACAGCAGTGGAAGAGGCAAC TCG AGTCAG C TTTGG AGCAGT GAGGC CTGGT
TGGTGCTTTTCAGCTAGGCC AGC TTAGTT G AGACT TCGTTA TTCCG GATCG
TTGAAAAATTGCTTCAGAGG T - G ---- AAAAG -- --------
TTGATTTCGA
GAM772 11168 TGGCACCAGCTTCCAAAGCC C TTCCAA A-- AGA A AG TG CCAC
AGGATGAAGAGGAGGAGAAA TGGCA CAGC AGCC GGATGA GG GGAGAA GA GGGT

GGATGGGGTCCACACCTTGT ATCGT GTCG TCGG CCTACT CC CCTCTT TT TCCA
TTTCTCCACCATCATCCAGG C TC---- GGA A-- A -- GT ----
GGCTCTGCTGCTGCTA
GAM779 10042 CCGATGAACCCAGGGCCGTT T GCC CC-- AC TT TTAGTAG A-
TTGATTAAGG
CCCTTCATACCCTTTCATTA CCGA GAACCCAGG GTTC TTCAT CC TCA CTCT AGATGT
GTAGCTCTAAGATGTTTGAT GGCT CTTGGGTTT CAAG GAGTA GG GGT GAGA TTTGCA

TAAGGTGTACGTTTACAGAG T A-- TTAC GT TT TGAG--- CA ----------
GAGTTGGTTGGTGATGAGCA TGT
TTGAACATTTGGGTTCTTCG
G

GAM785 10027 CCCGGAGTTTATGGTCTGGT GAG-- TCT- TG A C T TGCCA TCTA
GAGAAGATCCCTGCTCTGAG CCCG TTTATGG GG AGAAG TCCCTG TC GAGTCAC AGC

TCACTGCCAAGCTCTAGCTA GGGC AAATATC CC TCTTT AGGGAC AG TTCAGTG TCG

TGTGACTTTGAACAGGGAAT AAATA TATC TG A A T TA--- ----
TTCTGTCCCTATCTATAAAA
TAAACGGG
GAM801 10252 GAATTCCTAAGTATGTGGTC ATTC AGTAT--- C A- T T ---- - TATA
TGTATTGTGCTTGTACTGAC GA CTA GTGGT TGT TTG GCT GTACT GACCAT GTA
CATGTATATATGCTATGGTT CT GAT TACCA ACA AAT CGA CGTGA TTGGTA CGT
ATTTAGTGCTAGCTAAGAAC GAC- GACCCCTT T AG - T TTTA T ----
ATACCATTTCCCCAGTAGCA
GTC
GAM807 11034 TGACAATCTTGGTTACCATC ACAA GTTA TCCATTAA GCTGAT CATGAAAAAC

CATTAAGTGCTGCTGATTTT TG TCTTG CCA GTGCT TTTGGAAAGAT
GGAAAGATCATGAAAAACGT AC AGAAC GGT CACGG AAACCTTTCTG
CTTTCCAAACATGAAGGCAC GG-- ACG- TTGCTG-- AAGTAC ----------
GTCGTTTGGGCACAAGAGGC
A

GAM821 10085 CGCTGCCTCTCTGCAGGCCG CA G - T- G TGATCTT
TGTGCTTTGCTCGGTTGATC CGCTGCCTCTCTG GGCC TGTG CTT GCTC GT
TTGCAGAGCCTAAGACACAG GTGACGGAGAGAC CCGG ACAC GAA CGAG CG
GCCCAGAGAGGCAGTG -- - A TC A -------
GAM828 9655 ACTGGAGACACATCTAATGG - AATG -- TCAAG ACTTTCTAA
CTGTGCTGATGTCAAGGGAC ACTGGAGACA CATCT GCTGT GCTGATG GG
TTTCTAATCATGTTCATCAG TGACCTTTGT GTAGA CGATA TGACTAC CT
TTGATAGCAGATGCTGTTTC C ---- GT TTGTA ---------
CAGT
GAM834 10448 GCCCAGGCTAGAATTCAGTG CT AATT T TC A CAC C CGAACTCCT
GCAGGATCATAGCTCACTGC GCCCAGG AG CAG GGCAGGA AT GCT TG AGCCT
AGCCTCGAACTCCTAGGCTC TGGGTCC TC GTC TCGTCCT TA CGA AC TCGGA
AAGCAATCCTCCTGCTTCTG -- C--- T CC A --- - ---------
CCTCCTGGGT
GAM840 10568 GGAGAATCATTTGAACCCAG AA GA--- AGG A T A- TCAGATC
GAGGTGGAAGTTGCAGTGAG GGAG TCATTT ACCCAGG TGGA GT GCAGTG GC
CTCAGATCGCACCATTGCAC CCTC AGTAAG TGGGTCC ACCT CA CGTTAC CG
TCCAGCCTGGGTAACAAGAA AA AACAA G-- - - CA -------
TGAAACTCC
GAM842 10178 CTGGGGGCTGAGACCACCCT ------ - A CT - CCCTTCT--- GCCTTA
TGCCTGCCCCCTTCTTTCTG CTGGGG GC TGAG CCACC TGCCT GCC TTCT
CCTTAAGAATGTCCTTTTAG GACCCC CG ACTC GGTGG ACGGG CGG AAGA
GCTGGGCATGGTGGCTCACG AATGTC C - T- T ATTTTCCTGT ------
CCTGTAACCCCAG
GAM846 10989 TCCTGTGCTGCAGTAGAAAT C TG G T A TGT TTTAT
TAGAGCATGTCCTGCTTTAT TC TG CT CAG AGAA TTAGAGCA CCTGC
GCAGGCTTTGCTTTAGTTCT AG AT GA GTC TCTT GATTTCGT GGACG
TCTGAAGTGTATGA T GT A T - TTC -----
GAM869 10519 GGAAAGAATAAAGGCTTGGA GA AAT GA - C T TACTGCAT
CTCAGCCTAGGTTCAAGTAC G AAG AAAGGCTTG CT CAG CTAGGT CAAG
TGCATCTTGACCTGGCCTGT C TTC TTTCTGAAC GA GTC GGTCCA GTTC
AGGCAAGTCTTTTCACTTCT TC ACT G- T C - --------
C
GAM892 11175 TGGCTTTATCTCTTGCCTTG ---- T- CC C C A ACAAAG
ACCTCCTACATTATCAACAA TGGCTTT ATCTCTTGCCT GA TC TA ATT TCA
AGTGAGAGTTTAAGATCTCC ACCGAAG TAGAGGACGGG CT AG AT TGA AGT
TGGGCAGGAGATTTCAGAAG ACTT TC CT A T G ------
CCA
GAM933 9643 ACCTCTCATTTCTCCTCAAT TCAT C A AC A T AACT
GCCACTGCACTGATGTCAAC ACCTC TTCTC TCA TGCC TGC CTGA GTC
TGACTTAGGGCAGGCATGAG TGGAG AAGAG AGT ACGG ACG GATT CAG
AGAACTGAGGT TC-- - - -- G - ----
GAM965 11190 TGGGTAGCATGAACTAAGGT CAT A A- AAAG C G TTTGG
AGATAAAGGCTTCACGTGGT TGGGTAG GAACT AGGT GAT GCTT ACGT GTG
GTTTGGCATGGCGTAGGTGT ACCCGTC TTTGA TCCA TTA TGGA TGCG TAC
AGATTGGACCTCAGTTTTCT T-- C GG GATG - G -----
GCCCA
GAM973 9616 AAGTGCTGGATATTGCTAAG -- - G AGAA AG CG AGA CCATACTA
AATTCAGGTAGTCTCGGGAT AAGT GCTGGAT ATT CTA TTCAGGT TCT GGATCTCC GTCT

CTCCAGAGTCTCCATACTAG TTCG TGATCTG TAA GGT AGGTCCA AGA TCTAGAGG CAGG

GACAGGAGATCTTCAGAACC AC A A AAGG -- CT A-- --------
TGGAGGAATGGAAATAGTCT
AGTCAGCTT

GAM999 9667 AGACCACCTTATTCTTTTCT CCTTA T- TA---- ------ - TGAA
TATGGGTATGTGGCATGAAT AGACCA TTCTTT CT TGGGTA TG TGGCA
GCCATCATTTATTTACCCAG TCTGGT AAGAAG GA ACCCAT AC ACCGT
CTGCCAGTTGAAGAACATTT TTTAC TT CCGTCG TTATTT T ----
TGGTCT

GAM1017 10611 GGAGAATCGCTTGAATCTGG AA TGAA T G - GT A- TGAGATC
GAGGCGGAGGTTGCAGTGAG GGAG TCGCT TC GG AGGC GGAG TGCAGTG GC
CTGAGATCGCACCACTGCAC CCTT AGCGA AG TT TCCG CCTC ACGTCAC CG
TCCAGCCTGTTGACAGCGAG AG C--- - G A -- CA -------
ATTCC

GAM1032 10472 GCTAGTCACTGGGGCAAAGA TAGT CAAAG AAACACTT C CA TGT
TGACTAAAACACTTTTCCTG GC CACTGGGG ATGACTA TTCCTG CCTCGAGGAGCT
CAGTCTAGTA
CCCTCGAGGAGCTCACAGTC CG GTGGCTCC TACTGGT AGGGAC GGAGTTCCTCGA
GTCAGATCAT
TAGTATGTCTCATCCCCTAC TT-- ACTCA -------- A A- ---
TAGACTGAAGCTCCTTGAGG CTCATCCCC
ACAGGGATGGTCATACTCAC
CTCGGTGTTGC

GAM1033 10394 GAGGGGAGATTAAAGAATCA TTAAA AT A C- GGG G TTAAATTGTTT
ATGTTCCCAGGGGAAAAGGG GAGGGGAGA GA CA TGTT CCA GAAAAGG CC
CCTTAAATTGTTTGGTCTTT TTCCCCTCT CT GT ACAG GGT CTTTTCT GG
TCAATGGCTGACACTGTCTC CAAC- CT C TC AA- - ----------
CAACTCTCCCCTT

GAM1087 9741 AGGTGGCAGAGAGGCAATAT -- C -- AT-- ----- T CATCACA
CAATCCTTCTGCATCACACA AGGT GG AGAGAG GCAAT CAA TCCT CTG
GTGGGAAAAGTTTGTCTCAT TCCG CC TCTCTT CGTTA GTT AGGG GAC
TGCAGTTCTCTTCCAAGCCT AA T GA CTCT TGAAA T -------

GAM1088 10043 CCGCAGGGAGAAGAGCTGTG G -------- A - AT---------- TTATAAATT
TGCTGTGATGTGGTTTATAA CC CAGGGAGA AG GCTG TGTGCTGTG GTGGT
ATTACCATTTGGAAGGAGCT GG GTCCTTCT TC CGAC ACACGACAC TACCA
GCACAGCACAGCAGCCTGCA A CATCAACG - G GTCGAGGAAGGTT ---------
ACTACTCTTCCTGAGG

GAM1089 10834 GTCTGAAATCCAGGTGTGGG G TCC G CC G CC AGGC
CAGGGCCGTGCTCCCTCCGA GTCT AAA AGGT TGGGCAGGG GT CTCCCT GA
AGGCTCTAGGGGAGGATCCT CAGA TTT TTCA ACTCGTTCC TA GAGGGG CT
TGCTCAACTTATTTTTGAGA G TTA - -- G AT ----
C

GAM1099 10919 TAGTATGTTGAGCATCTTTT T - TT T TTGCC -- - TTTGGT
TGTAAGTGTACTTGCCATCT TAGTA GTTGAGCA TCT TTG AAGTGTAC ATCTG TAGAT CTTC

GTAGATCTTCTTTGGTGAAG GTTAT CAATTTGT GGG AAT TTTACGTG TAGAC GTCTG GAAG

TGTCTGTTCAGATCTGTGTG T T TT T TGTC- TT T ------

CATTTTTAATTGGGTTGTTT
AACTTATTG
GAM1144 10118 CTCTCATCATAGATTAATCA CA- - TT T ----- - T TTAAC GTGAA
CTTAGTTGCAAGGGACCAGT CTCT TCA TAGA AATCACT AGTT GCAAGGG ACCAG AAA
AGAATG
AAATTAACAGAATGGTGAAC GAGA GGT GTCT TTGGTGA TCAG CGTTTTC TGGTT TTT
TTTTAC
ATTTTCCTTTTCTTGGTGCT CAA C -- - TAGGT G C TCC-- -----
TTTGCTGGATGACTAGTGGT
TTCTGCTGGAACAGAG
GAM1163 10865 GTGGTGTATGGGATCTGCAT T GATC -- TG A AA AACCCCAGTGAG
GGAGGTGGTCTATGAGAAAG GTGG GTATGG TGCA TGGAGG GTCT TGAG AGCA
CAAACCCCAGTGAGTGCTGC CATC CGTACC ACGT ACCTCT TAGG GCTT TCGT
TTCGGGATTCTCTCCAACTG - A--- CA CT - CG ----------
CAACCATGCCTAC
GAM1191 11151 TGCTGGGCGTGTGAGGCGGC GGC A CTG CTGT A GA GG TACACC
TGTGCTGTGCCTGTGAGACA TGCTG GTGTG GGCGG TG GCCTGTGAG CAG AT TTCCAT

GGAATGGTTCCATTACACCA ACGAC TACAC CCGTC AC TGGATATTT GTC TA AGGGTA

TGGGAAATCACTGATTTATA --- A AA- CC-- A AC A- ------
GGTCCCAAACTGCCACACAT
CAGCA
GAM1193 10309 GAGCTGGAGTCTCGCTCTGT CT- TCTC C T- CC C -- T GATCTTG
CACCCAGGCTGGAGTGCAGT GAG GGAG GCT TG CAC AGG TGGAG TGCAGTGG GC

GGTGCGATCTTGGCTCACTG CTC CCTC CGA AC GTG TCC ACCTC ACGTCACT CG
CAACCTCCACCTTTGTGTTC CTT TTAA - TT TT - CA - -------
AAGCAATTCTCCTTCCTC
GAM1197 9685 AGATTTTTTCTGATACTACA TTT C- TGT- TTTTTAA C TTG TA AGAAAACA
TATTGTCAGTTTTTTAAATA AGATTT CTGATA TACATAT CAGT ATA TCAGT TGC AA
CTCAGTTTGTGCTAAAAGAA TTTAGA GACTGT ATGTATG GTCG TAT AGTCA ACG TT
AACATTCGGCAACTGATATC CCT CT TCTT TC----- - --- GC --------
TGCTGTTCTGTATGTATCTG
TCAGTCCAGATTT
GAM1216 11241 TTCAGTGGCATTGGGCCTTG G GCA G T G GGA GTTA ACT
GCTGGGATGCTGAGTTATCC TTCA TG TTG GCCT G CTG TGCTGA TCC
ACTGGAGCATCGGCAGTACA AGGT AC GAC CGGA C GAC ACGGCT AGG
GGCAGGCACAGAGGCAGTGG G GGA A - G ATG ACG- ---
A
GAM1217 9644 ACCTGCCTATATTACATTCA - ATATTACA CA GA TT C- G ACAGTGAACGAA
TTTTGATGGTTTGTATCTCA AC CTGCCT TT TTTT TGGT GTATCT AAA GAGT
AAGGAGTACAGTGAACGAAA TG GACGGA AA AGAA GCCA CATAGA TTT TTCA
CTTGTTTAAAGATACACCGG A GAAGAG-- AA AG -- AA G ----------
AAAGAAAAAGAGAAGAGGCA
GAGT
GAM1221 11031 TGAAGACTCCATCACAGTTC CTCCAT -- T- GGA AGGGCTGGG
CAGATGGGTAGGAATACCTT TGAAGA CACAGT TCCAGA GGGTA ATACCTTGC
GCAGGGCTGGGGCAAGGTAT ACTTCT GTGTCG AGGTCT TCCGT TATGGAACG
TGCCTTCTCTGGAAGGCTGT CTTAC- GA CT --- ---------

GCATTCTCTTCA
GAM1234 11221 TGTGGGGATCTGGTGCTGTG GA TG TGC- GC- GTAACGG
GTTCTGCATGAAGACAGTAA TGTGGG TC G TGTGGTTCT ATGAAGACA
CGGTGTCTTCATCCAGGAAC ACATCC AG C ACACCAAGG TACTTCTGT
CACATTGTCTGGACCTACA -- GT TGTT ACC -------
GAM1238 10560 GGAGAATCACTTGAACCTGG AA GA-- ---- - A TGTT GAGCCGAG
GAGGCAGAGGTTGTTGCAGT GGAG TCACTT ACCTG GGAG GCAG GGT GCAGT
GAGCCGAGATTGCACCACTG CCTC AGTGAG TGGGT CCTC CGTC CCA CGTTA
CACTCCAGCCTGGGTGACAG AG ACAG CCGA A A ---- --------
AGTGAGACTCC
GAM1293 10868 GTGTCCCTTCCAAGCTGTGT - CAAG- ACTG AA AG GT ACTC
TAACTGTTCAAACTCAGGCC GT GTCCCTTC CTGTGTTA TTCA CTC GCCT GTG
TGTGTGACTCCATTGGGGTG CA CAGGGGAG GGTACAAT AAGT GAG TGGG TAC
AGAGGTGAAAGCATAACATG A ACATG ACGA G- AG GT ----
GGTACAGAGGGGACAAC
GAM1294 10179 CTGGGTTCCCAAATTCTCCT - CCCAA - C T TG ATTGTCTA
TGCTGTTCTGCATCATTGTC CTGG GTT ATTCT C TTGCTG TC CATC
TAGATGGATTAGTAAAGAAG GACC CAA TAAGA G AATGAT AG GTAG
AATGAAAACTCCAG T AAG-- A A T -- --------
GAM1295 11006 TCTAGGGAGACCCAGGACCC ACCCA C G GTAGAGG - C--- CACCA
GGGAGAGAGGTAGAGGGGAG TCTAGGGAG GGAC CG GAGAGAG GGAGCAGA GA AGC

CAGAGACAGCCACCAGCTTC AGATCCTTT TTTG GC CTTTCTT TCTCGTCT CT TCG
TATCTTCTGCTCTAAGCACA GAA-- A A ACACGAA T ATCT -----
TTCTTTCACGAGTTTAAGTT
TCCTAGA
GAM1300 11148 TGCTAGGCTTATTCTCTTCC G TA C TTCA CT CAAT - ACT
TCATTCAGTCTCTCAATCAA TGCTAG CT TTCT TTCCTCA GTCT CAAT CAA TACTT
TCAATACTTACTGAGTACTT ACGATC GG GAGA AAGGAGT CAGA GTTA GTT ATGAG
GTCATTGCAAGACCTGAGGA G -- T C--- AC CT-- C ---
ATAGAGGGGCTAGCA
GAM1310 10701 GGCGTCTTGCTCTATTGGCA TC---- CTA-- C T A - T GATCTCA
GGCTGGAGTGCAGTGGTGCG GGCG TTGCT TTGG AGGC GG GT GCAGTGG GC
ATCTCAGCTCACTGCAACCC CCGT AACGA GACC TCCG CC CA CGTCACT CG
CCGCCTCCCAGATTCAAGCA CCTCTT ACTTA C C C A - -------
ATTCTCCTGCC
GAM1332 10431 GCACCCTGTGAGGTAGGTGC CCCT GA- GG ACT CCTG- AGGT
TTTAACTGTGTGCACCCTGT GCA GT GGTA TGCTTTA GTGTGCAC TGAGGT
GAGGTAGGTGCTTTAACTGT CGT CA TCGT ATGGAGT TACACGTG ATTTCG
GTGCACATTGTGAGGTAGGT ---- AAG GG GT- TGTCA ----
GCTGAAACTGC
GAM1338 10613 GGAGAATGGCATGAACCCGG AATG A- AA- AGG CT A AGAGATCAC
GAGGTGGAGCTTGCAGTGAG GGAG GC TG CCCGGG TGGAG TGCAGTG GC
CAGAGATCACGCCACTGCAC CCTC CG AC GGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGC AGAG AG AAC G-- -- - ---------
GAGACTCC
GAM1361 9954 CAGAAGGGGTTTTTATCAAA AG- TTTA GTAG---- - AA AG AAAGA
AATATGTAGATTCTACTACA CAGA GGGTT TCAAAAATAT ATT CTACTAC TATTTT CT
ATATTTTAGCTAAAGAAGAA GTCT CCCAG AGTTTTTATG TGA GATGATG ATGAAG GA
GAAGTAGTAGTAGCAGTAGT CAA TCCC ACTGATGA C -- AA -----

AGTCAGTATTTTTGACCCTG
ACCCAACTCTG
GAM1363 9672 AGAGCTGGTGTGTAGCGGGT T- ---------- TC TGCT
ACCTTCTGTCTGCTGGCACT AGAGCTGGTGTG AGCGGGT ACCT TGTC
AGGTATTTTACACATTAAAT TCTCGACTACAC TTGCTCG TGGA ACGG
CAGCTCGTTCTCACATCAGC TC ACTAAATTACACATTTTA TC ----
TCT
GAM1372 10468 GCTAGGATTGCACCACTGCA A -------- CCAA CA AGCAAGACC
CTCCAACCTGGACAACAGAG GCT GGATTGCA CCACTGCACT CCTGGA ACAG
CAAGACCCTGTCTCTAGGCC CGA CCTAATGT GGTGACGTGG GGATCT TGTC
AGGTGCAGTGGCTCACACCT C CCACACTC ACC- C- ---------
GTAATCCCAGC
GAM1423 10304 GAGCAAGGACAAGTTGTGAC GA T ---- CCA - AT A T CAAGCTT
CTTCCCAGTCCTCTCTCCAT GAGCAAG CAAGTTG GACCT TC GTCC TCTCTCC TTGC GA CAG

TTGCAGATCAGCAAGCTTCT TTTGTTT GTTCGAC TTGGG AG CAGG GGGGAGG AACG CT GTC

GTCAGCAAGGAGGGGTGGAC A- - TCAA TAA T -- A - -------
AATGAAACTGGGTTCAGCTT
GATTTGTTT
GAM1431 10261 GAGAACTGGGATGGAGGAGA A- AG A A GTG TGTTTC
ATTAGAGGATGGTGTGGTGT GAGA CTGGGATGG GAGA TTAG GGATG TGG
TTCCCAAGACATCCCCTGAT CTCT GACCCTATC TTCT AGTC CCTAC ACC
CTTGCTATCCCAGCATCTC AC G- - C AGA ------
GAM1440 10231 GAACACAAAGAGGTGTAGAA ------- -- AGAAT TT T TTCAA A TCATT
TCTGGGTTGGTCCTTCAAGG GAACA CAAAGAGG TGT CTGGG GG CC GGC GC
CAGCTCATTGCAGCTACTGG CTTGT GTTTCTCT ACA GACCT CC GG TCG CG
CCTCCAGTGAAACAGGTCTC TTATCGA GG AAGT- -- - TCA-- A -----
TTTGAGCTATTTGTTC
GAM1443 10137 CTGAAGGGTGGAGAGGGCCT GAAGGGTGGAGAGGG T -- G GAG- C-- G G
TGAG
CTCATGCAGGCATGTGTGAG CT CC CTCAT GCAGGCAT TGT CAG TGCA GT TG
CAGCTGCAGGTGTGTGAGCA GG GG GAGTA TGTCTGTG ACA GTC ACGT TA AC
AATGTGCATCACTGGGGAAC AGTGGGAGTGAAGGA - GG G AGGG ACT G A ----
AGGTGTCTGTGGATGAGGGA
GGAAGTGAGGGTGAGG
GAM1447 10818 GTCCACACTGACCTTCTGTG CAC - GT-- T A CATGTCA
TCATGGCATATGCCCATGTC GTCCA TGA CCTTCT G CATGGCAT TGCC
AGGCAGTGCTGTGCTAAAGG CAGGT ATT GGAAGG C GTGTCGTG ACGG
AAGGATTACATGGAC AC- A AAAT - - -------
GAM1456 10902 TAAGATGAGTTGATATTCAA TG GATA AAATA - TA- A AAAA
ATATCCAGTTAGTAATGAAA TAAGA AGTT TTC TC CAGT GTA TG
ACAATACAATACTGAGAGAA GTTCT TCGA AAG AG GTCA CAT AC
AAAGCTTGTCTTG GT AA-- ----- A TAA A ----
GAM1461 11213 TGTGAAACCATTATGCAGAT T AA A A T A- - A AGA- ATGAAACA
GAAGAAGATGAAGCCCGAGA TG GA CC TTATGC GA GA GAAGA TGA GCCCG GGTT
GGTTATGAAACAGACCCAAG GC CT GG AATACG CT CT CTTCT GCT CGGGT CCAG
TGGGCTCGCTCTTCAGTCTC - AA - G - GA C - GAAC --------
GGCATAAGGAATCCG
GAM1469 10816 GTCAGGACTGTTGGCTAAGG G CTAAGG A T CT T CAAT CCAACTA

GAATGTCTGCTTGGACTGAT GTCA GACTGTTGG GA TG CTGCTTGGA GATCAT GAA CTTT

CATTGAACAATCTTTCCAAC TAGT TTGACAGCC CT AC GATGAATCT TTAGTA CTT GAAA

TAAAAGCTTCTATGATTCTC A ACGA-- A - C- T C--- -------
TAAGTAGCAATCAGCACCGA
CAGTTATGAT

GAM1479 10721 GGGAAGGCAGTAGGTTGTAT GA C ATA A TTCCGA ACATCAC
AGTTATCTTCCGAGGGGCAA GG AGG AGTAGGTTGT GTT TC GGGGCA
CATCACTGCCCTGAAACCAC CC TCC TCATCCAACA CAA AG TCCCGT
ACAACCTACTACCTCACC AC A CAC - ------ -------

GAM1484 11202 TGGTTGCAAGGCAGGAAATA TGC -------- A A G CAAT TACTCT
TTGGTGAAATGCTAGCAAAG TGGT AAGGCAGG AAATATTGGTGAA TGCT GCAAA TCA TTC

TCACAATTTCTACTCTGAAC ACCA TTTCGTCC TTTATGACTACTT GTGA CGTTT AGT AAG

ATGATTTGCAGTGTTCATCA --- CAAGTCTT - - - AC-- ------
GTATTTTTCTGAACCCTGCT
TTACCA

GAM1490 10307 GAGCTCCCACGGCTTTTCTA ---------- C C T AGAA GG AA CCAA
GAAATTGGCACACAAACTCC GAG CTCCCA GG TT TCT ATT CACACA CT
AAAGCGTGTGTGGAAATGCA CTC GAGGGT CC AG AGA TAA GTGTGT GA
GATGACCTGGGAGACCCAAA CAACAAAACCCA - - T CG-- AG GC ----
ACAACCTC

GAM1500 10450 GCCCGGTGCTCGGTTTGTAG CCG CG GTA- TCA C - GTGGT
GCAGTGTCATTAGCTGATTG GC GTGCT GTTT GGCAGTG TTAG TGATTGTA CT
TACTGTGGTGGTTACAATCA CG CACGG CAAA CCGTCAC AATC ACTAACAT GG
CTAACTCCACTGCCATCAAA A-- AA ACTA CTC - T -----
ACAAGGCACAGC

GAM1502 9980 CATATATGTCTGGTATTCTT -- ATTCT GG-- - TAGT
GGGGTCTAGTAGTCTAGTAT CATATATGTCT GGT TG GT CTAG
AATACACATAGCCTAGGACA GTATGTACAGG CCG AC TA GATC
TGTATG AT ATAC- ATAA T ----

GAM1523 10010 CCCAAAGCTCACAGTTTGGC AAA CACA -- AA- AT - GTAGTTTG
ACTGAATCATATACAATCTC CCC GCT GTTTGGCA CTG TCATATACA C TC
GTAGTTTGGATGGCTGTGTG GGG CGA CAGATCGT GAC AGTGTGTGT G AG
TGACTGCAGACTGCTAGACA A-- ---- CA GTC CG T --------
GCAGGG

GAM1543 10622 GGAGAATTGCTTGAACCCAA AA TG GA-- AGA - GT A - CGAT
GAGGTGGAGGTTGCAGTGAG GGAG T CTT ACCCA GG TGGAG TGCAGTG GC CA
CCACGATTGTGCCATTGCAC CCTC A GAG TGGGT CC ACCTC ACGTTAC CG GT
TCCAGCCTGGGTGACAGAGT AG GT ACAG --- G -- - T ----
GAGACTCC

GAM1550 11229 TTACTGAGTATTCACCAGGT CT TTCA - G ----- A- AGA TAAAGATTCCCT
GCTGGGTGGAGAAAGAAGAC TTA GAGTA CCA GGT CTGGGT GGAGA AGA CT
TTAAAGATTCCCTAGACATC GAT TTTAT GGT CCA GACTCA CCTCT TCT GA
TCCTCTCCCCTAGACTCAGG CT TCAC A G GATCC CC ACA ----------
ACCATGGCACTTATTTTCTA
G

GAM1602 10237 GAAGAAGTAGATTGGGCTGC A AGA A ACACAAT - ACCAG- GACA GTA -

AATCACACAATGGGTGCATC GA GAAGT TTGGGCTGCA TC GGGTG CATC TGCG
CCTAGGC CA
ACCAGTGCGGACACCTAGGC CT TTTTA GACTTGACGT AG CCCAT GTAG ATGT GGGTTCG
GT
GTACAGGGAACCATGGCTTG A ACA - GAC---- T GAAGAA GAG- --- A
GGGAGTGTAAAGAAGGATGT GAA
TACCCCAGGATGCAGTTCAG GG
ACAATTTTATC CC

GAM1607 10917 TAGGCTGTATGCTGTTAATG T-- C A T- CCTC
CTAATCGTGATAGGGGTTTT TAGGC GTATGCTGTTAATGCTAAT GTG TAGGGGTT TTG

TGCCTCCAACTGACTCCTAC GTCCG TATGTGACAATTACGATTA TAC ATCCTCAG AAC

ATATTAGCATTAACAGTGTA TAG - - TC ----
TGATGCCTG
GAM1617 9897 ATAGACAGGTCTCACTCTGT TC-- A C TT - - AGT A TGACTGTAGCT
TGCCCAGGCTGGAGTGCAGT ATAGACAGG TC CT TG GCCCAGG CT GG GC GTGGTG

GGTGTGACTGTAGCTCACTA TATCTGTCC AG GA AC CGGGTCC GA CC CG TATCAC
TAGCCACCAAGTCCTGGGCT TCCT C - T- T A AC- A ----------
CAAGCGATCCTCCTGTCTAT
GAM1650 11198 TGGTGGCTTGGTTTGTGTAC T GG TG C-- G GTA G CTTTTA
CTATTTTTCTGCATTTGTAT TGG GGCTT TTTG TAC TATTTTTCT CATTT TTGGAAAA GTTT

TGGAAAAGGTTTCTTTTAAG ACT TCGGG GGAC GTG ATAAGGAGA GTGAA AACCTTTT CAGA

ACATTTTCCAAAAGTGGAGA T AA TT TGT G --- A ------
GGAATATGTGTGTTCAGGAA
GGGCTTTCA
GAM1653 10791 GGTGGAGCAGAAAGGCAGGA T A AA-- A A CC C CACCA
GTCCTGCTCCCTGGCACCAT GG GG GCAGA GGC GG GT TGCTCC TGG
CATGGAGCATGCCCAGCCCA CC CC CGTCT CCG CC CG ACGAGG ACT
GATCTGCCCCCC - C AGAC A - T- T -----
GAM1698 10870 GTGTGACCTTGGCCCTGTGA G G- GAG TCA AGC G A GA GTAC
GGCTTCACCTCTTGAGCCTG GTGT ACCTT GCCCTGT GCT CCTCTTG CTGAGAA CAG GGT CA

AGAAGCAGAGGTGACAGTAC CGCG TGGGG TGGGACG CGG GGGGGAC GATTCTT GTC CCG
GT
TGGCCCTGGTTCTTAGCAGG G GA GG- TG- --- G - -- ----
GGGGTGGCGGGCAGGGTAGG
GGGTGGCGC
GAM1735 10829 GTCTAACCAGTCCCAGTGAG AAC - T G -------- - C A TGGAAAT
ATGAACCAGGTATCTCAGCT GTCT CAG TCCCAG GAGAT AAC CAGGT AT TC GC
GGAAATGCAGAAATCACCTG CAGA GTC AGGGTC CTCTG TTG GTCCA TA AG CG
CCTTCTCTGTTGGTCTCCCT C-- G C G TCTCTTCC C A A -------
GGGAGCTGCAGAC
GAM1748 10998 TCGCTTGAACCCTGGAGGTG GA-- T GG GT A AGATCG
GAGGTTGCAGTGAGCTGAGA TCGCTT ACCC GGA TGGAG TGCAGTG GCTG
TCGTAGCCACTGCACTCCAG AGTGAG TGGG TCT ACCTC ACGTCAC CGAT

TCTGGGTGACAGAGTGA ACAG - G- -- - ------
GAM1770 10790 GGTGGAGCAGAAAGGCAGGA T A AA-- A A CC C CACCA
GTCCTGCTCCCTGGCACCAT GG GG GCAGA GGC GG GT TGCTCC TGG
CATGGAGCATGCCCAGCCCA CC CC CGTCT CCG CC CG ACGAGG ACT
GATCTGCCCCC - - AGAC A - T- T -----
GAM1782 10126 CTCTTAAACCTTTAGAAATG AAAC GAAATGCTA CT- CTA CAATA
CTACAGCATCTAGCTTCTCT CTCTT CTTTA CAGCAT AGCTTCT GAT
AGATCAATAATCACAGAGGC GAGAA GAAAT GTCGTG TCGGAGA CTA
TTAAGTGCTGACCTCATAAA ATA- ACTCCA--- AAT CA- -----
GATAAAGAG
GAM1820 10211 CTTGATCTGTCACCCAGGCT TCTGTC CT AG---- - A ATCT
GCAGTGTAGTGGCATGATCT CTTGA ACCCAGG GC TGTAGTG GC TG
CGGCTCACTGCAACCCCCGC GAACT TGGGTCC CG ACGTCAC CG GC
CTCCTGGGTTCAAG ------ TC CCCCCA T - ----
GAM1835 10904 TAATCTTAACATTCTCAACT AA AA-- TTCTC TTACCAAA - AAA- AAA A TCAC
CT
ATGATTACCAAAGCAGAAAA T TCTT CA AACTATGA GC AGA ATA CAC TTAAA ATG
ATAAAACACATTAAATCACA A AGAA GT TTGATACT TG TCT TGT GTG AATTT TAC
TGCTGGCTTATGAAAGCCTC -- ACCG TAC-- -------- C CACG ACA - C--- CT
CATCTTTAAGTGACATGTGC ATGA
ACTCTCGTTCATAGTTCATT GGCTT
GGCCAAAGAA CCGAA

GAM1860 11134 TGATGAAAATCCACAATGTC A- ---- T T TG TGTGTAAT
TTTGAGCTTCTGGTTGTGTA TGATG AAATCCACAA TG CTTTGAGCT C GT
ATGCTGGGGTTTAAAGTCAC ACTAC TTTGGGTGTT AC GAAATTTGG G CG
CATTTGTGGGTTTGGCATCA GG TACC T - GT --------
GAM1863 11240 TTCAGTATAGCAAGGTGCTA TATA T ---------- CCT--- C- TCTCT
GGTTTTTTCCTTTCCCCACC TTCAG GCAAGG GCT AGGTTTTTT TTCCCCA CTG
TGTCTCTTAGCCTGGGGAAT AAGTC TGTTCC CGG TCCGAAGAG AAGGGGT GAT
TAAATGAGAAGCCTTAGAAT CAG- - TGGGTAAGAT TAAATT CC -----
GGGTGGCCCTTGTGACCTGA
A
GAM1864 10017 CCCAGCATGATTCATACCTG GA TACCT ATCTT TGAT A- TTGG
TAATCTTACCCATTCTTGAT CCCAGCAT TTCA GTA ACCCATTCT TTAG TGAGAT
TTAGATGAGATTTGGATTTC GGGTTGTA GAGT CAT TGGGTAAGA AGTT GCTTTA
GAGTTGATGCTAGAATGGGT G- TTT-- AAT-- TCGT GA ----
TAATACTTTTGAGGATGTTG
GG
GAM1887 10077 CCTTTGAACCCTGTGTTAAC TTGAA TTAA G T ATTTGA
AATGAGAAGCTTGTTTATTT CCT CCCTGTG CAATGAGAA CT GTTT
GAAGGCTGGGTTCTCATTGG GGA GGGACAC GTTACTCTT GG CGGA
CCCACAGGGGTAGG TG--- CCG- G T ------
GAM1896 10004 CCATCTCTGCTTATTCCTCT T TATT G G- - - CCTC GCTCTCATAA
GCCACGTCTTTCCCTTCTCC CCATCTC GCT CCTCT CCAC TC TTTCCC TTCT TCT
TCTCTGCTCTCATAAAGAAG GGTGGAG CGA GGGGA GGTG AG AGAGGG AAGA AGA

AATGGGAGATGAAAGTGGAG T C--- - AA T T ---- ----------
GGGCAGCTGAGGTGG
GAM1914 10416 GATCCAGATAGATGATATGT T ATAGAT -- A - G - TTTCAG CGCT

TTCTACTAGTGGTTGATGGC GA CCAG GATAT GTTTCT CT AGT GTTGATGG CCTC CTCCAT

CTCTTTCAGCTCCATCGCTA CT GGTT CTGTG CAAAGA GA TCA TAACTACT GGAG GAGGTA

TGGAGGCGAGGTTCATCAAT - GAGAC- TT - C A T CG---- ----
AACTCAGAGAAACTTGTGTC
CAGAGTTGGTC

GAM1937 9624 AATGTTTACTGAGTATTCAC T --- TTCA - G ----- A- AGA TAAAGATTCCCT
CAGGTGCTGGGTGGAGAAAG AATGTT ACT GAGTA CCA GGT CTGGGT GGAGA AGA CT

AAGACTTAAAGATTCCCTAG TTATAA TGA TTTAT GGT CCA GACTCA CCTCT TCT GA
ACATCTCCTCTCCCCTAGAC C TCT TCAC A G GATCC CC ACA ----------
TCAGGACCATGGCACTTATT
TTCTAGTCAATATT

GAM1942 10777 GGTAGTGGTGATTCAAAGCA AGTGG-- AA- GA-- G A TG AGAGGA GT AGATGA

AGATGGTAGCATTGGAGAGG GGT TGATTC AGCAA TG TAGC T G TGAGATATG C
ATGAGATATGGTCAGATGAG CCA ACTAAG TCGTT AC ATCG A T ATTTTATAT G
GATATATTTTAAAAGTTGAG AGTGAAG GAG TAGG A - GT GAAA-- AG ------
CTAACAGGATTTGCTGAGGA
ATCAGAAGTGAACC

GAM1961 10694 GGCCTCCCAAAGTGCTGAGA CTC - -- TAC TGA CTGCACC
TTACAGGCATGAGCCACTGC GGC CCAAAGT GCT GAGAT AGGCA GCCA
ACCTGGCCCTTGCCTCTATT CCG GGTTTCA CGA CTTTA TCCGT CGGT
TCAAAGCTACTTTGGTGCC T-- T AA TC- TCC -------

GAM1975 9905 ATCTGTCTTTCCAAGCCTTC GT - GGG GTT TAAG
CCCGGGATCAGAGTTTTTAA ATCT CTTTCCAAGCCT TCCCC ATCAGA TT
GGATAATTTGGTGGGGAGAG TGGG GAAGGGTTCGGA AGGGG TGGTTT AG
GCTTGGGAAGTGGGGT GT G --- AAT ----

GAM1976 10517 GGAAAATGAGTGGAAGACCT AAATGAGT T CTCCCTC T CTC- GTTA
GGCTCCCTCTCTTCTCTCCC GGA GGAAGACC GG TC TCT CC
GTTAGGCACAAGACGGTGTA CCT CCTTCTGG CC GG AGA GG
AATCCTGGTCTTCCTCC -------- T TAAATGT C ACAC ----

GAM1997 10825 GTCCCTATCACTCGGAGCGG - C CG ACC A A ---- AGTGA
AGACCTGAGCTATGAGTCAT GTCC CTAT ACT GAGCGGAG TG GCT TGAGT CATC
CAGTGAGGTGCTATACTCAG CAGG GGTA TGG CTCGCCTT AC CGA ACTCA GTGG
AGCCATTCCGCTCAGGTCAT A C A- --- - G TATC -----
GGAGGAC

GAM2010 9634 ACAGGAGAATTGCTTGAACC G AA GAAC-- A GT A- CGAGATT
CTGGAGGTGGAGGTTGCAGT ACAG AG TTGCTT CCTGG GGTGGAG TGCAGTG GC
GAGCCGAGATTGCACCATTG TGTC TC AACGAG GGATC CCACCTC ACGTTAC CG
CACTCCACCCTAGGCAACAA - AA AACAAC - -- CA -------
GAGCAAAACTCTGT

GAM2014 10682 GGCAGGGAGGTGACGAGGTA C TGA- - CA--- C --- - AT GTTC
GGGGCAGAGCGGATGGAAGC GG AGGGAGG CGAGGTA GGGG GAG GGAT GGAAGCC GGAG
CCCAG CCG
CGGAGATCCCAGGTTCCCGG CC TCCCTCT GCTCCGT CCCC CTC CCTG TCTTCGG CTTC
GGGTC GGC

AATACTCCGGCTGGGGCCTT - TTGG G CATCC C TCC G CG ----
CGGGCTTCTCCTGTCCCCTC ATAC
CCTACCCCCGTGCCTCGGGT GA
TTCTCCCTCC CT

GAM2022 10258 GACCATGAAGCCAGAGTCTC CCAT - - T CCA ---- - GCCATGGA
CAGGACTCCTCACTCAACCT GA GAAG CC AGAG CT GGACTCCT CACTCAACCT CG
CGGCCATGGACGCAGGTTGG CT CTTC GG TTTC GA CCTGGGGG GTGGGTTGGA GC

GTGTGAGGGGGGTCCCAGCC TTAT T C C C-- GAGT C --------
TTTCGGTCTTCTATTTC

GAM2027 10467 GCTACTTCTATGTGTCCCAT T TATG- CCAT - AC -- CAGCTCTCTCCA
GGTACTGCCACAGAAGAGTC GC ACTTC TGTC GGTACTG CC AGAA GAGTCT
TCAGCTCTCTCCAGGATTCA TG TGAGG ATAG CCGTGAC GG TCTT CTTAGG
GTTCTAAGGTCAGTGCCTAA - TAAAA AAT- T AA GA ----------
GATAAAAATGGAGTGT

GAM2033 10236 GAAGAAGAAGAATGGGTTTG ---- A TGAGA CCAATATTAAC
GTGAGAGGGTTCCAATATTA GAAGA AGA GAATGGGTTTGG GGGTT
ACAACCCAACTTCAAGCTCA CTTCT TCT CTTACTCGAACT CCCAA
TTCCTCTAACCTCTTC CCAA C TCAA- ----------

GAM2051 9948 CACTCTGTAATAAAGAACTT - AATAAAGAA - AAG -- CAAG GGCCAA
GGAAAGGGAGGTTCCAAGAT CACTC TGT CT TGGA GGAG GTTC AT
GGCCAAATATGAACAGCTCC GTGAG GCG GA ATCT CCTC CAAG TA
AGTCTACAGCCCCCAGCGTG T ACCCCC--- C GA- GA TA-- ------
AGTG

GAM2058 10513 GCTTTGAAAGAGATGTGGTG GAAAGAGA - TG AGA---- GCCTTTTGTTT
TGTGAAGACGAAGATGCCTT GCTTT TGTGGTGT G A CGAAGAT
TTGTTTGTCTTTGGAGAATA TGAAA ACATCACA C T GTTTCTG
TTGCAACACTACAAAAGT -------- A GT ATAAGAG ----------

GAM2062 11181 TGGGCGCCTGTAATCTCAGC GC- A A --- TGAGACAGAGAATT
TACTTGGGAGGCTGAGACAG TGGGC CTGTAATCTC GCT CTTGGG AGGC
AGAATTGCTTGAACCCAGGA ATCCG GACGTTGGAG CGG GGACCC TTCG
GGCGGAGGTTGCAGTGAGCC AGT G A AAG ----------
TA

GAM2098 10197 CTTCACCAAGTTGTCATTTG A AAG C GAG C AG- G TAAGA
AGCACAGTTTGAGGAGTGTA CTTC CC TTGT ATTT CA AGTTTG GA TG
AGACAGTCATGCGGACTTGA GAAG GG AACA TGGG GT TCAGGC CT AC
GGGGTACAAGGGAAG - --- - GA- - GTA G -----

GAM2171 10110 CTCCCAGGCAATATTCCAGG CAATA - TA G -- TTGGA
ATAGGCTGCCAGTTGGACTA CTCCCAGG TTC CAGGA GGCT CC AG
AGGAAGCCACTCCTGCGGAA GAGGGTCC AGG GTCCT CCGA GG TC
CCCTGGGAG CA--- C CA A AA -----

GAM2221 9920 ATGTCCAAAGACTCAACAGT - - ACAGT TAC CCACTCATTTTA
TAGACTACTTTTCTTCCACT ATGTCCAAAG ACT CA TAGAC TTTTCTT
CATTTTAAAGAAAAATGTCT TATAGGTTTT TGA GT ATCTG AAAAGAA
ATGAAGTGTTTTGGATAT G A ----- TA- ----------

GAM2223 11022 TCTTACCCCAGTATCCTATT - GTAT - A TAC CAGTGAT TCTCA
ATCTCATACCTAAGGCAGTG TCTTAC CCCA CC TATT TCTCA CTAAGG GGTT
ATGGTTTCTCAGACCTCTTA GGAATG GGGT GG GTAG AGAGT GATTCT CCAG
GATTGAGAAGATGTGGCATG T AC-- T A TA- ------- -----

GGTGTAAGG
GAM2233 9755 AGTCTCTCTCTGGCTGGACC CTC - GG - TCACACTCT CTC
TGGACTGCAGTCACACTCTA AGT TCTCTGGCTGGAC CT ACTG CAG AAGAG
AGAGCTCCTCTTTCTACACC TCG AGAGACTGGCTTG GG TGAC GTC TTCTC
TCTGCCAGTGGGCGTTCGGT AAC C G- C TCCACATCT ---
CAGAGACAAGCT
GAM2251 11172 TGGCCTCTGGGACTCAGATT GC ---- GGA GAT-- TTTAAAAT-- ATAA
CCTCCTCTTTAAAATGGTGC TG CTC TG CTCA TCCTCCTC GGTGCTA
TAATAATAGCACCCACCCTC AC GAG AC GAGT AGGAGGAG CCACGAT
TGTGAGGAGGATGCTGTGAG TA TAAA AG- GTCGT TGTCTCCCAC ----
GACAAAATGAGATCA
GAM2260 10524 GGAAGCATCCCTGCTGCGGA TCCCT GGAC T ------- - GAG T AATAAGAGT
CGCTTTCACTTCTAAAGAGT GGAAGCA GCTGC GCT TCA C TTCTAAA TCTTG CTGCT
G
CTTGTCTGCTAATAAGAGTG CTTTCGT CGGCG CGG AGT G AAGATTT GGGAC GACGG
T
CCCATGGCCCAGGGTGGCAG ----- ATCA T AGTACGG A AGG - ---------
CAGGGGGATTTAGAAAGGGC ATGGCCCA
ATGATGATGGCACTAGCGGC CCC
TGCTTTC GGG

GAM2262 9724 AGGCTGAGGTAGGATGATTG - - -- - C AG---- AGGAGTTCA
CTAGCTAGAGTCCAGGAGTT AGGCTG AG GTA GG ATGATTG TAGCT AGTCC
CAGGATTAAAATGAGCTATG TCCGAC TC CGT CC TACTAGT ATCGA TTAGG
ATCATACCACTGCACTCCAG C A CA A - GTAAAA ---------
CCT
GAM2263 9619 AATGAAGTGGAATCAAGGTG - TC G - AAGAAAA - CT ACTTTC
GCAAGAAAATTTAGAATCGT AATGA AGTGGAA AA GTG GC TTTAGAAT CGTTT GATAGGG

TTCTGATAGGGACTTTCCCT TTACT TTACCTT TT CAC CG AAGTTTTG GTAAA CTATTCC

TATCCTAAATGTGTTTTGAA G TA G A G------ T TC ------
GGCACACGTTATTTCCATTG
TCATT
GAM2270 10841 GTGACTTTCCAGGTGTCACA G A-- - A-- -- - --- AA- GTACAA
CAGTGAGTGGCATAATCAGA GT ACTTTCC GGTG TCAC CA GTGA GT GGCAT TCAGA
GTACAATTTGAGTCATGCCC CA TGAAAGG CCAT AGTG GT CACT CA CCGTA AGTTT
ATACATCACATTGCCAGTGA G AAC T ACC TA A TAC CTG ------
TTACCCAAGGAAAGTGAC
GAM2272 9891 ATAAGCTGCTCTAATTGCCA C C A TG CA- T TG TTGT G ACT GAGA
AGAATTCACATGTGGTTGTA ATAAG TG TCTA T C AGAAT CACATG G ATGCA CTTT GG
TGCAGCTTTACTGGGAGACT TGTTC AC AGGT A G TCTTA GTGTAC C TATGT GAAG TC
GAAGTGTATCTGCATGTGAT - - - GT TCG - GT ---- - --- ----
TCTGCTGTGATGGACACTTG
T
GAM2290 9630 ACACTGCCTCTAGATTGTTA - CT TTGTTATTTTGTCC G A- ATG A TCTCT
TTTTGTCCAAGAGAGAGATC ACAC TGC CTAGA AAGA AGAG TC GAG GAG
ATGGAGAGAGTCTCTCTCGC TGTG ATG GATCT TTCT TCTC AG CTC CTC
TCACGGAGGCTCTGTCTTTC T AG ---------- G GG GCA G -----
TAGGAGTATGTGT

GAM2300 9665 AGACAGTGCTGGGTCAAACA CA GT AAC TTA - T- A CCTTT
GCCTTTATTTTAGCAGTTGT AGA GTGCTGG CA AGCCTTTATT GCA GTTG GAGACCCTAGAG
ACT
GAGACCCTAGAGAACTCCTT TCT TACGATC GT TTGGGGGTAA CGT CGAC CTCTGGGGTTTT
TGG
TGGTGTTTTGGGGTCTCCCC C- -- A-- CA- A CC G -----
AGCATGCACAATGGGGGTTA
TGCTAGCATCTCT
GAM2306 11288 TTTGAGATTTTATTGAGTAC AGATT G GT TG - TT GT GCACCA
TACTAATCTTGACATATTTT TTTG TTATT A ACTACTAATCT AC ATATT G TG
GGTTGGCACCACATTCTTGG AGAC GATAA T TGGTGATTGGG TG TATGG C AC
TATAGTGGGTTAGTGGTTGA GTTT- G -- -- A TT TT ------
ATAGTTTGCAGA
GAM2309 10021 CCCCACCCCAGTGGAGCTCA -- ---------- CCTT-- AGGTCTAA
CCTTCCAGTAGGTCTAAACT CCCC ACCCCA GTGGAGCTCA CCAGT
GGTTTGATTGAGTTCCATGG GGGG TGGGGT TACCTTGAGT GGTCA
AAAACAACAAAGTGGGGTAA AA GAAACAACAAAAGG TAGTTT --------
GGGG
GAM2350 9592 AAACGGATGGGCCTGGGGGC - TG- CC CACTT CA TCCA
CACTTTGCACAGGGTTCTCC AAAC GGA GG TGGGGGC TG CAGGGTTC
AGAGCCCTGCCCATCCTGCC TTTG CCT CC ACCTCCG AC GTCCCGAG
TCCACCACTTCCTGTTT T TCA -- TCCT- CC ----
GAM2384 10962 TCATTCCTCTTAATCTTCAC TTA - AAA A CATTGAGCACCT
TAAAATGGACAAGTATTCAT TCATTCCTC ATCTTC ACTA TGGACA GTATT
TGAGCACCTAATGCGTGTTC AGTAGGGAG TAGAGG TGGT ACTTGT CGTAA
AGTATGGTGGGAGATGAGGG --- G ATG G ----------
ATGA
GAM2391 10853 GTGCTGGGTCAAACAGCCTT GT AAC TTA - T- A CCTTT
TATTTTAGCAGTTGTGAGAC GTGCTGG CA AGCCTTTATT GCA GTTG GAGACCCTAGAG ACT

CCTAGAGAACTCCTTTGGTG TACGATC GT TTGGGGGTAA CGT CGAC CTCTGGGGTTTT TGG

TTTTGGGGTCTCCCCAGCAT -- A-- CA- A CC G -----
GCACAATGGGGGTTATGCTA
GCAT
GAM2393 9775 AGTTTGGGTAATGAAGCCAC T TA---------- ATTT GATACATTT CACGACT
AGAGATTTGCTGATACATTT AGTT GGG ATGAAGCCACAGAG GCT GCTAGG
GCTAGGCACGACTTCTGGTC TCGA CCC TACTTCGGTGTTTT CGA TGGTCT
ATTTAGAAAGCTATTTTGTG C TTATGGAATAAC AT-- AAGATTTAC -------
GCTTCATCAATAAGGTATTC
CCCAGCT
GAM2398 9611 AAGCCCTTGACTGGGGCTGC CCTT G -- CTCAG GC G CAGTGA
TGCCTTTCTCTCAGAGATGC AAGC GACTG GGCT GCTGCCTTTCT AGAT CCT CC
CCTGCCCAGTGAGGAGGAAT TTCG TTGAC CCGG TGACGGAGAGA TCTA GGA GG
CTAGAGAGGCAGTCTGGCCA ---- A TC ----- A- - ------
CAGTTGCTT
GAM2424 10997 TCGCTTGAACCCGGGAGGCA GAA-- AGGCA - A A- TGAA
GAGGTAGTAGTGAGCTGAAG TCGCTT CCCGGG GAG GTAGT GTG GC
TCCCGCCACTGCACTCCAGC AGCGAG GGGTCC CTC CGTCA CGC TG
CTGGGCAACAGAGCGA ACAAC GAC-- A C CC ----

GAM2440 11256 TTGCTTGAACCCAAGAGGCG GA-- AGA - GT A TAAGATCAT
GAGGTTGCAGTGAGCTAAGA TTGCTT ACCCA GGC GGAG TGCAGTG GC
TCATGCCACTGCACTCCAGC AACGAG TGGGT CCG CCTC ACGTCAC CG
CTGGGTGACAGAGCAA ACAG --- A -- - ---------
GAM2514 11159 TGGAACTGGAGGAGCTGTCC AC GAGCTG CA AATCAAA CAAAA
TGTGTCAGCCTGAAATAATC TGGA TGGAG TCCTGTGT GCCTGAAAT AGGAT
AAAAGGATCAAAAATCCTGT ATCT ACCTC AGGATACA CGGATTTTG TCCTA
TTTAGGCAACATAGGAAGAC CA AGA--- A- ------- -----
TCCAACTCTA
GAM2519 9913 ATGATGCCAGGACTGCAGCT AT CA ------- CTT GG T AGG
TCAGGGACTTGTGGCAGATG ATG GC GGACTGCA GCTTCAGGGA GT CAGA GCAC
CACAGGGTGCCTCTGGCTCC TGT CG CCTGACGT CGAGGTCCCT CG GTCT CGTG
CTGGAGCTCCACACTGCAGT CT AC CACACCT --- -- C ---
CCCAGCTCTGT
GAM2543 11152 TGCTGTAGGCTGTATGCTGT ---- T-- C A T- CCTC
TAATGCTAATCGTGATAGGG TGCTG TAGGC GTATGCTGTTAATGCTAAT GTG TAGGGGTT TTG

GTTTTTGCCTCCAACTGACT ACGAT GTCCG TATGTGACAATTACGATTA TAC ATCCTCAG AAC

CCTACATATTAGCATTAACA CATT TAG - - TC ----
GTGTATGATGCCTGTTACTA
GCA
GAM2565 10306 GAGCCTTTTAATGACACAGT TT- T -- T --------- TT---- CAC CCTG
GGGGCCAGTTGGAGCACTGA GAGCCT TAA GACAC AG GG GGCCAG GGAG TGAT
TCCTGGTCATTACTCCTGCA TTCGGG ATT CTGTG TC CC CCGGTC CCTC ACTG
CCCTGGCCTGCAGCCTTCCT TTT - AC T TTCCGACGT CCACGT ATT ----
CTCAGTGTCTTATTTGGGCT
T
GAM2591 10044 CCGGTAGGTTTAGAATGAGG - -- AGA A - T AT CG TTTTGACTGGT
TCTGTGTCACTGTGGTATTA CC GGTA GGTTT ATG GG TCTGTG CACTGTGGT TA ATA
CGATATTTTGACTGGTTATT GG CCGT CCAAA TAC CT AGACAC GTGACACCA AT TAT
ATAACCACAGTGTCACAGAG T AC AAC - G T -- AT ----------
TCCATCAAAAACCCATGCCT
GG
GAM2608 10221 CTTTTGAGCTGCTTCTTATA C TCT A T CT -- T C T TA GAAGCAG
ATGTGTCTCTTGTGTTAAGG CTTTTGAG TGCT TATA TG GT CTTGTGTTA AGG GCAT TAG GCAGT
GT
TGCATCTAGTGCAGTTAGTG GAAAATTT ACGA ATAT AT CG GGACACGGT TCC CGTA ATC
CGTCA TA
AAGCAGCTTAGAATCTACTG T C-- A C TC CT C A C TC -------
CCCTAAATGCCCCTTCTGGC CTTAGA
ACAGGCTGCCTAATATACAG
CATTTTAAAAG

GAM2618 11220 TGTGGGAAGATGCTGGCAAG AAG CT- GCT A GGAGGCAA
GTGCTGGAGGGCCCTGGAGG TGTGGG ATG GGCAAGGT GG GGGCCCT
CAAAGGGCCTGCCTCGACCT ACACCC TAC CCGTTCCA CC TCCGGGA
TGCCCCCCATAACCCACA AA- CCC GCT G --------
GAM2624 9903 ATCGTCTGAGCCCAGGAGTT - - AG - TGCA-- GCTACAA
TGAGGCTGCAGTGAGCTACA ATCG TCTG AGCCCAGG TTTGAG GC GTGA

ATCACACCCCTGCACTCAAG TAGT AGAC TTGGGTCC GAACTC CG CACT
CCTGGGTTACAGAGTGAT G A -- A TCCCCA -------
GAM2628 10846 GTGCACTACAGACTCCAGCC A- GA CAG C-- - AAGCC A TCCTCCCTTT
TCCCTTTGAAGCCAGGTTCC GTGCACT CA CTC CCT CCT TTG AGGTTCCAG GCT
AGAGCTTCCTCCCTTTGGCC CATGTGA GT GAG GGG GGA GAC TCCAAGGTC CGG
TGGAACCTCAACAGCAGGAT AG AG TA- TTA C AAC-- - ----------
TGGGATGAGGATGGAAGTGT
AC
GAM2631 11155 TGCTTCCTTACCTACAAGAA TA CAAGAAAATTTAGAAGTT C - TTTC-- TACTT

AATTTAGAAGTTGGTGCAAA TGCTTCCT CCTA GGTG AAATG GCA CATGAG
TGGCATTTCCATGAGTACTT ACGAAGGG GGGT CCAC TTTAT CGT GTACTC
CTCATGCATCTTTGCATATT -- ---------- - A TTCTAC -----
TCACCTGGGGGGAAGCA
GAM2640 11205 TGGTTTCATTAAAATGTGTA A GTAA TT---- - GCAGTA
AGGTTGGCTGGGTGCAGTAA TGGTTTC TTAAAATGT GG GGC TGGGT
CTCATGCCTGTAATCCCAGC ACCAGAG GATTTTACG CC CCG ACTCA
ATTTTAGGAGACCA - AC-- TAATGT T ------
GAM2672 10457 GCCTGCGGGGTATTGTAGAA -- A----- --- C - TGCCT AGCTT
ACGCTGCGCTGCCTATCACA GCCT GCGGGGT TTGTAGAA ACG TG CGC ATCAC
GCTTGTGATGTGACACGTTC TGGA CGCTTCA AACGTCTT TGC AC GTG TAGTG
ATTCTGCAAGTTTAAACTTC TC AATTTG ACT - A ----- -----
GCCTAGGT
GAM2732 10785 GGTCTGTGTGAAGCATCACT T T TG A ACT GC TAATG G- GC TCT A- TT
TTGCAGGGATTACTAATGGT GG CTG G A GCATC TT AGGGATTAC GTG GGCA AGG GTGA
TTAAG
GGGGCAGCAGGTCTGTGAAT TC GAC C T CGTAG AA TCCTTAATG CAC CTGT TCC CACT
AGTTC
TAAGTTATCTCTTGACCTCA T - GT A AAC A- TAAA- AA AC --- CC --
CCCTCATGTCAACACAAATG ATCT
TAATTCCTAAACAAGATGCA
TTGCCAGTCT

GAM2762 10200 CTTCTCACTTTCCCTTCACA CT- TTCC TCAC GT- TTT- C T G TAATCTCTT TC
CACAGTCGTGTAGTTTTGCG CTT CACT CT ACACAGTCGT AG TG GCT GCTT AT GGCC

CTTGCTTGATTAATCTCTTG GGG GTGA GA TGTGTCGGTA TC AC TGG TGAG TA TTGG
GCCTCAGTCGGTTTTCTACC TGT CCT- ---- AGC TCTT T T G TACCATCTT --
ATATGGAGTTGGTTCATTCT AGTC
CTCGAATGGCTGTGTAGTCC
AGTGTGTGGG

GAM2770 10537 GGACTACAGGCACATGCAAC A CACA CA CA C TTTCT T AGAG
CACATCTGGCTAATTTTCTT GGACT CAGG TG ACCA TCTGG TAAT TGAG TTTAGT
GAGTTTTAGTAGAGACTGGG CTTGA GTCC AC TGGT GGACC GTTG ACTC GGGTCA
TCTCATTATGTTGTCCAGGC - TCGA CC C- T TATT- T ----
TGGTCCCAAGCTCCTGAGTT
C
GAM2780 10174 CTGGGAGGCAGAGGTTGCAG GG- - A-- G - AATT- CACT
TGATCAGGAATTGTGCCACT CT GAGGCAGAG GTTGC GT A TCAGG GTGC

GCACTCCAACCTGAGTGACA GA TTCTGTCTC CAACG CA T AGTCC CACG
GAGCAACACTCTGTCTTAAA AAA A AGA G G AACCT ----
AG
GAM2799 9754 AGTCTCACTCTGTTGCCCAG TC C TT C-- -- T GATCTCA
GCTGGAGTGCAGTGGTGCGA AG TCACT TG GCCCAGG TGGAG TGCAGTGG GC
TCTCAGCTCACTGCAACCTC TC AGTGA AC TGGGTCC ACCTC ACGTCACT CG
CACCTCCTGGGTTCAAGTGA TT - T- TCC CA - -------
TTCT
GAM2807 9926 ATTGTATTGCAGCAGGTTGG - C G --- - A AAATCTCCAT AAATG-- A C A
CAGCCTCAGTAAATCTCCAT ATTGTAT TG AGCA GT TGGCA GCCTC GT TTGT TGAC GT
AGC
TTGTAAATGTGACAGTCAGC TGATATA AC TTGT CA ACCGT CGGGG CG AACG ACTG CA
TTG
AGAATCTCCAGTTACAGTCA T - A TAC A A ---------- AAACTCA A - -
ACTCAAAGCAAGCAGGGGCA GAATCTCCA
TGCCACATACATGTTCATAT
ATAGT

GAM2808 10475 GCTATTGTGACAATCTTGGT ATTGTGACAA GTTA TCCATTAA GCTGAT
CATGAAAAAC
TACCATCCATTAAGTGCTGC GCT TCTTG CCA GTGCT TTTGGAAAGAT
TGATTTTGGAAAGATCATGA CGG AGAAC GGT CACGG AAACCTTTCTG
AAAACGTCTTTCCAAACATG ---------- ACG- TTGCTG-- AAGTAC ----------
AAGGCACGTCGTTTGGGCAC
AAGAGGC
GAM2817 10420 GATGGTCTCATAACTGAATA T- ACTGA - AA TTGTATAC
TATTAAAAACTTAAATTGTA GATGG CTCATA ATATA TTA AACTTAAA
TACTTTAAGTTGGTGATTGT CTATT GAGTAT TATGT AGT TTGAATTT
ATGATATATGAGTTTTATC TT ATAG- T GG --------
GAM2839 10129 CTCTTGACCAGAGGGTCTCA -- - - AG C T TA TGCCA
AATGAGGGACATTTTACCTG CTCT TGACCAGAGG GTCTC AAATG GGA AT T CC
CCAGGGGACATTTCCAATGT GAGA ATTGGTTTTC CAGGG TTTGT CCT TA A GG
TTGGGGACACTTTTGGTTAT CT A G AA T C GG -----
CAGAG
GAM2846 10104 CTCAGCCTCTCCCTGATGTA A CCTGATG ---- TGTGG - A-- AAGAAAGGA
ATCTGGGTTCCTTGTGTGGC CTC GCCTCTC TAATCT GGGTTCCTTG CAAC AGTA TGGG

AACAGTAATGGGAAGAAAGG GAG CGGAGAG ATTGGA CCCAGGGAAC GTTG TTAT GTCC

ACCTGAAATATTAGTTGATT A ------- ATCT CTTA- A AAA ---------
CCAAGGGACCCTCTAAGGTT
AGAGAGGCAGAG

GAM2868 10046 CCGTGGCCCGTGTTCTCTCC TG - TT --------- T C-- T GTGAC GCCA
TTTTGTCCCCATAGTGTGAC CCG G CCCGTG CTCTC CTTT GTC CCA AGT TCC
TCCGCCAGGAACTTGGAATG GGT C GGGTAC GAGAG GAAG CGG GGT TCA AGG
GCTGAAGACTGTGAATGAGA GT T T- TAAGTGTCA T TAA - ----- ----
GTCATGGGTCTGTGG
GAM2887 10789 GGTGCAAACACCCCGTTCAT CAAA CC ACAC C A CAGTAGAG AGTATT

GTAACACGGGCCTGAGGTCA GGTG CA CCGTTCATGTA GGGC TG GGTCAG GACC
GCAGTAGAGGACCAGTATTG CCGC GT GGTAGGTGCGT TCCG AC CCGGTT TTGG
GTTTTGGCCCCAGCCTCTGC AA-- TA C--- - C -------- ------
GTGGATGGATTGAACGCC
GAM2908 10680 GGCAGGAGAATTGCTTGAAC GAA GAA A------ - A- AT A T AGATCA
ACAGGAGGCAGAGATTGCAG GGCAGGA TTGCTT CAC GGAG GC GAG TGCAGTG G CA

TGAGTCAAGATCATGCCACT TTGTCCT AACGAG GTG CCTC CG CTC ACGTCAC C GT
GCACTCCAGCACTCCAGCCT AG- ACA AATCCGA A AC -- - - ------
AAGTGACAGAGCAAGATCCT
GTT
GAM2911 10165 CTGCCTCTCTGCAGGCCGTG CA G - T- G TGATCTT
TGCTTTGCTCGGTTGATCTT CTGCCTCTCTG GGCC TGTG CTT GCTC GT
GCAGAGCCTAAGACACAGGC GACGGAGAGAC CCGG ACAC GAA CGAG CG
CCAGAGAGGCAG -- - A TC A -------
GAM2920 10706 GGCTGAGACCACCCTTGCCT - A CT - CCCTTCT--- GCCTTA
GCCCCCTTCTTTCTGCCTTA GGC TGAG CCACC TGCCT GCC TTCT
AGAATGTCCTTTTAGGCTGG CCG ACTC GGTGG ACGGG CGG AAGA
GCATGGTGGCTCACGCC C - T- T ATTTTCCTGT ------
GAM2927 10001 CCAGTATATTTCTGCAGTCT - - --------- GTA CCC A AAC
GGTATGTTTTTCCCCCTAAG CCAGT ATATTTC TGCAGT CTG TGTTTTTC CT AG
AACCTCAGCTGAGAAATAAA GGTCA TGTAAAG ATGTCG GAC ATAAAGAG GA TC
GCAGGTTAACAAAGCTGTAT C T AAACAATTG GAA TC- C ---
GAAATGTCACTGG
GAM2931 10668 GGATTAGTTCTGGAGAGAGC GTTC GC TT T A AAT TCTTC
AGGTTGCTAAGAAGAATCTG GGATTA TGGAGAGA AGG GC AAGA G CTGGCT
GCTTCTTCAGTCAGCGCTCT TCTAGT ACCTCTCT TCC CG TTCT C GACTGA
TGCTTCCTATCTCTCCATGT GT-- A- TT - - GC- -----
GATCT
GAM2950 10005 CCATCTGGCAGAACACTGGG CTG ACAC C - GA GTTACT T- ACAA
CAAAAGAGGTTCTGATTCTG CCAT GCAGA TGGG AAAAGAG GTTCT TTCTGGCCT TGC GT

GCCTGTTACTTGCTGTACAA GGTG CGTCT ACCC TTTTCTC CAGGA GAGACCGGA ACG CA

ACTTGCACAAGGCCAGAGAG AAA ---- - T -- AC---- TT ----
GACTCTCTTTTCCCATCTGC
AAAGTGG
GAM3004 10037 CCCTGTCCTGTCTTCGAGTA CC C GA A TAA GGG GATCGA
TTTGTTTTTAATGCTGGGTG CCCTGT TGT TTC GT TTTGTTTT TGCT TGTC
TCGATCGAGACAACAAGCGC GGGGCA ACG AGG CG AAACGAGA GCGA ACAG
TCAGAGCAAAGCAAGGATGC TT T AA - CTC ACA ------
ATTACGGGG
GAM3028 9743 AGGTTCTGGTGAATTCAGGA T ---- A T TATTTTT TTT TAG TT G TT ATAGT
TGGTATTTTTGTCTTTGAAT AGGT CT GGTGA TTCAGGA GG GTC GAA T CTGGTT CAT CT

AGTTTCTGGTTGCATTTCTA TCCG GA TCACT GAGTCCT TC TAG CTT G GATCGA GTG GG

TAGTGGGGGTGAAGCTAGGG T AACT G - ------- TGT CAA GG A GG -----
GAACTTCTGTGATCTTCCTG
AGGTCACTTCAAAGTGCCT

GAM3057 10217 CTTTCTGTGCCACTCAGGAA TT---- CCAC A AA G - A CA A A--- TTT AA
GCAATGGGCATGATTCAGCA CT CTGTG TCAGGA GC TGG CA TG TT GCAG GGAG GGAGAG
AG
GAGGAGAGGAGAGTTTAGAA GA GACAC AGTCCT CG ACC GT AC AA CGTC CCTC CCTCTT
TC
CTGGTTATGCTTCCTTCTCC CAGAAT TAC- - -- G C A AA - CCAA CCT --
AACCCTCCCTGCAAAAACAC CTGGTTATG
TGGCCAGCTCCTGACATCAC
AGTAAGACAG

GAM3061 10250 GAATCTGGTTGGTTCCTTAA T TCCT G A ATG GG
GAAAACTATTTGATCATTA
AGATCACTTGACATGGACAG GAATCTGGT GGT TAAA ATC CTTGAC GACAG TTTG
GGTTTGGAAAACTATTTGAT TTTGGATTA CTA ATTT TGG GAACTG CTGTC AGGC
CATTACGGAGACTGTCACCG - TT-- G A CCA AG ----------
TCAAGAGGTGTTTATTATCA
TTAGGTTT
GAM3064 10671 GGCACTTGGAACCGTCTTGG ACTT A G TGG ATA T AACT C- TTAT
GGAATATAGCTTGGTAATTG GGC GGA CC TCT GGAAT GCTTGG AATTG GCTTAAG TTA
AACTGCTTAAGCTTATTATT CCG CCT GG AGA CCTTA CGGACC TTGAT CGAATTT AAT
AATATTTAAGCTATAGTTCC ACCC - - --- CC- - AT-- AT ----
AGGCCCATTCCAGAGGTCCC
CCAGCC
GAM3065 10649 GGAGACATGATGTAGCAGAT C AG- AT GGG---- C ATA G TA ACTA
GATGGGACTGTCTTACATAA GGAGA ATGATGT CAG GAT ACTGT TTAC ACT GATCTTT GA
CTGGATCTTTTAGAACTATC CCTTT TATTGTA GTT TTG TGGTA AATG TGA TTAGAAG CT
GAAGATTAAGTAGTAAAATG - ACA CT AAAAATA A A-- A -- ----
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ATGTTATTTTCC
GAM3077 9975 CAGGTGTGGACTACCATGCC T GGACT T TTTTGTATTTT ACAGGG
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GGTAGAAACAGGGTTTTACC GTCT CA TGGT CGGACCGGTTG ACCATTTT
ATGTTGGCCAGGCTGGTCTT T AGTTC - T---------- ------
GAACTTCTG
GAM3081 10054 CCTCAGCCTCCCAAAGTGCT G CCCAAAGT A AC T C CA CCG
GGGATTACAGGTGTGAACCA CCTCA CCT GCTGGG TT AGG GTGAA CAC TGC
CCATGCCCGGCAGTGATTCA GGAGT GGA CGACCC AA TCT TACTT GTG ACG
TTTCTAAACCCAGCTTGTTA - AAATTGTT A -- T A -- ---
AAAGGTGAGG
GAM3089 11035 TGACACTTTCTGTAAACGCC C ---------- T CATCT TTTCTCCCATT TGCC
ATCTGTGCTTTTCTCCCATT TGA ACTTT CTG AAACGC GTGCT TGTAC
TGTACTGCCCTGTATATCCC ACT TGAAG GAC TTTGTG TACGA ATATG
CGTTCAGCATTGCCAGTGTT T TCTTACGAAATTCTCCACC C ACCGT CTTGCCCCT-- ----
TCCAGCCACCTCTTAAAGCA CT
TTCTGAAGTTTCA

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                    --
GAM3091 10253 GACAGCAGAACTTTTCTATC      GA  TTTCTATCC   AAT-  G   T  A TGG
        CAAATGAATGCCGTCCCATG GACAGCA  ACT       AAATG   GCC TCCCA GGA AG
        GAAAGTGGCTGTCCTGGGAG TTGTCGT  TGG       TTTGC   CGG AGGGT CCT TC
        GCTACACGTTTCTCCAATGG      AG  TAACCTC--   ACAT  -   -  G ---
        TGATGCTGTT
GAM3123 10050 CCTACCATGACTGTTCTCAA    CAT   GT    A -     ----- A-   ACCG
        AGTTTGAAGTTGAGCATACC CCTAC   GACT  TCTCAA GT TTGAAGT    TG  GCAT
        GATGCGCCACTCCTGCTTCA GGATG   CTGA  AGAGTT CG AACTTCG    AC  CGTA
        ATGCTTGAGAAGTCGTAGG     ---  --    - T     TCCTC  CG   ----
GAM3126 11212 TGTGAAACACAGCCAGTTTC   GAAA     ----  T  ----    -    ACGTA  T  GATCTT
        TTTGATGACTCAAAACGTAC TGT   CACAGCCA   GTT CTT   TGATGA CTCAAA    CTT GT
        TTTGTGATCTTGCCAAGCTT ACA   GTGTTGGT   CGA GAA   GCTACT GAGTTT    GAA CG
        TGAGATCATCGTTACAAGCA   AAAA      TTTA  C  CATT    A    C----  C ------
        GCATTTTGGTTGTGAAAAAC
        A
GAM3132 9697  AGCTATTGTGACAATCTTGG  CTA   GACAA   GTTA  TCCATTAA   GCTGAT
CATGAAAAAC
        TTACCATCCATTAAGTGCTG AG  TTGT   TCTTG   CCA     GTGCT    TTTGGAAAGAT
        CTGATTTTGGAAAGATCATG TC  AACG   AGAAC   GGT     CACGG    AAACCTTTCTG
        AAAAACGTCTTTCCAAACAT  TA-  G----   ACG-  TTGCTG--   AAGTAC       ----------
        GAAGGCACGTCGTTTGGGCA
        CAAGAGGCAAATCT
GAM3138 9652  ACTCTTTGAGATGACTGGTA  T   G   T   TG  A   AAT   AG   G  AG C   A  CT  CTAACT
        TTGAATGGAGCAGTCTTTGA AC CTTT AGA GAC  GT TTG   GGAGC  TCTTT AA  G ACCA CC  TC

        AAGGCACCAACCCTTCCTAA TG GAAA TCT CTG  TA AAC   TCTCG  AGAAA TT  C TGGT GG  AG

        CTGATGGTGGTCTCTTGAAA  T   G   T   TT  -  CT-   G-   G  CT -   - T- ------
        GAGGCTCTTCCAAATTTGTC
        TTCTGAAAGTGT
GAM3140 9763  AGTGTGAAGACAAAAGCCAC    GAA   AAAGCCACT   TAA  T  T  A    AA--  A  A  CC    C  C
        TTTCTAAGGATGGTGGAGCA AGTGT   GACA      TTC   GGA GG GG GCAGA   GGC GG GT
TGCTCC TGG
        GAAAGGCAGGAGTCCTGCTC TTACG   TTGT      AAG   TCT CC CC CGTCT   CCG CC CG  ACGAGG
ACT
        CCTGGCACCATCATGGAGCA    ---   CCTTT----  ---  C  -  -   AGAC  A  -  T-    T  -
        TGCCCAGCCCAGATCTGCCC ACCA
        CCCTCTGAATTTCCTGTTGC
        ATT
                    ----
GAM3143 10699 GGCGTATCAGGTTTCAGAGG    ATC  G TT       -   G  A   GA    A  TGAGGGG
        ATGCGGCTGGGAACGGGAGT GGCGT   AG T  CAGAGGATGCG GCTG GA CGG  GTAG GG

        AGAGGTGAGGGGTCGTTGCA CCGCG   TT G  GTTTTCTATGT TGGC CT GTC  CGTT CT
        TCTGTCGCGGTGTGTATCTT    AC-  G GG       G   G  -  TA   G -------
        TTGGGGGTTCAGCGCC
GAM3157 11285 TTGTTGAAGGGCAGTGAAGG    TG A--    T  A    GTTT     GTTTTA
        TAGGTTTCAGGTTTGGTTTT TTGT  A   GGGCAG GA GGTAG   CAGGTTTG
```

ACAAACCTGTTAACTACCTC GACA T CCTGTC CT CCATC GTCCAAAC
CTGTCCAGCTTGACAG GT CGA - - AATT ------
GAM3163 11019 TCTGCTCATGATTACTGGGC A TTA G -- CC TGAC C CTTGTGAA
CAATACCACTGCAATGACTG TCTGCTC TGA CT GGC CAATA ACTGCAA TGT AGAACAATT

TCAGAACAATTCTTGTGAAA AGACGGG ACT GA TTG GTTGT TGATGTT ATA TTTTGTTGA

GTTGTTTTTATAAGCCTTGT A TG- G AA T- CCGA T --------
AGTTTGTTGAAGTTGAGGTT
CAAGGGCAGA
GAM3174 9656 ACTTTTGGCTCATTTTTTGA G TTTTT - - G ATAAA ATTAGG
TGCATGTGACCTGGGATTAT ACTTTT GCTCA TGATGCATG TGAC CTGG ATT TGTGAA

AAATGTGAAATTAGGTTTAC TGAGGA CGGGT ACTACGTGT ACTG GACC TAG GCATTT

GAAAGGATCCAGTGTCATTG A ----- T T - GAAA- ------
TGCATCATGGGCAAGGAGT
GAM3183 9906 ATCTTGTACATTTTCCCCAC C ------ CA - A C TCCAG
ACTTGGAATCAGCCATTCCT ATCTTGTA ATTTTC CCCA CTTG GAATC GC ATTCC
CCAGGGAGTGCAGGTTCACA TGGAATAT TAAGAG GGGT GGAC CTTGG CG TGAGG

GGCTGGGCTCTAAGAGAATT - AATCTC C- A A - -----
ATAAGGT
GAM3190 10415 GATCATTTGAGACCAGAAGT CA AGACCA GT- T CT A- A ACGT
TCCAGGCTGTAGTGCACTAT GAT TTTG GAA TCCAGGCTG AGTGCA ATG TG TCGT
GATGATCGTACGTATGAACA CTA GAAC CTT GGGTCCGAC TCACGT TAC AC AGTA
GCCATTGCACTCCAGCCTGG CA GA---- AAC C -- CG A ----
GCAATTCAGCAAGACATC
GAM3195 10884 GTTCCTTAGGCCACACCCTG TT ----- C CCT G--- - CGCTCCA
CCCTCCCTGGACTGCCTGAC GTTCC AGGC CACACC TGCCCTC GGACT CCTGA CCT

CTCGCTCCAAGGCTCAGGGG TAAGG TTCG GTGTGG ACGGGAG CTTGG GGACT GGA

AAGGTTCTGAGGGCAGGTGT -- TAAAA - T-- AAGG C -------
GAAAATGCTTGGAAT
GAM3211 10984 TCCTCCCCCAGGCATTCTGG -------- - A TTC-- TCA T- TT - T TCTCG
TCACTGTTCCTTTTTGTTGA TCCTC CC CC GGCA TGG CTGT CCT TTGT TGAGA CAT
GATCATTCTCGGTGTCTCAT AGGAG GG GG CCGT GCC GACG GGG GATA ACTCT GTG

ATAGCTGGGTTGCAGCTCCG ATAATGGT A A TTCTT TC- TT TC T - -----
TTCTTTGCCAGGAGGTGGTA
ATAGAGGA
GAM3227 10618 GGAGAATGGGCCTGAACCCG AATGG - AA- AGGC C T A- CGAGATT
GGAGGCGGACGTTGCAGTGA GGAG GC CTG CCCGGG GGA GT GCAGTG GC
GCCGAGATTGCACCACTGCA CCTC CG GAC GGGTCC CCT CA CGTCAC CG
CTCCAGCCTGGGCAACAGAG AGAG- A AAC GA-- - - CA -------
CGAGACTCC
GAM3236 10435 GCAGCGACGCTGAGTTTCAA GACG G C AAA AAGA C CACA
GAAAGCCAAGATGGCTGAGT GCAGC CT AGTTT AAG GCC TGG TGAGTC
CCACAGGCTCACCCACGGGT CGTCG GG TCAGA TTT TGG ACC ACTCGG

GCGTTTAGACTGGGATGCTG TA-- G - GCG GC-- C ----
C
GAM3263 10041 CCGAGGCTACGTGAAGGAAC A- TAC - - TTTGCCT CATTTC - ACCAATG
ACTTTGCCTGGAGACATTTC CCG GGC GTGAAGG AA CAC GGAGA TACTGG TACCTT

TACTGGTACCTTACCAATGA GGC CCG TACTTCC TT GTG CCTCT ATGACC ATGGGA
GGGTATCCAGTATCTCCGTG CC TC- A A ------- ------ T -------
ATTACCTTCATCTGCCCCCG
G
GAM3266 10068 CCTGTACAAAGCAGCCTTGG T AAA CA AAAACCCCA CTGC
ACCAGGAGGGAAAACCCCAA CCTG AC GCAGCCTTGGAC GGAGGG AGGCT
GGCTCTGCAGCCTCCCTGCT GGAC TG TGTCGGAATTTG CCTCCC TCCGA
CCCCTCCGTTTAAGGCTGTG - G-- -- CTCGTCCC- ----
GTCAGG
GAM3271 10413 GATATGTTTCTACTAGTGGT -- A - G - TTTCAG CGCT
TGATGGCCTCTTTCAGCTCC GATAT GTTTCT CT AGT GTTGATGG CCTC CTCCAT
ATCGCTATGGAGGCGAGGTT CTGTG CAAAGA GA TCA TAACTACT GGAG GAGGTA
CATCAATAACTCAGAGAAAC TT - C A T CG---- ----
TTGTGTC
GAM3293 9998 CCAGGCCTGACCTGTCTCTT - C-- A- AA AGTATTTG- AG GGTGGTAA
GAAGGAGTATTTGTGTTGAA CCA GG CTG CCTGTCTCTTG GG TGTTGA ATG
GATGGGTGGTAACGTTCAGC GGT CC GAC GGACAGAGGAC CC ACGACT TGC
AAAAGCCATGCCCAGGAGAC A CAT AC -- GTACCGAAA -- --------
AGGCACAGTACCCATGG
GAM3298 11281 TTGGGTCCTAGTAGTACCAA G- T T CA- G GT- TTGGCAT
AGTGCTCATAGTGCAGGTAG TTG GTCC AG AGTAC AAGTGCTCATA TGCAG AGTT
TTTTGGCATGACTCTACTGT AAC TAGG TC TCATG TTCACGGGTAT ATGTC TCAG
AGTATGGGCACTTCCAGTAC AA T - ACC G ATC -------
TCTTGGATAACAA
GAM3311 10726 GGGACTGCTGTCTGCTGTCT GCT C ACAC TACT- CTGC
ACACTACACACTACTACACT GGGACT GTCTG TGTCT TACACAC ACA
GCTGTCTGCTGTGTGTGATA TCCTGA TAGAC ACAGG GTGTGTG TGT
AGGACACAGATAGTCCT --- - AATA TCGTC ----
GAM3330 10049 CCTACATGTGTTACACTCAG TG -- CA GTA - AAGA AT A AGCAA
TGTGTAAATAACTGTGAAGA CCTACA T GTTA CTCAGTGT AATA ACTGTG GGCA TGTC GAT

GGCAATTGTCAGATAGCAAA GGATGT G CAGT GGGTCACG TTAT TGGCAT TCGT ACGG TTA

TTGGGCACCTGCTGTGTACG GT GG CG --- A GTG- CC G -----
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CGGGTGTGTAGG
GAM3350 10894 GTTTTGACAAATGCAGATAC TT A-- C CAT- AACT A- C- CTTATA
ATGTGTAACTGAACTTATGA GT TGACAA TG AGATA GTGT GAACTT TGA TTTC
CTTTCCTTATAGAAACTTCA CA ACTGTT AC TCTAT CATA CTTGAA ACT AAAG
GAAAGTTCCCTCATACCCCT TC CTA - TCCC CTCC AG TC ------
TATCTCAATCTTGTCACTAC
GAM3368 10953 TCAGATCAGTAGTGACATGA G TGA G A--- GA ----- A AACTCCAAA
GATTTTCATAGGAGCAGAAA TCAGATCA TAG CAT AGATTTTCATAGG GCA AACC CT TTGTG

CCCTATTGTGAACTCCAAAC AGTCTAGT GTC GTA TCTAAGAGTATTC CGT TTGG GG AACAC

ACAAGGGATCTAGGTTATGC A C-- A ATCA A- ATCTA G ---------
ACTACTTATGAGAATCTAAT
GCCTGATGATCTGA
GAM3414 9917 ATGGCATGCACGTGTTGGAA A ACG GG GCT- C C -- GT AAAGGA
GTTAGTGGAGGCTATCTCCC ATGGC TGC TGTT AAGTTAGTGGAG AT TC CCAGT G C
CAGTGGTCAAAGGAGGTCTT TGTCG ACG ACGA TTCAATCATTTT TA AG GGTCG C G
GCTGGAGAAATTATATTTTA - --- AG ATAT A A TT TG ------
CTAACTTGAAGCAGCAGCTG
T
GAM3422 10760 GGGGGACAGAGCGAGACTCC GG A - A A CT ---- ATTG
ATCTTTTCTGGGAGACTCCA GGG AC GAG CG GACTCC TCTTTT GGGAGAC TCC
TTGGGAGACTGTCTTTTTTG CCC TG TTC GT CTGAGG AGAGGG TTTTCTG AGG
GGAGACGGAGTCGTGCCTTA TT A C G C TT TCAG ----
GTTTCCC
GAM3426 9899 ATCAATCACACTGGGTGACC ATC----- C C- TGTCA
TTTACTCCCTGTCAGGTCAG ATCA ACACTGGGTGAC TTTACT CC
TAAGAGTCACCCAGTGTAAA TAGT TGTGACCCACTG GAATGA GG
CAGCATGAT ACGACAAA A CT -----
GAM3431 10749 GGGCGGGGGCCCTCGTCTTA CT - A T T GGTTGGGA
CCCAGCAGTGTTTGGGTGCG GGGCGGGGGCC CGTC TTACCC GCAGTGTT GGG GC

GTTGGGAGTCTCTAATACTG CCTGTCCCCGG GTAG AATGGG CGTCATAA CTC TG
CCGGGTAATGATGGAGGCCC AG T C T - --------
CTGTCC
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CCCAAGCCCAAGCGGGCCTT TG GTCGG CCGGGG CT GTCAAG CT CGGG CG
TCCTCCAGAACTGCTCCGGG T- T C C-- ACCTC TTC- -- ----
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GAM3461 9941 CACCTGCCTATATTACATTC - ATATTACA CA GA TT C- G ACAGTGAACGAA
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GAAAGAAAAAGAGAAGAGGC
AGAGTG
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AATATAGCAAATAGAGGGTC GGGA GGAAA TGCAGA AGCA AGGGT CT TTTCC
TTTTCCTGTCATGGAAATCG CCCT TCTTT ACGTCT TCGT TCCCG GG AAAGG
GTCAGCCCTGATGCTTCTGC T - -------- AG--- ACT CT ------
ATTTCTTTCCC
GAM3479 10822 GTCCATCTTCAGTGGCATTG T A --- G------ T G GGA GTTA ACT
GGCCTTGGCTGGGATGCTGA G CCATCTTC GTGG CATTG GCCT G CTG TGCTGA TCC

GTTATCCACTGGAGCATCGG C GGTGGAGG TACC GTGAC CGGA C GAC ACGGCT AGG

CAGTACAGGCAGGCACAGAG - C TAG GGAGACA - G ATG ACG- ---
GCAGTGGATCCATCGGAGGT
GGC
GAM3486 10003 CCAGTTCTCCTTTAGTGTTC T TT T CTCAAA--- GCCA
AGGCTCAAATGAAAGGCCAC CCAGT CTCC TAGTGT CAGG TGAAAG

TTTCAGCAAGTTTTCCTGAC GGTCA GAGG GTTACA GTCC ACTTTC
ATTGTCGGAGACTGG - CT - TTTTGAACG ----
GAM3513 10229 GAAATGGAGTCTTGCTTTGT AAT- TCTT TT TCA -- C -- - TGATCTC
CACCGAGGCTGGAGTGCAGT GA GGAG GC TG CC GAGG TGGAGT GCAGTG GCA
GGCATGATCTCTGCTCACTG CT CCTC CG AC GG CTCC ACCTCG CGTCAC CGT
CAAGCTCCACCTCCCGGGTT CCGT TTAC C- TTG CC - AA T -------
CACGCCATTCTCCTGCCTC
GAM3535 10223 CTTTTTCTCTGCCCTTCGTC ---- CTTC -- T A G T GGGAA
ATTATGCAGCCTGTGAACAG CTTTTTCTCT GCC GTCA TTATGCAGCC GTGA CA CG CT

CGTCTGGGAAAGTGGTGGTC GGAAAGGAGG CGG TAGT AATACGTTGG TACT GT GT GA

ATTGGTTGCATAATTTGATC TATT AGTC TT T G G - -----
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CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACAT GCA GT TGT AC
TAGGTATACATGTGCTATGT TCAA CCCA GT C GTG TTGTA CGT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G T G C - ----
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GAM3595 9681 AGAGTCTTGATCTGTCACCC -- TCTGTC CT AG---- - A ATCT
AGGCTGCAGTGTAGTGGCAT AGAGT CTTGA ACCCAGG GC TGTAGTG GC TG
GATCTCGGCTCACTGCAACC TCTTA GAACT TGGGTCC CG ACGTCAC CG GC
CCCGCCTCCTGGGTTCAAGC CC ------ TC CCCCCA T - ----
CATTCT
GAM3605 10089 CGGACCCTGCTGTGAGCAGC - - - TGAGC T -- A- TGTT GCTC
TCCCTATTCCATGACAGTGT CGG ACC CT GCTG AGC CCCTATT CC TGACAGTG GA
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TAGAGGTGCCG
GAM3630 10831 GTCTATTATGAGTCTGACTG - - C C CTG GAAGGA
GCACAGACATCTGTCAAGGA GTCTAT TATG AGT TGACTGGCACAGA AT TCAAGGAA

AGAAGGATTCTTTGAGCGTA CAGGTA ATAC TCA ACTGACTGTGTTT TG AGTTTCTT
TTTGTGTCAGTCAACTGCAT T G - A CG- ------
ATATGGAC
GAM3640 10803 GGTTTCCTGGAACTTTGGGG TG ACT G- CATTATAAAAA AAAAAAGCA
GATCATTATAAAAATACTAG GGTTTCC GA TTG GGGAT TACTAGGGT
GGTAAAAAAGCAACCTTAGT CCGGAGG TT AAC CCCTA ATGATTCCA
AATCCCAGCAATTTGGGAGG GT --- GA ---------- ---------
CC
GAM3666 10476 GCTCACAAAACCTAGGTGGG CACAAAACCT GA AA C AA C G TTC GATCA

GATGAAAGCTGAGAAAGCGA GCT AGGTGGG TGA G TGAGA G GAA AGGTGG AGGG

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CTCTTTCCTACTTGTTCCTC CACGTCATCT AA -- C -- - G CTT -----
TCACCTCAAACTCACCTTCT
ACTGCACAGC
GAM3691 10139 CTGAATGACCTGCAGTCAGG AAT - A T GACTCTATA
GCCCAGAGTTGGGACTCTAT CTG GACCTGCAG TCAGGGCCCAG GT GG

ACTACCCTGGGCTCTGGTCT GAT TTGGATGTC GGTCTCGGGTC CA TC
GTAGGTTTGTAG GT- T C - ---------
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GGTGAGATGAGTTGCTTGGC AGAGGGT AGG TGGTGAG TG GTT GC GGC CAGAT GC
CAG
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CCTGGTGATAAGGCATCTGG TTACCT- -- - - T TT - -- GAATAGTG ----
CTTTGCTAACCACTTATCAT
CTTCCATTATTCTCT
GAM3768 10892 GTTTGTGGGAGGAGGACTGG T A C CAA A A A A TG CTTG
CAAAAATATGAGAGTAGGAG GTT GTGGG GGAGGA TGG AAAT TGAG GT GG GTT GGCT

TTTGGGCTCTTGAGCTTGGG CGA CACTC CTTTCT ACC TTTA ACTT CG TC CGG TCGA
CCTGGCCTTCAAATTTCCAC T A C --- A C G - GT ----
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TGATAGTAAAGTCATGTAAC GCAAGGTT GGAA TAA CTG ATAG AAAGT
ACTTTCTGTGCAGGTTAACA CGTTCCAG CTTT ATT GAC TGTC TTTCA
TTTCTGGACCTTGC GT ACA G G - --------
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AGCTACCCATGAAGAAACCC CACTGTGTGATTT CAAG ACC TGA
AGACTCAGAGGTCACTTGCC GTGACACACTGGG GTTC TGG ACT
TAGGGTCACACAGTG ATCC- AC AG ----------
GAM3810 10439 GCAGGGAGACTGGAGAGAAA GG A G A GA A ---- C CATAGT
GCGAAGATGTAGCCCAAAGC GCAG AG CTG AG GAAAGC AG TGTAG C CAAAGC
CATAGTGCTTTGTGTGCCCT TGTC TC GAC TC CTTTCG TC ACGTC G GTTTCG
GCAACTGAGCTTTCCCTGCA TT - G C AG A CCGT T ------
GCTTTCTGT
GAM3890 11222 TGTGGTCCACAAGGGGAGAG T - ACAAG--- A GG---- CACAGCA - CCTCAAA
CAGGGGACACAGCATTGGCA TG GGT CC GGGAG GCA GGA TTGG CAGGAA
GGAACCTCAAATTCCTGACC AC CCA GG CCCTC CGT CCT AACC GTCCTT
AAACCCTCTTCCACACAATG - A AAAGAAAG - AACACA TCTCCCA A -------
CCTCCCGAAAGAAAGGAACC
CA
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AAAACTCAACTAAGCTAAAG GC GCTGCT AGTCA CTGA AACTCA CTA GCT
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ATGACTGGCAGTGC - -- A CA A C ----
GAM3946 10833 GTCTCTGTTGCCCAGGCTGG T GTT C-- -- C AATCTCA
AGTGCAGTGGCGCAATCTCA GTC CT GCCCAGG TGGAG TGCAGTGG GC
GCTCACTGCAACCTCCACCT TAG GA TGGGTCC ACCTC ACGTCACT CG
CCTGGGTTCAAGCGAT C ACT TCC CA - -------
GAM3978 10752 GGGCTTGCTGGGTTTACAGA TG -- ACAGA- AAAGATCT AAATTAAAAATA

TGGCAAAGATCTGGCAAATT GGGCT CT GGGTTT TGGC GGC
AAAAATAGCCTTAGGCCAAA TTCGG GG CCCAAA ACCG CCG
GATCAAACCCAAGGTGGGCT GT AA CTAGAA GATT---- ----------
T
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TTTTGGCTCACTGCAACCTC TC ACGA AC TGGGTCC ACCTC ACGTCACT CG
CACCTCCTGGGTTCAAGCAT TTT - T- TCC CA - -------
TTCT
GAM4008 10952 TCAGAGACACCTCTCATTTC GAGAC TCAT C A AC A T AACT
TCCTCAATGCCACTGCACTG TCA ACCTC TTCTC TCA TGCC TGC CTGA GTC
ATGTCAACTGACTTAGGGCA GGT TGGAG AAGAG AGT ACGG ACG GATT CAG
GGCATGAGAGAACTGAGGTT ACATT TC-- - - -- G - ----
TACATGG
GAM4011 9765 AGTTCAAGGCTGCCTCCTCT C -- -- T T T ATTGAA GTCA
CTGTCTTCATTATGTGAATT AGTT AAGGCTGC CTCCT CTCTG CTTCA TATG GA TGTG
GAATGTGGTCACACATCTGT TCGA TTTCGACG GGGGA GAGAC GAGGT GTGT CT ACAC

GTTGGAGCAGAGGCAGGGGC C TC CG - T - ------ ----
TGCAGCTTTCAGCT
GAM4020 9615 AAGGTATTTTCTGAGCTGTG T A-- - G CC A TCTAAAAATT
AGCCTGCCTTCCAGTGACAT AAGG ATTTTCTG GCTGTGA GCCT CCTT AGTGAC TGT
GTTCTAAAAATTGCAAGTTA TTCT TGAAGGAT CGACATT CGGA GGAG TTATTG ACG
TTTGAGGAGGCTTTACAGCC - AAC T - T- A ----------
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GAM4027 11191 TGGGTCCCAGATTCTTCCTG G-- TT- - G GA C GCAACACCC GCCTTAA
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ACACCCTGGCCTTAACACAC ACC AGGGTCT GA GGGG CAC CT TAAGTTTCT AC
TACATATCTTTGAATTTCAC AAA TCC C G A- T ATACATCAC -------
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AAACCA
GAM4064 10022 CCCCAGCCCGGAAGCCTCCA A-- GGAAG ACTA CCA - ACAAACC
CTATCTCCAGCCCAGACAAA CCCC GCCC CCTCC TCT GCC CAG
CCCTGTGGTCCAGAGGAGGA GGGG TGGG GGAGG AGA TGG GTC
ATGAGGGTGCAGGGG ACG AGTAA ---- CC- T -------
GAM4074 10140 CTGACATGTGCATTATCCAT TG T G T TTTAAA A - ATGGAA
GTCATTTTAAACAAAGTGAC C ACA GT CATTA CCATGTCAT CA AGTG ACCT
CTATGGAAGGGTACGCTGTG G TGT CG GTAAT GGTACAGTG GT TCGC TGGG
CTGTGACATGGTAATGGGCT GT - G - TC---- G A ------
GTTGG
GAM4085 9711 AGGCACCTGGGGGTGTAGAC - G AGACC GAGCC G-- G GGTGTAGA
CGGGGTGGAGCCGCATGGGC AGG CACCTGGG GTGT GGGGTG GCATGG CACCT GG

ACCTGGGGGTGTAGACCGGG TTC GTGGACTC CACA CCCTAC TGTATC GTGGG CC

GTGGAACTATGTAAACATCC A A ----- AAA-- AAG G --------
CACACACTCAGGTGACTT
GAM4130 10199 CTTCCATGGGCAGGGGCCAT GG GG GACA AT CCACA
GACAGGGAGATAGGCCACAC CTTCCAT GCAGG CCAT GGGAG AGG
CTTTCCCAGGTGGAACCTGC GGAGGTA CGTCC GGTG CCCTT TCC
AGATGGAGG GA AA GA-- -- -----
GAM4136 9668 AGACGTGGGGTCTCGCTATG TG TC--- - - - -- A- C CCTC ATTC
TTGGCCAGGTTGGTCTTGAA AGACG GGGTC GCTA TGTTGGC CA GGTTG GTCTTG ACT TTGG
AAGC
CTCTTGGCCTCAAGCATTCC TTTGT TTCAG TGAT ATAACCG GT CCGAC TAGGAT TGA AACC
TTCG

TCCTGCCTCAGCTTCCCAAA TT TAAAA G A A AT CG - C--- ----
GTGCTAGGATTACAGCCATG CTCCTGCCTCA
AGCCAATAGTAGTAAAATGA
CTTTTTGTTT

GAM4142 10081 CGAATGGACCACTGGAGGGG T- A A T TTCCA AATATG
TTCAAAGATTCCAGTTCTAA CGAA GG CC CTGGAGGGG TCAAAGA GTTCT
TATGGGAATGAGCCTCTTTG GCTT TC GG GGCCTTCTC AGTTTCT TAAGG
ATCTCTTCCGGGGCTTTTTC TT - - T CCGAG ------
G
GAM4147 11207 TGTATTGCAGCAGGTTGGCA - C G --- - A AAATCTCCAT TAAA
AGTCAGCAGAAT
GCCTCAGTAAATCTCCATTT TGTAT TG AGCA GT TGGCA GCCTC GT TTG TGTGAC
GTAAATGTGACAGTCAGCAG ATATA AC TTGT CA ACCGT CGGGG CG AAC ACATTG
AATCTCCAGTTACAGTCAAC T - A TAC A A AACGAAACTC TG-- ----------
TCAAAGCAAGCAGGGGCATG CTCCA
CCACATACATGTTCATATAT
A

GAM4152 10154 CTGCAGCCCAAGCAAAATGG G CAA AAAAT ACAAG A ATG A T C A
CAGGAACAAA
AAATACAAGCAATCATGTAG CT CAGCC GC GGAAAT CA TC TAGTTC CTG GTC ATC GA
TTCACTGTGTCCATCAGACA GA GTCGG TG CCTTTA GT AG GTTAAG GAC CAG TAG CT

GGAACAAATCAGATGACCAG G --- GACT- CAA-- C AGA - - - A ----------
GAATTGAGAGACTGAACATT
TCCTCAGGTGGCTGGAG

GAM4188 9909 ATGACAGCAAGACACTGGCC TG - TGGC-- GAAT--- TC TCA
CTGGAATCCTCCGTGTCACA A ACAGCAAGA CAC CCTG CC CGTG
TGTGGGCTGCTGACAGGAAG T TGTTGTTTT GTG GGAC GG GTAC
AATGTGCTTTTGTTGTTGT GT C TAAGAA AGTCGTC GT ---
GAM4189 9666 AGACATGTCAAGGCAGGAGC -- AA - CAT ATCGACCTTA AAGCTGGTG
CATCTGATCGACCTTAGACT AGACA TGTC GGCAG GAGC CTG GACTTGGC
TGGCAAGCTGGTGGCTAAGT TCTGT ACAG CCGTC CTCG GAC CTGAATCG
CCAGTGCTCACTGCCGACAT CT -- A T-- ---------- ---------
CTGTCT
GAM4199 10173 CTGGCTGCTCCTCTCCATGT CCTCTCCATGTACC TT---- CAAGCCACAC
ACCCATTCCCCTTGGGGTGC CTGGCTGCT CATTCCCC GGGGTG
AAGCCACACCACCCTTCACT GACCGACGA GTAGGGGG TCCCAC
TGGGGGATGATAGCAGCCAG TA---------- TTCACT ----------
GAM4205 10494 GCTGTCAGATCAGGTTCCTG TGT- T T --- T- TGCTCT
ATTGGAGTTCTCTTATCTGC GC CAGA CAGGTTCCTGA TGG AGTTCTCT ATC
TCTGGTTTGGAGGGCTGCCC CG GTTT GTCTAAGGGCT ACC TCGGGAGG TGG
CATTCGGGAATCTGTTTTGT TTTT T T CCG TT ------
TTTGC
GAM4238 10112 CTCCTGTAGTCCTAGAGCGT GTA AGAGC TT - - A- - CAAAGAGT
TTCTCTTGAACCCTAATTTT CTCCT GTCCT GT CT CTTGAACC CT ATTTTT AGGTCT
TAGGTCTCAAAGAGTGGGCT GAGGA CGGGA CA GA GGATTTGG GA TAGAGA TTCGGG

TCAGAGATAAAGAGGTTTAG G-- ----- GG C A AA C --------
GCAGGGACAGGGCGAGGAG
GAM4243 9595 AAAGGCAGACGGTGAATGCC AC AA - ---- ATTG
TTGAGAAATTGTTCAGATTC AAAGGCAG GGTG TG CCTTGA GAA
AAGGACAAGCATTTGTTGCC TTTCCGTT TTAC AC GGAACT CTT
TTT GT GA A TAGA ----
GAM4298 10843 GTGAGGCTCTGGCAAGGTGT AG --- - GGG - C CT AGTT
GGGCTAGAGATGCGACTCAG GTG GCTCTG GCAAGGT GT CT AGAGATG GA C
TTGGATCTATCTCTCAGAAG CAC TGAGAT TGTTCCA CG GA TCTCTAT CT G
GCTACCTTGTAAGTAGAGTT CT GAA T GAA C - AG ----
CCAC
GAM4315 9960 CAGATTGCACGAACATTTCA ATTG AAC TTTTTCACAC ------ A- TCAATTTTT
TTTTTCACACAGGGTCACCA CAG CACG ATTTCA AGGGTCAC CAG ATACCA
GAATACCATCAATTTTTTGG GTC GTGC TAAAGT TCCTAGTG GTC TATGGT
TATCACTGTCAAAAGTGATC GA-- AA- CTTCCACGA- AAAACT AC ---------
CTAGCACCTTCTGAAATAAC
GTGAGCTG
GAM4364 9623 AATGTTCTGGCACATAGTAA TG C- TAA ATCG - TA ACCTAG
TTAATTAAGAAAATCGAGCA AATGTTC GCA ATAG TTAATTAAGAAA AGCA CCCT ATT
CCCTTAATTACCTAGAATGC TTACGGG CGT TGTT AGTTGGTTTTTT TTGT GGGA TAA
AGGGTTGTTAGTTTTTTGGT GT TT TTC GA-- T CG ------
TGACTTTTGTTTTGCTGGGG
CATT
GAM4376 10325 GAGGCAGGAGAAATTGCTTG G AAA GAA--- AGGTA GT A T AGATCA
AACCCAGGAGGTAGAGGTTG GAGGCAG AG TTGCTT CCCAGG GAG TGCAGTG G CA

CAGTGAGTCAAGATCATGCC CTCTGTC TC AACGAG GGGTCC CTC ACGTTAC C GT
ATTGCACTCCAACCTGGGCG - AA- AACAGC AAC-- -- - - ------
ACAAGAGCAAAACTCTGTCT
C
GAM4377 10976 TCCCTCTGCTAGTGAGTACA ------ - --- TG A A- T CAA A GAGGAGCA
AATGAAGTCTGTGGGCCAAC TCCC TCTG CT AG AGT CAAATG AGTCTG GGGC CA GGAGC

AAGGAGCGAGGAGCAGTTTC AGGG AGAT GA TC TCA GTTTGT TCGGGT CCCG GT CTTTG

CTGGAAGCCCTGGGCTGGTG TAAATA A GTT GT - GG - AAG C --------
TTTGACTTGCTTTGAGATAG
AATAAATGGGA
GAM4382 9983 CATCAGCTATTCCTGTTCTA CA AT G AGAA GG GG G- AATGT
GAAAGGGCACTCTGGCTGCA CAT GCT TCCT TTCT AG CACTCT CT C
ATGTGGAGGAGGGAGTGACT GTG TGG AGGG AGGA TC GTGAGG GG G
GGAGGAAGGGAGGTAAGTG AA -- A GG-- A- GA AG -----
GAM4398 11199 TGGTGGGACACAGAGCCAGT - CACA GC GAC A- T - G G A TACA
GACTGACATAGAAGAGCAGT TGGTGG GA GA CAGT TG CA AGAAGAG CA T GGGT GAAT

GGGGTAGAATTACAGTTCCA ACCACC CT CT GTCG AC GT TCTTTTC GT G TCTA CTTG
TCTGGTGCCTTTTCTCTGAG A AC-- AT AA- GA C C - G C ----
CAAAGCTGTATCCATCACCA
CCA
GAM4408 9746 AGTATCTGGAATTCTATTGT ATTCTATTGTGTGT - GC A AT T GAAAAAA

GTGTGAGTCTGTGCAGGAAC AGTATCTGGA GAGT CTGT AGGAAC CA GAGTC CAAAGT

ACAATGAGTCTCAAAGTGAA TCATAGACTT TTCA GACA TCCTTG GT CTTAG GTTTCA
AAAAACTTTGGATTCCTGGT GTT---------- C -- - C- - -------
TCCTACAGCACTTTTGTTCA
GATACT
GAM4423 10486 GCTGCAGTGGAAAGGAGTTT C GAA-- - --- A A TT AG GAAA
GTGACATTGACATTGACAGC GCTG AGTG AGG AGTTT GTG CATTG CA GAC CAT
ATGAAAATGGGTCTTGCCAG CGAC TCAC TCC TCAGA TAC GTGAC GT CTG GTA
TGCATGTGAGACTGCCTCCC - AACCC G GTG - C T- G- ----
AACACTCAGC
GAM4426 11283 TTGTGGATATTGAAGTTTGA ------ C GTTG-- TAGATGCAC
AGCCTGTTGTTCATCTATAG TTGTGGA TATTGAAGTTTGAAG CT TTCATCTA
ATGCACTGGATGGGATTGGA AACACCT ATGACTTTAGACTTC GA GGGTAGGT
AGTCTTCAGATTTCAGTAGG TTTGGG T AGGTTA ---------
GTTTTCCACAA
GAM4429 10859 GTGGCTCGACTCTTGACCAT - AC- CT C-- GAGGATG
GGCTGGGGTTCCTGAGGATG GTGGC TCGACTCTTG CATGG GGGGTT CT
AGCTAAACCCTTTCCATGTA CACCG AGTTGGGGGT GTACC TCCCAA GA
CTGGGGGTTGAGGCCAC G CAT TT ATC -------
GAM4432 9931 CAACAGGTGCAAGTGTTAAA AGG A AAA ----- - GA AAAGCCTCC
GGGTATGATCCTTCAGTGGA CAAC TGCA GTGTT GGGTATG ATCCTTCAG TG AC
ACAAAGCCTCCGTGTCACCT GTTG ACGT CACGA TCCGTAC TAGGGAGTC AC TG
GAGGGATAGCAACATGCCTA AGA - ACA AACGA C TG ---------
CAAGCACTGCAAGAGTTG
GAM4446 10969 TCCCACAGTCGGGAGGAAAA --- G AA TC TTGTT
GAAAGAAGACTCTGTTGTTC TCCCACAG TC GGAGGAAAAGA GAAGAC TG
ATTGTTTTTATCTTTTTCTC AGGGTGTC AG CCTCTTTTTCT TTTTTG AC
CAGATGCCTGTGGGA CGT A A- TT -----
GAM4448 9953 CACTTTCATGTCTGCCTTCT C - TCTTTGC AGGTG T TAT A CTTTGGA
TTGCTGGAAGGTGCCTCCCT CA TTTCAT GTCTGCCT TGGA CC CCC TCCAC GA
ATTCCACAGACTTTGGATCA GT AAAGTA CAGACGGA ACCT GG GGG GGGTG CT
GTGGGTGTGGGGGAATCCAA - C ------- AA--- - TGT A -------
GGCAGACCATGAAATG
GAM4459 10240 GAAGAGGCCTTTACTCCTGT GGC---- -- TT -- C - ------ TCTG AG
TTTCTTCCATTCTCACCCCT GAAGA CTTTACT CCTGT TCT TC ATTCT CAC CCC
TTTCTGCC
CTGTTTCTGCCAGAATTGTG CTTCT GAAGTGA GGACA AGA AG TGAGA GTG GGG
AAAGACGG
ACAGCAGGGCAGAAAATGGG AAGAACA TG T- AC T C CTTTTC TA-- --
CTTTTCGTGCAGAGTTGACA AA GACA
AGATACAGGGTAGTGAAGAC TTGT
AAGAATCTTC GACG
-- ----
GAM4516 10651 GGAGACGAACACATACACAG A AACACATACA A AGA A GCA--- AT- GATTC

AAGATTCAGACACACTTGCA GGAG CG CAGA GATTC CAC CTT ATGT TGCTGGG
ATGTATTGCTGGGGATTCTC CCTC GC GTTT CTAAG GTG GAG TACG ACGACCT
CAGCATTGGCATGATGGAGA C CA-------- A AG- G AGGTAG GTT -----
GGGTGGAGAATCATTTGACC

GCCTCC
GAM4538 10975 TCCCTCCTGTGTCCCAAAAC - G AAACGAAA CCTATA A G TTCCAGAAT
GAAAACACTCCTATATTTTG TC CCTCCT TGTCCCA ACACT TTTTGT GC CC
TAGCGCCTTCCAGAATGGGG AG GGAGGA ACAGGGT TGTGA AAGGCG CG GG
CAGCGGAAACTAGTGTTGGG C A -------- TCA--- A G ---------
ACAAAGGAGGCGA
GAM4544 10926 TATGAACTGGCCACTTTTCA G A C AA-- G TG CCAGC
GATGAAACCTGGTGGGCCAG TATGAACTG CC CTTTT AGATG ACCT G GG
CTCTGTGGGGTGATGCATTT GTACTTGAC GG GAAAA TTTAC TGGG T CT
AAAAGGGCAGTTCATG - - - GTAG G GT -----
GAM4557 11230 TTAGCACCTGCCTATATTAC T - - ATATTACA CA GA TT C- G
ACAGTGAACGAA
ATTCATTTTGATGGTTTGTA T AGC AC CTGCCT TT TTTT TGGT GTATCT AAA GAGT
TCTCAAAGGAGTACAGTGAA G TCG TG GACGGA AA AGAA GCCA CATAGA TTT TTCA
CGAAACTTGTTTAAAGATAC T G A GAAGAG-- AA AG -- AA G ----------
ACCGGAAAGAAAAAGAGAAG
AGGCAGAGTGGCTTG
GAM4561 9992 CCACACCAGAGGCTGTGACC ---- AG-- TG CTA- - --- ACA--- T CCC
ATGGCTAGTAGACAGTGGCA CCAC ACCAG GC TGACCATGG GTA GACAGT GGCA TAG
CATC
ACATAGTCATCCCCAAGATG GGTG TGGTC TG ACTGGTACT CAT CTGTCA TCGT ATC
GTAG
CTAATCTTCTGCTGGAACTG TGTT CAAA TA ATTG A AGG CTTCTA - ---
TCATACGTTATCATGGTCAA AA
TGTAAACCTGGTTTGTGTGG

--
GAM4571 9771 AGTTCTGCAGGGCTGCTGCC T- G T CAA TT TAGCTGTATTC
TCAACATTTTAGGTTCTGAT AGT CTGCAGG CTGC GCCT CATTTTAGG CTGA
AGCTGTATTCTCAGTCCTGG TCA GACGTCC GATG TGGA GTGAGGTCC GACT
AGTGACAGGTGTAGCCTGCA TT - - CA- T- ----------
GTTACT
GAM4633 11142 TGCATTACCCTCCCCAACTT AT CCTCCC TT AT T------- GCAG
AAAATCTTTTGATAACCCAG TGC TAC CAAC AAA CTTT GATAACCCAG
GCAGCTGGGTTATCCCCAAT ACG ATG GTTG TTT GAAA CTATTGGGTC
TTAAAGTCTTTTTGTTGTAG GT TCGAT- TT CT TTTAACCC ----
CTGTATGGCA
GAM4650 10553 GGAGAATCACTTGAACCCAG AATCA GA-- AGG GT A CAAGATCGT
GAGGTGGAGGTTGCAGTGAG GGAG CTT ACCCAGG TGGAG TGCAGTG GC
CCAAGATCGTGCCACTGCAC CCTC GAG TGGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGTGATAGAGC AGAAC ATAG G-- -- - ---------
AAGACTCC
GAM4656 10921 TAGTGACAAGGGCATCCCAA T A- C CCC A G A-- A T TGTGC
GGCACTTGCCCAGAGCTGCA TAG GAC AGGG AT AAGGC CTT CCC GAGCTGCAG GT GTG

GAGTTGTGTGTGCCATACCT ATC TTG TCCC TA TTCCG GAA GGG CTCGGCGTC CA TAC

GCGGCTCAAAGGGAAGGCCT T AG C TC- - - AAA - - -----
TCTATCCCCTGAGTTTCTA
GAM4671 10032 CCCTGCCGCAGGAGAGCCAC CT - G CAC------ - A C- A ATCGT

TTTCAGAGATGCCCTGAGTG CC GCCGCAGG A AGC TTT CAG GATGC CTG GTG
ATCGTCACCAGCTGCATCCT GG CGGTGTCC T TCG AAA GTC CTACG GAC CAC
GCAAACTTCATCTTGCTGTC TT C G TTCTACTTC C - TC - -----
CCTGTGGCTTGG
GAM4685 11293 TTTTCAATTTTTAAAAATTA T-- AATTAGATTTATTGC A CTCA- --------- A T
GATTTATTGCAGACTGGCCT TTTTCAA TTTTAAA AG CTGGC AGCTCC CAG CTA
CAAGCTCCCAGACTATATTT AAAAGTT AGAGTTT TC GACCG TTGGGG GTC GAT
TTTAGCTGCATTATTTAGGG TTC ---------- - TAAAG ATTTATTAC - -
GTTGAAATGCCAGCTTTTGA ATTTTT
GACTTTTGAAAA

GAM4690 10888 GTTTCCCACTTTTCTCCCAT CTC A TCA T CCATAAAAAGC GTGA
CTGTCATTTTTCTCTTTCCA GTTTCCCACTTTT CC TCTG TTTTTC CTTT TAATG
TAAAAAGCTAATGGTGACGT CAAGGGGTGGGAA GG AGAC AGGAAG GAGA ATTGC

TATCAAAGAGTGAAGGAGTC TC- - TG- T AACT------- ----
AGAGGCTAAGGGTGGGGAAC
GAM4707 10352 GAGGCAGGAGAATCGTTTGA CA AA GAA--- AGGC - T T CCGAGAT
ACCTGGGAGGCGGAGGTTGT GAGG GGAG TCGTTT CCTGGG GGAG GT GTG TGAG

GTTGAGCCGAGATCTCGCCA CTCT CCTC AGCGAG GGATCC CCTC CG TAC GCTC
TTGCACTCCAGCCTAGGCAA A- AA AACAAC GA-- A T C -------
CAAGAGCGAAACTCCATCTC
GAM4709 10157 CTGCAGTGGTGATGTGTTGT T ---------- T C ACACCCCACTA
CACTTCAGGACACCCCACTA CTGCAG GGTGATG TGTTG CA TTCAGG
CCTGAATTGCAGCAGTGTTG GACGTC TCACTAC ACGAC GT AAGTCC
CGAATCATCACTCTGCAG - TAAGCGTTGTG - T ----------
GAM4733 9593 AAACGTGTGGTGATTGATGC G ATTGAT TCAT C TTGCCC
TTTCATGGACTCTGTTGCCC AAACGT TGGTG GCTT GGACT TG
CAAGTCCCCAAGCCTTGTAC TTTGCG ACCAT CGAA CCTGA AC
CAGCGTTT - GTTC-- CC-- - ------
GAM4738 9729 AGGCTGTATGCTGTTAATGC T-- C A T- CCTC
TAATCGTGATAGGGGTTTTT AGGC GTATGCTGTTAATGCTAAT GTG TAGGGGTT TTG

GCCTCCAACTGACTCCTACA TCCG TATGTGACAATTACGATTA TAC ATCCTCAG AAC
TATTAGCATTAACAGTGTAT TAG - - TC ----
GATGCCT
GAM4769 10176 CTGGGATTACAGGCACCTGC TA CACC CT A TTTT ATTTTTAATA GGG
TGCCAAGTCTGGCTAATTTT CTGGGAT CAGG TG GCCA GTCTGGCTAAT GT GAGAC
TGTATTTTTAATAGAGACGG GACTCTA GTCC GC TGGT CGGACCGGTTG CG CTTTG
GGTTTCGCTATGTTGGCCAG -- TCAA TC - TAT- ---------- ---
GCTGGTCTCGAACTCCTGAT
CTCAG
GAM4796 10896 TAAAACTCACCATCAAATAG TCAC C A T TTATT ---------- A AA
ATGTAATCTTATTAATTACA TAAAAC CAT AAAT GA GTAATC AATTAC ACATTTTGT TTTT
TTA
CATTTTGTATTTTAATTATT GTTTTG GTA TTTA CT CATTAG TTGATG TGTGGGACA AAGA
AGT
TCAAGGAGTGAAGAAAACAG TTAC - - - TC--- TTTTTGTTTT A --

GGTGTTTTTGTTTTTGTAGT CAAG
TCTGATTACTCATTTATGCA TTT
TTGTTTTG GAG

GAM4800 10690 GGCCACTTCCACCTTCCAGG - C--------- ---------- TGACC
GCATAGGTGACCCCTGTGGA GG CCACTTCCAC TTCCAGGG CATAGG
AAACAAGTACCCCTGGAACA CC GGTGGAGGTG AAGGTCCC GTGTCC
TCCTAGAAGTGGAGGTGGAC A AAGATCCTAC CATGAACAAAAG -----
C
GAM4803 11165 TGGAGGAATGGGAGCTATGG ATG- T CA AC G C GA CCAGGATA
GCAAATACTGGGAGCTGGCT TGGAGGA GGAGCTA GGG AAT TGG AG TGGCTG TG
GGATGCCAGGATACAGCAGC ATCTCCT CTTCGAT CCC TTA ACC TC ACCGAC AC
CATCTGCCATCATTACCCTA AGGA - A- CT G T G- --------
GCTTCAGGATCCTCTA
GAM4814 10992 TCGCTCTTTGTTGCCCAGGC CTT TT C-- -- - A ATCT
TAGAGTGCAGTGGCATGATC TCGCT TG GCCCAGG TAGAG TGCAGTG GC TG
TCGGCTCACTGCAACCTCTG AGCGA AC TGGGTCC GTCTC ACGTCAC CG GC
CCTCCTGGGTTCAAGCGA --- T- TCC CA T - ----
GAM4821 10930 TATTATTGGGCACCTGTTAT A CAC TA TGTC--- AC- -
ATAACAACAGCAAACA
GTGAGACACTGTCCTAGGCA TATT TTGGG CTGT TGTGAGACAC CTAGGC TGTG GG

CTGTGGGATAACAACAGCAA ATAG AATCC GACA ACATTTTGTG GGTCCG ACAC CT
ACACTTCACACAACAGCCTG A TC- -- TCCTTCC ACA A ----------
GCCTTCCTGTGTTTTACAAC CT
AGCTCCTAAAGATA

--
GAM4844 11226 TGTTGATGGTCTCATAACTG T- ACTGA - AA TTGTATAC
AATATATTAAAAACTTAAAT TGTTGATGG CTCATA ATATA TTA AACTTAAA
TGTATACTTTAAGTTGGTGA ATAACTATT GAGTAT TATGT AGT TTGAATTT
TTGTATGATATATGAGTTTT TT ATAG- T GG --------
ATCAATA
GAM4895 10116 CTCGTGGCTGCTGCTGCTCC GTG CT ---- - C CT TCC-- T GC -- TTCAT
TGCTCTCCCTCTCCCTCCTC CTC GCTG GCT GCT CCTG TCTCC C CTCC CCAG CAC GGAT

CAGGCCACGGATTTCATGTC GAG TGAC TGA CGA GGAC AGAGG G GGGG GGTC GTG
CCTG
CCTGTGACTGGTGGGGCCCA ACG CT ACTC A - AG TACCC T A- TC -----
TGGAGGAGACAGGAAGCCTC
AAGTTCCAGTGCAGAG
GAM4904 10792 GGTGGCACTGGCAGGATGTG T C - AG - TGA G A TTCTC
CCTCCTGAGGTGTGTCGAGT GG GG ACTG GC GATG TGCCTCC GGTGT TCG GTG
GTTCTCTACATGGGGCACTG CC CC TGAC CG CTAC GTGGAGG TCACG GGT CAT
TGGAGGTGTCATCGGCTCAG - T T G- T TG- G A -----
TTCCCC
GAM4913 9599 AAATCTCTCAACCACTGCAA ------ CT AA T ---------- T CGCAT
GCTTTTAAAAGTCTGGCGCA AAATCTCTCAA CCA GC GCT TTA AAAGTC GG
TCTTGACTTTCTTTTCACCT TTTAGAGAGTT GGT CG CGA AAT TTTCAG TC
ATAACAGCCAGCTTGGATTC TACTTA T- AC C ATCCACTTTTC T -----

ATTTGAGAGATTT
GAM4932 11218 TGTGGAGAATTAAAAAGGGT T ATTAA -- T CATTTATAGA TGTATTGGGT
AGTGAGGCTGGCATTTATAG TG GGAGA AAAGGGT AG GAGGCTGG ATCTGGCTTTCT

AATCTGGCTTTCTTGTATTG AC CCTCT TTTTCCG TC CTTTGACC TAGATCGAAAGG
GGTGGAAAGCTAGATGAAAC T C---- AC T AAAG------ ----------
CAGTTTCTCTCAGCCTTTTC
TCTCCTCA
GAM4946 10922 TAGTGAGATGAACCCGGTAC T- T ACCC TA TC -- A ATC - TCT T AC
CTCAGATGGAAATGGAGAAA TAG GAGA GA GG CC AGATGG AAATGG GAA GC CTG TCTGCG
CTCTC
TCGCCTGTCTTCTGCGTCTC GTC CTCT CT CC GG TCTACC TTTATC CTT CG GGC AGATGT
GAGGG
TCACGCTGGGAGCTGTAGAC TC - ---- TC T- GG - GT- A C-- C --
CGGAGCTGTTCCTATTTGGC GCT
CATCTTGGCTCCTCTCTCCT
CTG

GAM4969 10491 GCTGGATGATGAATCCTTGT GA AA C TT CA CAAAAAGAATGTTGCATG
ACCATC
TTTTCAGGTGGCTCCAAAAA GCTGGAT TG TC TTG TTT GGTGGCTC TGTTCAG
GAATGTTGCATGTGTTCAGA CGATCTG AC AG GAT AAA CCACCGAG ACGAGTC
CCATCCTGAGCAGAGCCACC TG -- T TT -- ---------- ------
AAATTTAGTGACAGTGTCTA
GC
GAM4971 10965 TCCAGACACTTTCTTCCTTC ACACTT C GAAC - ACA-- GTAAGAA
AGTTCAGGGAACCCTCAATA TCCAG TCTTCCTT AGTTCAGG CCT CAAT CA
CACAGTAAGAATGAAGAGGT AGGTC AGGAGGAG TCGAGTCT GGA GTTG GT
TGCAGGTCTGAGCTTGAGGA ------ T ---- C GAGAA -------
GGACTGGA
GAM4975 9993 CCACAGTGGGGGTGCCCGGG A TG TGC G CCCACT--- CT A CAGC
CTGGGTCCCACTGGGGAAGC CCAC G GGGG CC GGCTGGGT GGGGAAG CA GG
TCAAGGCAGCCCTGGCCTTT GGTG C CCCC GG CTGACCCA CCCTTTC GT CC
CCCTCATTCTCCACCCAGTC - GT --- A CCTCTTACT CG - ----
AGGCCCCTGCGTGG
GAM4986 9981 CATCAAAGAATAAATAAGCT A AAA ---- C C A TG CA- T TG TT AG TTA
GCTCTAATTGCCAAGAATTC C TC GAATAA ATAAG TG TCTA T C AGAAT CACATG G GTATGC
CA
ACATGTGGTTGTATGCAGCA G AG CTTGTT TGTTC AC AGGT A G TCTTA GTGTAC C TATGTG
GT
TTACTGGGAAATTGAAGTGT - GTC TGAA - - - GT TCG - GT -- AA ---
ATCTGCATGTGATTCTGCTG CTGGGAAAT
TGATGGACACTTGTAAGTTT
GTTCCTGGAG

GAM5000 10518 GGAAACTGGGGCCTTCTTTG A TG CT--- G A GA ACAT
AGTACTAGTGAGTAAGACAT GGA AC GGGCCTT TT AGTACT GT GTAAG
TTTGCAACAGTGCTGAGTAT TCT TG CCCGGAA GA TCGTGA CA CGTTT
GAAAGGCCCTGGTCTCT C GT AGTAT G - A- ----
GAM5008 10156 CTGCAGGGCTGCTGCCTCAA G T CAA TT TAGCTGTATTC

CATTTTAGGTTCTGATAGCT CTGCAGG CTGC GCCT CATTTTAGG CTGA
GTATTCTCAGTCCTGGAGTG GACGTCC GATG TGGA GTGAGGTCC GACT
ACAGGTGTAGCCTGCAG - - CA- T- ----------
GAM5011 10837 GTCTTCATATCTCCAGGTTC CA- C CT AATTACCTCCCCCATCTG
TGCTGGAGCAATTACCTCCC GTCTT TATCTC AGGTTCTG GGAGC
CCATCTGGCTCCTTAGGACC CGGAA ATGGAG TCCAGGAT CCTCG
TAGAGGTAGTAAAGGC ATG A T- ----------
GAM5035 10820 GTCCACTGGCCCTTCTTGTC TC C- T TAG--- T ACA- T TCA AATCACCCA
TTAGGTCCTCACACACAGCT G CACTGGC CTTCT GTCT G CCTCAC CAGC CTGC GTTC

CTGCTCAGTTCAATCACCCA C GTGACTG GAAGA CAGG C GGAGTG GTCG GACG TAAG

GAATGCAGGCTGGTTGGTGA CT AA - TTTAAA - GTTG - --- ---------
GGCAAATTTGGACAGAAGAA
GTCAGTGTCC
GAM5048 10510 GCTTGCTGGGTTTACAGATG TG -- ACAGA- AAAGATCT AAATTAAAAATA
GCAAAGATCTGGCAAATTAA GCT CT GGGTTT TGGC GGC
AAATAGCCTTAGGCCAAAGA CGG GG CCCAAA ACCG CCG
TCAAACCCAAGGTGGGC GT AA CTAGAA GATT---- ----------
GAM5058 10645 GGAGAATTGCTTGAATCCAG AA TG GA-- AGGCA GT A - AGAT
GAGGCAGAGGTTGCAGTGAG GGAG T CTT ATCCAGG GAG TGCAGTG GC TG
CTGAGATCATGCCACTGCAC CCTC A GAG TGGGTCC CTC ACGTCAC CG AC
TCCAGCCTGGGTGACAGAGT AC GT ACAG GAC-- -- - T ----
GACACTCC
GAM5082 10778 GGTATACTTACTAGCATATT - AGAGTG
ATATAGCTCTAAGAGTGTAG GGTATACT TACTAGCATATTATATAGCTCTA
AGTTATATGATGTGCTAGTG TTATGTGA GTGATCGTGTAGTATATTGAGAT
AAGTGTATT A ------
GAM5085 10724 GGGACATCAAAGAATAAATA TCAAAG AA C C A TG CA- T TG TT AG TTA
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CA
ATTCACATGTGGTTGTATGC CCTTGT TTG TGTTC AC AGGT A G TCTTA GTGTAC C TATGTG
GT
AGCATTACTGGGAAATTGAA ------ AA - - - GT TCG - GT -- AA ---
GTGTATCTGCATGTGATTCT CTGGGAAAT
GCTGTGATGGACACTTGTAA
GTTTGTTCC

GAM5090 10160 CTGCCCCCGCCCTCTGGACC GC C C AC----- T----- AG TTTGT TTCCT
CGAGTGACTCAGGCCTTTGT CT CCC GC CTCTGG CCGAG GACTC GCCTTTG CC
TTGTCCTTCCTGGTAGAGGC GG GGG CG GAGGCC GGCTC TTGGG CGGAGAT GG
GGGTTCCCTCCCTCGGCAAG TA T T GTAGAAC CCTCCC -- ----- -----
ATGCCGGAGTGCTGGGATGG
GAM5127 10734 GGGAGGAGAGAAGGAACCAT ---- G ACCAT AT AAA A A GA AGGCCTGG
AGATTCTGAGAAACACACCA GGGAGG AGA AAGGA AG TCTGAG CAC CC GGAT CT
GGATGACTAGGCCTGGAGGA CCCTCC TCT TTCTT TC AGACTC GTG GG CCTG GA
GTCCAGGGTGGGCCTCAGAC ACGG G CAC-- CC CGG - A AG --------
CCTCACTTCTTGTCTGGCAC
CTCCC
GAM5142 9751 AGTCTCACTCTGTCACCCAG ACTC TCA -- T -- -- TGATCT

GCTGGAGTGCAGTGGCATGA AGTCTC TG CCCAG GC GGAG TGCAGTGG CA
TCTTGGTTCACTGCAACCTC TTAGAG AC GGGTC CG TCTC ACGTCACT GT
TGCTTCTGGGATTCAAGAGA A--- TTA TT - CA TG ------
TT
GAM5209 10525 GGAAGCCTTCCCTTACCTCA CTTC- TT - TTGAG C TG CTGT CT AT- TAT
GCCTGGTTGAGGGCCCCCTG GGAAGC CC ACCTCAG CCTGG GGCCC C GG TTTCA
GGTTG GG
GGCTGTTTTCACTGGTTGAT CCTTCG GG TGGAGTC GGACC CCGGG G CC GGAGT CCGAC
CC
GGTATCTGATCCCTTCCAGC TACTT TC T TGA-- A GT TT-- -- CTT ---
CTGAGGTTCCTGGAGGGCCA CTGATC
GTCCAGGTCTGAGGTCTGGT
TCATGCTTCC

GAM5217 9631 ACACTGGACAGATGGATGTT GA GGAT A- G- GCAG TACT
GATGAGCTTGTGTGCAGCAG ACACTG CAGAT GTTG TGAGCTT TGTGCA TTC
TTCTACTGGAAGTATGTACA TGTGGC GTTTA CGAC ACTCGGG ACATGT AGG
AGGGGCTCAGCCAGCCAATT AG AC-- CG GA ATGA ----
TGGACGGTGT
GAM5222 9898 ATATGCTGAGTTGGGACAGG TG T C A-- AA -- AACCC GACAACAGCGACA
AGCTAAGGATAGAGGTGAGG ATATGC AG TGGGA AGG GCT GGAT AGAGGTGAGGA GCA

AAACCCGCAGACAACAGCGA TGTGTG TC ACCTT TCC CGA CCTG TTTCTACTCCT CGT

CATGCTCCTCATCTTTGAGT TG - - AAG C- AG ----- ----------
CCCAGCGAACCTTTCCACTG
TGTGTGT
GAM5254 11132 TGAGTGTATGTGTGAGAGAG T - A TTATGTTTATCAC-- TTCCCATTGTTTCATT

AATGTTATGTTTATCACTGA TGAGTG ATGTGTG AGAGAG ATG TGAG
GTTCCCATTGTTTCATTCTC GCTCAT TACACAT TCTTTC TAC ACTC
ATAGCACTTATTTCTTCATA T A A TTCTTTATTCACGAT ----------
CTTTCTATACACATTTACTC
G
GAM5266 10941 TCACTCTGTTGCCCAGGCTG C TT --- C -- T AATCTTG
GAGTGCAGTGGTGCAATCTT TCACT TG GCCC AGG TGGAG TGCAGTGG GC
GGCTCACTGCAACCTCCACC AGTGA AC TGGG TCC ACCTC ACGTCACT CG
TCCCGGGTTCAAGTGA - T- CCC - CA - -------
GAM5270 10016 CCCAGACAGTGCCCGTTTTG A -- - TG ATG AC T CCAAATGCCT
AGATGTGACCTGGTGGCCAC CCCAG CAGT GCCC GTTT AG TG CTGG GGCCA
CAAATGCCTTGGCCTCAGTG GGGTC GTCA CGGG CGAA TC AC GACT CCGGT
CAAACTAAGCAGGGCACACT C CA A -- AA- GT - ----------
GCCTGGG
GAM5272 10727 GGGACTTAACTGAGAGGATC ----- - GAT A - C CCCTAAGAGCATGTCAT
TGAGTAGCAGACACCCTAAG GGGACTT AACTG AGAG CTG GT AG AGACA
AGCATGTCATTGTCTTCTCA CCCTGAG TTGAC TCTC GAC CA TC TCTGT
CCAGTTACTCTCCAGTTGGC ATCGG C ATT - C T ----------
TAGAGTCCC
GAM5278 10980 TCCCTTTTATTAACCATCTT T TA AA TTC A- A- AAGTAGAAAAGAAACA
CCCTTTCTCGAGTATACACA TCCC TT TT CCATCTTCCCT TCG GTAT CAC

AGTAGAAAAGAAACAGTGAA AGGG AG GA GGTGGGAGGGA AGC CATG GTG
GTACCCCGATAGGGAGGGTG T GA GG T-- CC AA ----------
GGGAGAGGATGGGA
GAM5292 11143 TGCCCTGTTGACCAGAATTT TGT--- AGAATT -- TAC CTGATTA
GTTAGATTGCTATTACAATG TGCCC TGACC TGTTAG ATTGCTAT AATG
CTGATTATATTTTATAGCAA ACGGG ATTGG ACAGTC TAACGATA TTAT
TTACTGACATAAGGTTATAC TTTCAT AAT--- AT TT- -------
TTTGGGCA
GAM5324 10951 TCACTTTGGTGATATCATGG C AG T C- TGATG
GAAGGTGTACTTCCGGTGAT TCA TTTGGTGATATCATGGGA GTG ACTTC GG
GCCTAGAGGTCACGTCCTGT AGT GGATTACTGTAGTGTCCT CAC TGGAG CC
GATGTCATTAGGCTGA C G- - AT -----
GAM5329 11139 TGATTCAAAGCAAGATGGTA AA- GA-- G A TG AGAGGA GT AGATGA
GCATTGGAGAGGATGAGATA TGATTC AGCAA TG TAGC T G TGAGATATG C
TGGTCAGATGAGGATATATT ACTAAG TCGTT AC ATCG A T ATTTTATAT G
TTAAAAGTTGAGCTAACAGG GAG TAGG A - GT GAAA-- AG ------
ATTTGCTGAGGAATCA
GAM5340 9709 AGGCACACACGCATGGTTTT C A ATG- T-- T ----- ATT CC- ACAG
CTCTTTTATATGCTAGATTT AGG AC CACGC GT TTCTCT TTATA TGCTAG TCAT CTG
CATCCCTGACAGCAGAAAAT TCC TG GTGCG CG AAGAGG AGTAT ACGGTT AGTA GAC

GATTGGCAATGGTTATGACG - - ATAA TAC C TGGTA --- AAA ----
GAGAACATGCAATAGCGTGG
TCCT
GAM5342 9601 AACCTCCAGCACACCACCAA C A CCA T--- - ATAC T TCTG
TGAATAGCAGTAATACCAGC AACCT CAGC CA CCAATGAA AGCA GTA CAGCA AATTG

ATAATTGTCTGCAGTTCTGC TTGGA GTCG GT GGTTATTT TCGT CAT GTCGT TTGAC
TGAGATACGTGCTCTATTTT T - TC- TATC G AGA- C ----
ATTGGCTTGGCTGTAGGTT
GAM5354 11223 TGTGTCAGTCAGGATAGGTC C - TCAACT ACAAA-- - CAAATCTC
AACTGCTGTAACAAACAGCC TGTGT AGTCAGGA TAGG GCTGTA CAGCC CT
CTCAAATCTCAGTGGCTGAA ACACA TCGGTCTT GTCT CGACAT GTCGG GA
CACCATACAGCTCTGCTTCT C C ------ ACCACAA T --------
GGCTCACACA
GAM5370 9902 ATCCTGGGAAGGACCCTACC TGGGA C - TCT CCAACCAT
CAGTCATTTTATCTACCCCA ATCC AGGAC CTAC CCAGTCATTTTA ACC
ACCATGGTTAAAGTGGCTGG TAGG TTCTG GGTG GGTCGGTGAAAT TGG
AGTGGAGTCTTGGAT ----- A A --- --------
GAM5371 9757 AGTCTTGCTCTGTCACCCAG -- CT TCACCC T -- T ATCTT
GCTGGAGTGCAGTGGTGCCA AGTC TTG CTG AGGC GGAG TGCAGTGG GCC
TCTTGGCTCACTGCAACCTC TTAG AAC GAC TCCG CCTC ACGTCACT CGG
CGCCTCCCCAGTTCAAGTGA TG TT CCC--- - CA - -----
TT
GAM5374 9987 CATTAAAACTCACCATCAAA TTA TCAC C A T TTATT ---------- A AA
TAGATGTAATCTTATTAATT CA AAAC CAT AAAT GA GTAATC AATTAC ACATTTTGT TTTT
ACACATTTTGTATTTTAATT GT TTTG GTA TTTA CT CATTAG TTGATG TGTGGGACA AAGA

ATTTCAAGGAGTGAAGAAAA --- TTAC - - - TC--- TTTTTGTTTT A --
CAGGGTGTTTTTGTTTTTGT CAAG

AGTTCTGATTACTCATTTAT TTATTT
GCATTGTTTTG AGTGAG

GAM5385 9977 CAGTGGGAAGGGGGGCCGAT A ATA AC G- AGTAG
ACACTGTACGAGAGTGAGTA CAGTGGG AGGGGGGCCG CACTGT GAGA TG
GCAGGTCTCACAGTGAACCG GTCATCC TTTCTCTGGC GTGACA CTCT AC
GTCTCTTTCCCTACTG C CAA -- GG -----
GAM5415 10133 CTCTTGCCCAGGCTGGAGTT - CCC T T TATG AACTC AGCCTCAAACACC

CAGTGGTATGATCACAACTC CT CTTG AGGCTGGAGT CAG GG ATCAC TCCTA
TCCTAAGCCTCAAACACCTG GA GAAC TCCGACTTCG GTC CC TAGTG AGGGT
GGATCAAGTGATCCTCTGGC T CC- - T ---- AACT- ----------
TTCAGCCTCCCAAGTAG
GAM5422 10860 GTGGGAGGAGGACTGGCAAA A C CAA A A A A TG CTTG
AATATGAGAGTAGGAGTTTG GTGGG GGAGGA TGG AAAT TGAG GT GG GTT GGCT
GGCTCTTGAGCTTGGGCCTG CACTC CTTTCT ACC TTTA ACTT CG TC CGG TCGA
GCCTTCAAATTTCCACTCTT A C --- A C G - GT ----
TCACTCAC
GAM5444 10242 GAAGGGTACCTGCTGGAGAC TG GG CCTGT TT TGGGTT
CTGTGTGGTTTGTGGGGTGG GAAGGGTACC CT AGA GTGGT GTGGGG
GTTTCTTATATCACTGAATC CTTTCCGTGG GA TCT CACTA TATTCT
TAAAGTGGGTGCCTTTC GT AA AAGT- -- ------
GAM5454 10545 GGAGAAGAGGTCTTGCATAC G GT GCATA C T --- AT-- TGTGA
CAGCACAGTGGATGGGGAAT GGAGAA AG CTT CCAGCA AG GGA TGGGGA GG
GGTGTGACCTCTGTCCCTGC CCTCTT TC GGA GGTCGT TC TCT GTCCCT CC
TCTCTTCTCTGCTGGCTTAA A TG ATTC- C T CTC GTCT -----
GGGTCTATTCTCC
GAM5486 10210 CTTGAGAAAAGACAACTAGT G AA- CTAGT A AA-- GAGAA G AAA--
GTAGATGAG
ATTTGAGGAAGGTGTGAGAA CTT AGAA GACAA ATTTG GG GGTGT AT AGCCT GAG
ATGAGCCTAAAGAGGTAGAT GAA TCTT TTGTT TGAAC TC CCATA TA TCGGA CTC
GAGACTCAAAGGAGGCTGAT G ATA TT--- A GACA GAAA- G GGAAA ---------
AAAGATACCACAGCTACAAG A
TTTTTGTTATATTCTGAAG

-
GAM5498 9766 AGTTCACAGTGGCTGAAGCT T AAGCT CCATAAGACCCT
GTTCCCATAAGACCCTGAAT AGT CACAGTGGCTG GTTC
CTAGCAGCCACTGTGTACT TCA GTGTCACCGAC TAAG
T GATC- ----------
GAM5512 9703 AGGAGGGAAAGGCCCAGGAG GA- AAAG CCA- G AAGGCAGA G GGGA
GGGGAGAAAGGCAGACTCAG AG GGG GC GGA GGGGAGA CTCA CCA
CCAGGGATGGGTGAGGGTTT TC CCC CG CCT TCCCTTT GAGT GGT
CCCTGTCCCAAAGCAAGACC GAA AGAA AAAC G GG------ G ----
CAAGCT
GAM5514 10801 GGTTGCCGTGATTGAGGAGG - - - A A CTAC- G GCAGAGA
TGCTACCAGCGTCTGCTGGG GGTTG CC GTG ATTG GG GGTG CAGCGTCT CTGG
CAGAGACCAGGGATGCTGCT CTAAC GG CAC TAAC CC CTAC GTCGTAGG GACC
CCACATCCCACAATGCACAG A A G A - ACCTC - -------
GACAATC

GAM5526 10393 GAGGGCTTTAGAAATGCTGT AGAA - AGA C C-- CCAACAAAATCAGAC
GCCAGAGCTGCACCCCAGAC GAGGGCTTT ATGCTG TGCC GCTGCA CC AGA
CAACAAAATCAGACTCTCCA CTTTCGAAA TATGAC ACGG CGGCGT GG TCT
GGATGCGGCCAAGGCATCAG GGTG T AAC A ACC ----------
TATGTGGAAAGCTTTC
GAM5560 11007 TCTATATGAGACTAACTAAG A ACTAACTA-- TT CC TG - ------ TAAAAT
GTATTTGCCCCTTGGAGCTT TCT TATGAG AGGTA TG CCT GAGC TTTTATAG TCTT
TTATAGTCTTTAAAATGAGA AGA GTACTC TCCGT AC GGA TTCG AAAGTGTC AGAG
TAATGTCTGTGAAATGCTTT A ACAAATACGG C- A- TT T TGTAAT ------
TAGGACACTGCCTGGCATAA
ACACTCATGAAGA
GAM5597 9764 AGTGTTGGGTTGACTTGAAT --- TGA TGAT AGAA TC CTAGATTTGC
GGAGGTGATTGTTTTAGAAG AGTGT TGGGT CTTGAATGGAGG TGTTTTAGA GG AGAAGA

AAGGTCAGAAGACTAGATTT TTACA ACCCA GAGCTTATCTTC ATAAAGTTT CC TCTTTT

GCTTTTCTCTCCAATTTGAA AGG CAG TCC- AA-- TC ----------
ATACCTCTTCTATTCGAGGA
CACCCAGGAACATT
GAM5615 10117 CTCTCACCCCTCTAGCCTTA AC-- T CTTAAA TCTAGA---- TG ATG GAATG
AATCCAGAATCTAGACTGAA CTCTC CCCTC AGC TCCAGAA C AAT GACT
TATGGACTGAATGGGTCAGA GAGAG GGGAG TCG GGGTCTT G TTA CTGG
TTTGGGGAAATGTGTTTCTG ACCA - ACAG-- TGTGTAAAGG GT GA- -----
GGGACAGCTGAGGGACCAGA
GAG
GAM5617 10703 GGCTAAGAGTAACAGGTGCT TAACAGGT T CCA C-- C- TCTACCAATTT
GGAGCCAGACTTCCTGGGTT GGCTAAGAG GC GGAG GA TTCCTGGGTTCATAT CTGGT

CATATCCTGGTTCTACCAAT TTGATTCTC CG CCTC CT AAGGATTCAAGTGTG GACCA

TTACCAGCTGTGTGAACTTA -------- - TC- TAA TC ----------
GGAAAATTCCTCTCCGCCTC
TTAGTT
GAM5623 9692 AGCATATGACAGCAAGACAC T TG - TGGC-- GAAT--- TC TCA
TGGCCCTGGAATCCTCCGTG AGCA A ACAGCAAGA CAC CCTG CC CGTG
TCACATGTGGGCTGCTGACA TTGT T TGTTGTTTT GTG GGAC GG GTAC
GGAAGAATGTGCTTTTGTTG - GT C TAAGAA AGTCGTC GT ---
TTGTTGTT
GAM5640 9747 AGTATTATTAAGACTTTTCC TATT A GGTC T C GCTGCCTCTGA
TGGGTCTGGGCTGTGCCTGT AG ATTAAG CTTTTCCTG TGGGCTG GC TGTT
TGCTGCCTCTGAGACAAGTC TC TAATTC GAAAAGGAC ATCCGAC TG ACAG
AGCCTAATACAGGAAAAGCT TCT- - ATA- - A ----------
TAATTCTCT
GAM5653 10648 GGAGAATTTCTTGAACCCAG AAT-- TGAA AGG GT A - AGAT
GAGGTGGAGGTTGCAGTGAG GGAG TTCT CCCAGG TGGAG TGCAGTG GC CG
CCGAGATTGCGCCACTGCAC CCTC AAGA GGGTCC ACCTC ACGTCAC CG GT
TCCAGCCTGGGCAACAGAAC AGAAC CAAC G-- -- - C ----
AAGACTCC
GAM5654 9597 AAATACAAATTCCTGGGTCT A T C CTTG AAATC
CCTGGCAGACTTGCTAAATC AAATAC AATTCC GGGTCTCCTGG AGA CT

AGAATCTCCAGGGGATCCTG TTTGTG TTAAGG CCTAGGGGACC TCT GA
GAATTGGTGTTT G T - AA-- -----
GAM5657 10736 GGGAGGATCGCTTGAGCCTA G GA GA-- - TCAA C AGC AGAT
GGAGGTCAAGGCTGCAGTGA GG AG TCGCTT GCCTAGG AGG GG TGCAGTG TG
GCTGAGATCACACCACTGCA CT TC AGTGAA TGGATCC TCC TC ACGTCAC AC
CTCCTGCCTAGGTGACAAAG G AG ACAG G ---- - CAC ----
TGAGACTGTC
GAM5673 9761 AGTGGTAATGCCGTGTGTTG ATG T ------ A AA - GATC- TG G- AATT
ATAGAAATATGTAATCGATC AGTGGTA CCG GTGT TG TAG ATATGTA ATC TTTTCTT GTG
GC
TTTTCTTTGGTGGGCAATTA TTACCGT GGT CACA AC ATC TATGTAT TAG GAAAGGA TAT
CG
GCAATATTGAGGAAAGTTAA AAA C AAGTTC C CC G AAATT GT AA ----
AGATGTATGTATCCCTACCA A
CTTGAAACACCTGGAAATGC
CATT
-
GAM5691 10719 GGGAAAGGCCCAGGAGGGGG AAAG CCA- G AAAG AGA G GGGA
AGAAAGGCAGACTCAGCCAG GGG GC GGA GGGGAG GC CTCA CCA
GGATGGGTGAGGGTTTCCCT CCC CG CCT TCCCTT TG GAGT GGT
GTCCCAAAGCAAGACCC AGAA AAAC G ---- G-- G ----
GAM5697 9911 ATGAGTATTGATCTGTCCCA AT TCT GC C AGG GTTC
GCCTGTGCATTGCTCCGAGG ATGAGT TGA GTCCCA CTGTGCATTG TCCG CA
CAGTTCTGAGTGGATGATGT TACTCG ACT TAGGGT GACATGTAGT AGGT GT
ACAGATGGGATTCCTCAGCT -- CCT A- - GA- ----
CAT
GAM5703 10256 GACATGTCAAGGCAGGAGCC -- AA - CAT ATCGACCTTA AAGCTGGTG
ATCTGATCGACCTTAGACTT GACA TGTC GGCAG GAGC CTG GACTTGGC
GGCAAGCTGGTGGCTAAGTC CTGT ACAG CCGTC CTCG GAC CTGAATCG
CAGTGCTCACTGCCGACATC CT -- A T-- ---------- ---------
TGTC
GAM5728 10119 CTCTCATGCAGGCATGTGTG -- G GAG- C-- G G TGAG
AGCAGCTGCAGGTGTGTGAG CTCTCAT GCAGGCAT TGT CAG TGCA GT TG
CAAATGTGCATCACTGGGGA GGGAGTA TGTCTGTG ACA GTC ACGT TA AC
ACAGGTGTCTGTGGATGAGG GG G AGGG ACT G A ----
G
GAM5744 10924 TAGTGTTCACATGTTGCTCA T A ----- CTC T A GATAAATCATTTAA - CT T
GTTTTGCTAACTGATAAATC TAG GTTC CA TGTTG AG TTTGCT ACT TC CTCTT TCATA G
ATTTAATCCTCTTCTTCATA ATC CAAG GT ACAAC TC GAACGA TGG AG GAGAA GGTGT
T
TGTATGAGTACTATCTTATA - A CCCAG C-- - A ---------- T CT C
TCTGTGGTCAAGAGTGAGGT TACTAT
AAGCAAGCTCCAACAGACCC TATGAG
TGAGAACCTA ATATTC

GAM5749 9769 AGTTCCTATGTGCCCCACAG C- - CCA----- CCC C GATG
GAAAGCGCCCTTAACCACTG AGTTC TAT GTGCC CAGGAAAGCG TTAAC ACT
ATGAGTGTTGATGTTTTTCT TCAAG GTA CACGG GTCTTTTTGT AGTTG TGA
GCACTAGAAGGCACTATGTT TT T AAGATCAC --- - ----
GAACT

GAM5764 10531 GGACATCAAAGAATAAATAA A CAAA AA C C A TG CA- T TG TTGT G AC
GCTGCTCTAATTGCCAAGAA GG CAT GAAT ATAAG TG TCTA T C AGAAT CACATG G ATGCA
CTTT
TTCACATGTGGTTGTATGCA CC GTG TTTG TGTTC AC AGGT A G TCTTA GTGTAC C TATGT
GAAG
GCTTTACTGGGAGACTGAAG - ---- AA - - - GT TCG - GT ---- - --
TGTATCTGCATGTGATTCTG T GAGA
CTGTGATGGACACTTGTAAG GG
TTTGTGCC TC
- ----
GAM5798 10000 CCAGGGAAAGTAGTAAGTTG AAA- A ATCTTCTAAT CCTAATATCCCTA
TATAGTTATCTTCTAATTGG CCAGGG GTAGTAAGTTGTAT GTT TGGGG
GGCCTAATATCCCTACCCCA GGTCCC CATCATTCAACATA CAA ACCCC
CAACAATACAACTTACTACC ACTC A C--------- ----------
TCACCCTGG
GAM5800 11225 TGTTCCTCTAAGGTTGTCAT - CTA --- A G A TAC - ATTA GTA TTG
AATAAGTGCATCATTACCAA TGTT CCT AGGTTG TC TAATAA TGC TCAT CAA GT CAGCAG
CTGGT
GTATTACAGCAGGTACTGGT ACAA GGG TCTAAC AG ATTGTT ACG GGTG GTT CA GTCGTC
GACTA
TTGCATCAGGGCTGCTGACG A --- CAA A - - TCT G ---- GG- ---
TTGTCTGTGGGCATTGTTAA C
GAAACCAATCTGGGAAACA
-
GAM5806 11215 TGTGAGCTCCTGAGGAGTCA AGCTCC A CA CC TCT GT- - -- C TAAT
GGCCTGAGTCTGTGGGTCAT TGTG TGAGG GT GG TGAG GTGG CATCTAG CA CAT CT
CTAGCACATCCTTAATAGAA ACAC ACTCC CA CC ACTC CACC GTAGGTC GT GTA GA
TGATTGCCTGGATGTGACCA ------ - AC CC C-- AGT C TA A ----
CCCTCACCCCCAACCCTCAC
ACA
GAM5809 11252 TTCTGTCTTTTGAATTCTGT G GAA--- C GA GG AAACAAC GGCA
CGTGACTGGGGCTAAACAAC TTCT TCTTTT TTCTGT GT CTG GCT TGTCACT
TGTCACTGGCAAGTGACAAG AAGA AGAAAA GGGACG CA GAC CGG ACAGTGA
AGGCACAGACAGCAGGGGAA G ATAAAG A -- A- AGA---- ----
ATAAAAAGAGAGAA
GAM5814 9664 AGACACTGAATTGGACATTG T -- A ATTTC CT CGAA
ATTTCCTTTTCTCTGCGTCG AGACAC GAATT GGAC TTG CTTTTCT GCGT
AAATGTCAAGGAAAGTTGCA TTTGTG TTTAG TCTG AAC GAAAGGA TGTA
AGTCTGTGATTTTGTGTTT T TG - GTT-- AC ----
GAM5823 10909 TAGAAATATGTAATCGATCT AA - GATC- TG G- AATTA
TTTCTTTGGTGGGCAATTAG TAG ATATGTA ATC TTTTCTT GTG GC
CAATATTGAGGAAAGTTAAA ATC TATGTAT TAG GAAAGGA TAT CG
GATGTATGTATCCCTA CC G AAATT GT AA -----
GAM5826 10710 GGCTGGGACTGAGGTCATGT CTG--- A CA CCAA CGCCAGGAAGA
TCTGTCAGGTTCCAAAGAGC GGCTGGGA AGGTC TGTTCTGT GGTT AGAG
GCCAGGAAGACTCTGAGACC CCGACCCT TCCGG ACGAGACA CCAG TCTC
ACAGAGCACGGCCTGCTTTC CTTTCG C -- AG-- ----------
TCCCAGCC

GAM5836 9774 AGTTTCACTCTTGTCACCCA TT ACT TCACC-- T -- T ATCTT
GGCTGGAGTGCAGTGGTGCC AG TC CTTG CAGGC GGAG TGCAGTGG GCC
ATCTTGGCTCACTGCAACCT TC AG GAAC GTCCG CCTC ACGTCACT CGG
CCGCCTGCCGAGTTCAAGCG TT C-- TTGAGCC - CA - -----
ATTCT
GAM5859 10392 GAGGGCTGTCACCATTAGCA G -------- TT - A -- GAAG
CTCTCGGAGCTGGGAGAAGT GAG GCTGTCA CCA AGCACTCT CGG GCT GGGA
CCCTGAGCCCTGAAGGGTGT CTC TGACAGT GGT TTGTGGGA GTC CGA CCCT
TTTGGGCAGTATGTGACAGT G GTATGACG T- A C GT ----
GCTC
GAM5868 9982 CATCACCCAGTGGTTCTCTC A--- CCAGT TC - AACA-- - A- A TA TGAC T
AGCAACAGACATGTCCAGTG C TCAC GGT TCT CAGC GACATGT CC GTGG CCG GTGTTG
GG
GACCGTAGTGTTGTGACGGT G AGTG CCG AGA GTCG TTGTACA GG TACT GGC CATGAC
CC
CGCCCATCTGCGCCCAGTAC CAAC T---- TT C AAACTG A CG A TC ---- -
CTCGGATCATGCGGAACATG CCATCT
TTGTCAAAGCTGCAGATTGC CGC
CTGTGACAACG GCG

GAM5872 10886 GTTTAAATGGTTATCCGGGA TTAAAT TCC TTGTGT --------- T C TTCTTCA
GAATTCCTGTTGTGTGGAAG GT GGTTA GGGAGAATTCCTG GGAAGAT GCT TG CCT
ATGCTTTGCCCTTTCTTCAT CA CCAGT TCTTTTTAAGGAC CCTTTTA CGA AC GGA
CTGGAAATCATTTTTCCATC ------ C-- ------ GTACAAATT C T TTTCCT-
CTTTAGGTCACAGCTTAAAC TC TCATT
ATGATTTTCCCAGGAATTTT TGGAAA
TCTCTGACCAC ACCTTT
-- -----
GAM5874 10189 CTGTGCTCTTGATAACAGAG - G- AGAGT GA C TCACATTT
TGTTTGAGGGACAACTTTCA CTGTG CTCTT ATAAC GTTT GGGA AACTT
CATTTGAGTTTTTCCAAAAT GACAC GAGAA TGTTG TAAA CCTT TTGAG
TAAAGGTTGTAGAAGAGTCA T GA GAAAT A- T --------
CAG
GAM5884 10741 GGGATAGCTCATTTTTGAAA A TCATT--- AATCAG CATTT AAT GG A -
AATAAAAA
TCAGTTTAGAACATTTAAAA GGG TAGC TTTGA TTTAGAA AA GTG AA TT CA
TGTGGGAAATTCAAATAAAA CCC GTCG AGACT AAATCTT TT CAC TT AA GT
ATGCAAATTTTCACTGTTTT G TTACAACT GAA--- ----- GT- TT A C --------
CTAAAAAGTCAGATCAACAT
TGCTGGCCC
GAM5886 10717 GGCTTTATCTCTTGCCTTGA ---- T- CC C C A ACAAAG
CCTCCTACATTATCAACAAA GGCTTT ATCTCTTGCCT GA TC TA ATT TCA
GTGAGAGTTTAAGATCTCCT CCGAAG TAGAGGACGGG CT AG AT TGA AGT
GGGCAGGAGATTTCAGAAGC ACTT TC CT A T G ------
C
GAM5910 11032 TGAATCACTGTGGAAAACAT ATCAC- AAA- AA- AC -------- CCTCTTAT
CAGTAATTCAACAACCTTGC TGA TGTGGA CATCAGT TTCAACA CTTGCT GCTGA
TGCTGACCTCTTATTCAGTT ACT ACACTT GTGGTCG AAGTTGT GAACGA TGACT
AAATGAGAGCAAGTGTTGAA AAAACT GGTG ACA -- GAGTAAAT --------
ACAGCTGGTGGTGGTTCACA

TCAAAATCA
GAM5916 10182 CTGTACAAAGCAGCCTTGGA T AAA CA AAAACCCCA CTGC
CCAGGAGGGAAAACCCCAAG CTG AC GCAGCCTTGGAC GGAGGG AGGCT
GCTCTGCAGCCTCCCTGCTC GAC TG TGTCGGAATTTG CCTCCC TCCGA
CCCTCCGTTTAAGGCTGTGG - G-- -- CTCGTCCC- ----
TCAG
GAM5958 9620 AATGCTGGACATTTATCTGG C GA TTA A G- G A T TC G AAAT
AGCTGCAGGGGGTAAAGTGT AATG TG CAT TCTGG GCT CAG GGGTA AG GTCA CTT GG

CATCCTTGGGAAATTCAAAG TTAC AC GTA GGACC CGA GTC TCCAT TC CGGT GAA CT

CTGGCCTGTACCTGCTGAGA - TG TAG A GA G G - C- A ----
GCACCAGGGATATGGTCACA
TT
GAM5963 9617 AAGTGTTCTCCTGAGGACCC TG-- TC GAG AG- C GCT
TTAGGTCAGACAGAGAAGCT AAG TTC CT GACCCTT GTCAGA AGAGAA
TTCTCTTTCTGATGGGAAGG TTC AAG GA CTGGGAA TAGTCT TCTCTT
GTCAAAGTGGAAATCTCTT TCTA GT AA- GGG T ---
GAM5971 9950 CACTGTAGGGCAGTAAGGAA - TAAG TTTT G TG GCCAA
AGAATGTTCTTTTTCAAAAA CAC TGTAGGGCAG GAAAGAATGTTCT CAAAAATA TC A
TAGTCTGAGCCAATTGGATG GTG ACGTCCCGTT TTTTTTTATAAGG GTTTTTGT AG T
TTTTTGTGGAATATTTTTTT T TAA- T--- - GT -----
AATTTGCCCTGCATGTG
GAM5973 11167 TGGAGTATTTAAGAGTGACT - ATTT T TAAA ATGT TAC T G- GG AAAGT
TAAACAACAGATGTTCATAC TG GAGT AAGAG GACT CAACAG TCA TCTGCCAGT CT GA
TTGG
TCTGCCAGTTCTGGAGGTTG AC CTCG TTCTC TTGG GTTGTC GGT AGACGGTCG GG CT
AACC
GAAAGTCCAAGATCAGGGTG G GTTC - ---- GTT- TT- T GA AG -----
CTGGCAGATTTGGTTGCTGT
TGGGTTCTCTTCTTGGCTCG
CA

GAM5990 11186 TGGGGGCACTGGCTTCTGCT CT CTTCT TT- TCT A TTATTC
CTTGCTCTTTCTTCTGGAAA TGGGGGCA GG GCTCTTGCTC TCT GGAA CA
CATTATTCTGTTCCTTTGGA ATCCCTGT CC TGGGAACGGG AGG CCTT GT
CATGGGCAAGGGTCCTGTCC -- ----- TAC TTT - ------
CTA
GAM5998 10074 CCTTGGCCCTGTGAGGCTTC TG GAG TCA AGC G A GA GTAC
ACCTCTTGAGCCTGAGAAGC CCT GCCCTGT GCT CCTCTTG CTGAGAA CAG GGT CA

AGAGGTGACAGTACTGGCCC GGG TGGGACG CGG GGGGGAC GATTCTT GTC CCG GT

TGGTTCTTAGCAGGGGGGTG GA GG- TG- --- G - -- ----
GCGGGCAGGGTAGGGG
GAM6014 10685 GGCATGGCAGAGCCTTGATT ATG A- - - - TGTTTGCTAAT
TGTAATGTTTGCTAATTTAC GGC GC GAGC CTTG ATT TGTAA
GTGGTACAAGTGCTCCAGTA CCG TG CTCG GAAC TGG GCATT
CGGCC GCA AC T A T ----------
GAM6024 10230 GAAATGTGGAGAATTAAAAA AA T ATTAA -- T CATTTATAGA TGTATTGGG

GGGTAGTGAGGCTGGCATTT GA TG GGAGA AAAGGGT AG GAGGCTGG ATCTGGCTTTCT

ATAGAATCTGGCTTTCTTGT CT AC CCTCT TTTTCCG TC CTTTGACC TAGATCGAAAGG

ATTGGGTGGAAAGCTAGATG GG T C---- AC T AAAG------ ---------
AAACCAGTTTCTCTCAGCCT T
TTTCTCTCCTCAGGTC

-

GAM6051 9651 ACTCTTGAGCTCCCTCCACT - ACTTC -- TC-- ACACATTCAA
TCTGAGGACGTTTCCTGACA ACTCTT GAGCTCCCTCC TGA GGACGTT CTG
CATTCAACAGCATCAGCGTC TGAGAA CTCGAGGGAGG ACT CCTGCGA GAC
CAATCAGGAGGGAGCTCAAA A ----- AA CTAC ----------
GAGT
GAM6055 10862 GTGGGTGGTGCAGGGGTGGT TGCAG- GT TAGGAG - TGAA
CTTAGGAGGGCTTTCCTGAA GTGGGTGG GGGTG CT GGCT TTCC
GGAGTGGCCAGGGTTCACCC CACCCACC CCCAC GG CCGG GAGG
ATCTTTCCACCCAC TTTCTA TT GA---- T ----
GAM6083 9939 CACCCCGTTCATGTAACACG CC ACAC C A CAGTAGAG AGTATT
GGCCTGAGGTCAGCAGTAGA CA CCGTTCATGTA GGGC TG GGTCAG GACC
GGACCAGTATTGGTTTTGGC GT GGTAGGTGCGT TCCG AC CCGGTT TTGG
CCCAGCCTCTGCGTGGATGG TA C--- - C -------- ------
ATTG
GAM6102 11170 TGGCCATGCACAGTGGCTCG T ACAG - C GTA- CACTT G A- CAAG
CAACTGTAATCTCAGCACTT TGGCCA GC TGG CTCG AACT ATCTCAG TC GA GC
TCGGAAGCCAAGGCGGTCAG ACCGGT TG ACC GAGC TTGA TGGAGTC AG CT CG
ATCACCTGAGGTCAGGAGTT C ---- A - GGAC CACT- A GG ----
CGAGACCAGTCTGGCCA
GAM6121 10148 CTGAGGCAGGAGAAATTGCT G AAA GAA--- AGGTA GT A T AGATCA
TGAACCCAGGAGGTAGAGGT CTGAGGCAG AG TTGCTT CCCAGG GAG TGCAGTG G CA

TGCAGTGAGTCAAGATCATG GACTCTGTC TC AACGAG GGGTCC CTC ACGTTAC C GT

CCATTGCACTCCAACCTGGG - AA- AACAGC AAC-- -- - - ------
CGACAAGAGCAAAACTCTGT
CTCAG
GAM6161 11182 TGGGCTGAGGGAAAGCATGT TGAG- ---- T C ---- -- - TCT TG TTTG
CCACACCAGGTGCCCAGACA TGGGC GGAAA GCA GTCCA AC CAGGTGCC CAG ACA GGT
GC
TCTGGTTGGCTTTGGCTGAT ACCCG CCTTT CGT TAGGT TG GTCCACGG GTC TGT TTA CG

TTGTCCTGCAGGCACCTGCC TTGAA CACA T C TTCC AC C --- GT ----
TTGTCTGGATTTGCACACTT
TCCAAGTTGCCCA
GAM6172 10977 TCCCTGACCACACCTTTACT C ACC TTACT AA AG TTT CCTG
CAGAAGTCTAAGGAACAGAC TCC TG ACACCT CAGAAGTCT GGAAC ACTG AA
TGTTTAACCTGTTTCCAGTG AGG AC TGTGGG GTCTTCAGG CTTTG TGAC TT
GTTTCAGGGACTTCTGTATT A GA- TTAT- GA G- CT- ----
GGGTGTAGCAAGGA
GAM6234 11250 TTCTGAACTTGGGCCAGATC AA TG -- CTTAACCT TAAA CT-- TG TTTA- C

TTAACCTGCTGGTAAAGCAC TTCTG CT G GCCAGAT GCTGG GCA GGC AGGG GACTTT
AA
TGGCTGAGGGTTTAGACTTT GAGAC GA C CGGTCTG TGACC CGT CCG TCCC TTGGAG
TT
CAAGGAATTTGAGGTTGTTT CA GT GT -------- CAA- TATT -- TTTTG T
TCCCTGCCTTATTGCAACCC GGAA
AGTGTCTGGCTGCTGAGACC
AGAG

GAM6250 11290 TTTGCGCTATTAAAGGCAAG GCG A CTGA TAGA T -- TG
TCTATATTTAAAT
CTGATATAAATTAGAACTCT TTT CTATT AAGGCAAG TATAAAT AC CTTCT GAA GGCCT
TCTGAATGGGCCTTCTATAT AAA GGTAA TTCTGTTC ATGTTTA TG GAAGG CTT TCGGG

TTAAATGGGCTTTTTCTAGG AAA G AA-- TA-- T AT TT ----------
AAGTGTATATTTGTAAACTT
GTCTTGAATGGAAAAAA

GAM6265 11294 TTTTGAGATTTTATTGAGTA AGA T ---------- TG - TT GT GCACCA
CTACTAATCTTGACATATTT TTTTG TTTTAT GAGT ACTACTAATCT AC ATATT G TG
TGGTTGGCACCACATTCTTG AAAAC AAAGTG TTCA TGGTGATTGGG TG TATGG C AC
GTATAGTGGGTTAGTGGTTG --- T GACGTTTGATAAGT -- A TT TT ------
AATAGTTTGCAGACTTTGTG
AAACAAAA
GAM6271 10422 GATTCAAAGCAAGATGGTAG AA- GA-- G A TG AGAGGA GT AGATGA
CATTGGAGAGGATGAGATAT GATTC AGCAA TG TAGC T G TGAGATATG C
GGTCAGATGAGGATATATTT CTAAG TCGTT AC ATCG A T ATTTTATAT G
TAAAAGTTGAGCTAACAGGA GAG TAGG A - GT GAAA-- AG ------
TTTGCTGAGGAATC
GAM6296 10979 TCCCTTCAGAGCCCATGGGT G- T CCATTCCCTCCT GCCC
TTCCCATTCCCTCCTGTCAG TCCCTTCAGA CCCA GGGTTTC GTCA
CCCTGGCCATGAAATCCTGG AGGGAGGTCT GGGT CCTAAAG CGGT
GGATCTGGAGGGA AG - TAC--------- ----
GAM6306 11208 TGTCCCTTCCAAGCTGTGTT CAAG- ACTG AA AG GT ACTC
AACTGTTCAAACTCAGGCCT TGTCCCTTC CTGTGTTA TTCA CTC GCCT GTG
GTGTGACTCCATTGGGGTGA ACAGGGGAG GGTACAAT AAGT GAG TGGG TAC
GAGGTGAAAGCATAACATGG ACATG ACGA G- AG GT ----
GTACAGAGGGGACA
GAM6329 10848 GTGCAGTACAAAGACAGTTC A A- CAGTG CC ATACCATGGAAGA
AGTGACAAGTTCCATCCATA GTGC GT CAAAGACAGTT ACAAGTT ATCC
CCATGGAAGAGGGTTAAACT TACG CA GTTTTTGTCGG TGTTCAA TGGG
TGTGGCTGTTTTTGCCACAG A CC ----- AT ----------
CAT
GAM6361 10433 GCAGCAGGCAGGGCCAGGCA C C-- ---- CC C GCC GTCCG
GGGCCGGGCCTGGGGCCTGG GCAG AGGCAGGG CAGGC AGGG GGGC TGGG TGGT

TGTCCGACCGCAGCCCAGCC CGTC TCCGTCTC GTCCG TCCC CCCG ACCC GCCA
CCCCTCATCGCCTGACACTC - ACA CTAC -- - GAC -----
TGCCTCTGC

GAM6366 9678 AGAGTATACCTGTGCCCGGT ATA CCC -- TAG TGC - --------- A-
TGCTGTAGCTCATGCCTGTA AGAGT CCTGTG GGTT GCTG CTCA CTG TAATC CCACC
CTTTGG
ATCCCACCACTTTGGGAGGC TCTCA GGGTAC CCGG CGAC GAGT GAT ATTGG GGTGG
GGAACC
CAAGGCGGGTGGATCATTTG AAG AA- TT CA- TT- G AGTTTACTA GC
AGGTTAGTAGTTTGAGACCA GAGG
GCTTGGCCAACATGGGGAAA
CTCT

GAM6388 10201 CTTCTTGCAGGCAGTGTTGT T AG C TGTT CTG AGTCTAGTTTATC AATT
TCCTGATTGCCCCAGTCTAG CTTCT GC G AG GTTC ATTGCCCC GCAAGGG
TTTATCGCAAGGGAATTTCT GAAGA CG T TC CGAG TGACGGGG CGTTTCT
TTGCGGGGCAGTGAGCTCCC - GT T CCT- --- ---------- ----
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GAM6414 10893 GTTTTGAAGGATGCGGTGTG T GG CC AT- G GGTT
GAGCCAGAGGATGTGTGGGA GTTTTGAAGGA GC TGTGGAG AGAGG GTGT GGAGG

GGGGTTTCTCTAACACTGAC CGGAACTTTTT CG GTACCTT TCTTC CACA TCTCT
TTCTATTCCATGAGCTTTTT - A- A- AGT A ----
CAAGGC
GAM6417 10520 GGAAATGTGGAGAATTAAAA AA T ATTAA -- T CATTTATAGA TGTATTGG
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ATCTGGCTTTCT
TATAGAATCTGGCTTTCTTG TCT AC CCTCT TTTTCCG TC CTTTGACC TAGATCGAAAGG

TATTGGGTGGAAAGCTAGAT GG T C---- AC T AAAG------ --------
GAAACCAGTTTCTCTCAGCC GT
TTTTCTCTCCTCAGGTCT

--
GAM6431 10700 GGCGTCACTGCCCTGATGGG ---- TGAT GG- TG A- CAAAA
CGGTTGGGAAGGCAAAACCT GGC GTCACTGCCC GGGC T GG AGG
GCCCTGAAAAGCCTTTGGGT CCG TAGTGATGGG TCCG A CC TCC
AGTGATTCTAGCC ATCT TT-- AAA GT CG -----
GAM6440 10971 TCCCCTAGGCCAGATTATCT CTAG- GATTA CAGCT CCAGTT TTTCCT-
CACAAC
TATCAGCTACTGACCCAGTT TCCC GCCA TCTTAT ACTGAC AGC ACTT
AGCTTTCCTACTTCACAACA AGGG CGGT AGAGTG TGACTG TCG TGGA
GGTTTCTAATGCTTTATGTC TTGAA AAAG- ----- TATT-- TAATCTT ------
AGTGTGAGAGAAATGGCAAG
TTGGGA
GAM6459 9612 AAGCTGGGGGCACTGGCTTC C CT CTTCT TT- TCT A TTATTC
TGCTCTTGCTCTTTCTTCTG AAG TGGGGGCA GG GCTCTTGCTC TCT GGAA CA
GAAACATTATTCTGTTCCTT TTC ATCCCTGT CC TGGGAACGGG AGG CCTT GT
TGGACATGGGCAAGGGTCCT A -- ----- TAC TTT - ------
GTCCCTAACTT
GAM6466 9733 AGGGCAAGATCCTCGCTCCA CAA TCCT C ACCGT TT --------- T C-- T G
ACCGTGGCCCGTGTTCTCTC AGGG GA CG TCCA GGCCCGTG CTCTC CTTT GTC CCA
AGT

CTTTTGTCCCCATAGTGTGA TCCC CT GC AGGT CTGGGTAC GAGAG GAAG CGG GGT
TCA
CTCCGCCAGGAACTTGGAAT TA- C--- A GT--- T- TAAGTGTCA T TAA - -
GGCTGAAGACTGTGAATGAG TGAC GCCA
AGTCATGGGTCTGTGGAACG TCC
CTCATCCCT AGG
---- ----
GAM6467 10124 CTCTGTGATGCTTGGGGACC TCT T- GGGGA - TC ACACCCCA - G GAA -
GGCTCCTCGGTCACACCCCA C GTGA GCTT CCGG CTCC GGTC GTC CT CTCT
GGTTGCCGTT T
GTCCTGCTCTGAAGGTTGCC G CACT CGAA GGTC GAGG TTAG TAG GG GAGA
TCGATGGTAG A
GTTTTCCAAACAGAAGGATG TT- TC A---- T TC AACGA--- A G --- G
GTAGCTAGAGGGGAGATAGC CAAACA
AAGATTCTGGAGTCTGGAAA TC
GCCTTCACTTG AG

GAM6506 10811 GTAGTCCCAGCTATTCAGGA C---- AT AG A G GATCA
GCTTGAGGTGGGAGGATCAC GTAGT CCAGCT TCAGG CTTG GGT GGAG
TTCGGCCCAGGAGTCTGAGG TATCG GGTCGG AGTCT GGAC CCG CTTC
CTGGAGTGAGCTAT AGTGA -- GA - G -----
GAM6509 10051 CCTAGATGGGATCTGCTGCA A TG TC C CAA TATTCCC TCA C A CTTCT
GGCAAGATATTCCCGGCCTC CCT GA GGA TGCTG AGG GA GGCC GAAG TG GGGGAGAAC

AGAAGCTGAGGGGAGAACCT GGA TT TCT ACGAC TCC CT TCGG CTTC AC CCCTTCTTG

TCTGTTCTTCCCCACCTTCG A CT -- T TC- TACGT-- --- C - -----
GCTTGCATTCCTCCTTCAGC
ATCTTCTTAAGG
GAM6531 11009 TCTCCCAGGCAATATTCCAG CAATA - TA G -- TTGGA
GATAGGCTGCCAGTTGGACT TCTCCCAGG TTC CAGGA GGCT CC AG
AAGGAAGCCACTCCTGCGGA AGAGGGTCC AGG GTCCT CCGA GG TC
ACCCTGGGAGA CA--- C CA A AA -----
GAM6541 10012 CCCAAGGTTACTTGGTAAGT A TACTTGGTA- C A T-- GCCT
AAAGAGAGAAGCCAGAAGCC CCCA GGT AGTAAAGAGAGAAGC AG AGCC GGG
TGGGGCCTCCTGACGGCTCC GGGT CCG TCATTTTTCTCTTCG TC TCGG TCC
TGCTTCTCTTTTTACTAAGG A TCTTCTGGAA - C CAG ----
TCTTCTGCCATGGG
GAM6564 10670 GGCAAGATCCTCGCTCCAAC - A- CCT C ACCGT TT --------- T C-- T G
CGTGGCCCGTGTTCTCTCCT GG CA GAT CG TCCA GGCCCGTG CTCTC CTTT GTC CCA
AGT
TTTGTCCCCATAGTGTGACT CC GT CTA GC AGGT CTGGGTAC GAGAG GAAG CGG GGT
TCA
CCGCCAGGAACTTGGAATGG A CC CTC A GT--- T- TAAGTGTCA T TAA - -
CTGAAGACTGTGAATGAGAG TGAC GCCA
TCATGGGTCTGTGGAACGCT TCC
CATCCCTGACC AGG
---- ----
GAM6567 10424 GCAAAGCAAGTGGCTTGGAG A-- A TTGGAGA G TTA-- AAGAGG
AGATAGTGATTTAGCTCAAG GCA AGCA GTGGC GATAGT AT GCTC

AGGGAGTGAGATGTGACTGT CGT TTGT CACCG TTGTCA TG TGAG
TGCCACATGTTAAATGC AAA A ------- G TAGAG ------
GAM6618 10920 TAGTCTCATCCAGGTATGAC T ATC A A T- ACT AT-- GAGCACCG
ATGTGCCACTGTGTCTGAAA TAG CTC CAGGT TG CA GTGCC GTGTCTGAA TCCT
TTCCTGAGCACCGAGGGCCG GTC GAG GTCCA AC GT CACGG CACGGACTT GGGA

CTTCAGGCACCAGGCACTTT - A-- - C TT AC- CGCC --------
GCCAACCTGAGAGCTG
GAM6638 10161 CTGCCTAATGATGGTGTATG TAAT- -- AT CTGTA- T CCTGCCAACT
GAAGCTGTAGCATTTCTGGC CTGCC GAT GGTGT GGAAG GCA TTCTGGCA
ACCTGCCAACTTGTCAGAGC GACGG CTG TCACG CCTTC CGT GAGACTGT
TGCCTTTCCCTTCCTGGCAC TGTAT TT GT CCTTTC C ----------
TTTGTCTATGTGGCAG
GAM6674 9689 AGCAGAGGCTGGGGAATGGG G GAA- TGCT GAAT
GGTTCTGCTCTCACTGAATG AGCA AGGCTGGG TGGGGGTTC CTCACT
GTGGGGAACCTTCAACTGCT TCGT TCCGATTC ACTTCCAAG GGGTGG
TAGCCTGTGCT G GTCA ---- ----
GAM6700 9606 AAGAGACTTTGTAGATGTGA A GTAGA A G - - GA-- TG GATTA
TTAAATTAAGGCTCTTGAGA AAG GACTTT TGTGATTA ATTAAG CT CT TGA T GGA
TTGGGAGATTATCCTGGATT TTC CTGAGA ACACTAAT TAGTTC GA GA ACT G CCT
ATCAGAGTAGGCTTGATGTA - ----- G G T G ATTA GT -----
ATCACAAGAGTCCTT
GAM6773 10819 GTCCACTGATATTCACTAGC -- A TG--- ACCC GAA GATAAACACA
CTGTTTGTCCTCACCCCTGA GTCCACTGAT ATTCACT GCCTGTT TCCTC CT GCA
AGCAGATAAACACATGTAGA CGGGTGACTA TGGGTGG CGGACAG AGGAG GA TGT

TGGAGGAAAAGTGACAGGCA CT A TGAAA GTA- --- ----------
GGTGGGTTCATCAGTGGGC
GAM6774 10155 CTGCAGCTCCAATAAAATTG AG- TGC G- G G GTGCT ACATT
CCGAGATGATGTTTGGGTTT CTGC CTCCAATAAAAT CGAGAT AT TTTGG TTT GG
GTGCTGGACATTCCTGAGAG GACG GGGGTTGTTTTA GTTCTG TG AGACC AGG CC
GAGCCAGAGGTGAGTCTTGA AGA --- AG G G AGAGT -----
TTTTGTTGGGGAGAGCAG
GAM6799 10936 TCACCCAGTGGTTCTCTCAG CCAGT TC - AACA-- - A- A TA TGAC T CC
CAACAGACATGTCCAGTGGA TCAC GGT TCT CAGC GACATGT CC GTGG CCG GTGTTG GG
CGC
CCGTAGTGTTGTGACGGTCG AGTG CCG AGA GTCG TTGTACA GG TACT GGC CATGAC CC
GCG
CCCATCTGCGCCCAGTACCT T---- TT C AAACTG A CG A TC ---- - --
CGGATCATGCGGAACATGTT ATCT
GTCAAAGCTGCAGATTGCCT
GTGA

GAM6807 10082 CGAGTGATTTTTGAGGTAAG ATTTT GTAAGTA A TG AAG TG TATATAGAA A T
AAA
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ATGAAAAGGAGGAGATGCCG GAC-- AATG--- - GT A-- GT TA------- - T A--
CTATCTTGGCAGGGATGATC A AGATG
ATGTATTTGAAATAGTAACT G GG

CACAGCATTTG C CC
G -----
GAM6811 10193 CTGTTTCCTATAGGTGCTGT TTTCCTATAGGT TGT- T T --- T- TGCTCT
CAGATCAGGTTCCTGATTGG CTG GC CAGA CAGGTTCCTGA TGG AGTTCTCT ATC
AGTTCTCTTATCTGCTCTGG GAC CG GTTT GTCTAAGGGCT ACC TCGGGAGG TGG
TTTGGAGGGCTGCCCCATTC TCACATAAACT- TTTT T T CCG TT ------
GGGAATCTGTTTTGTTTTGC
TCAAATACACTCAG
GAM6818 10771 GGGTTCTTTTTCCGCTTTCT TTCT--- G CCTTTTATACCTTAC
GAGCCCTTTTATACCTTACG GGG TTTTCC CTTTCTGAGC
TTTAGAAGGGGAAAATCATC CCC AAAAGG GGAAGATTTG
CTCCC TCCTACT - ----------
GAM6836 10334 GAGGCAGGAGAATCATTTGA AG AA A- A- AAG GT - CAAGATC
ACCTGGGAAGTGGAGGTTGC GAGGC GAG TC TTTG ACCTGGG TGGAG TGCAGTGA GC

AGTGAGCCAAGATCGTGTCA CTCTG CTC AG AAAT TGGATCC ATCTC ACGTCACT TG
CTGCACTCTAGCCTAGGTGA A- AG CG AG G-- -- G -------
TAAAGCGAGACTCAGTCTC
GAM6840 10967 TCCAGTTCTTCTGGGAGAAA - - ------- -- A - GGGGAA
AATGGCAGGCTTCTGGGGAA TCCAGT TCTTCTGGG AGA AAAAT GGC GGCTT CT
AGAAAGCCAGCTGAATTTTG GGGTCG AGAAGACCC TCT TTTTA TCG CCGAA GA
ACTCCATCTCCCCAGAAGAT T C ACCTCAG AG A A ------
GCTGGG
GAM6842 10938 TCACGTCTCTGCAAAGTAGC C C T AA AGCAA AT-- --- --- GAG GA
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TG TA
TTTTGAAAGCTGAGTGGATA AGT CA AG CGT CA CACTAA CAAG TGTAGTAAGGCTT TCGA
AC AT
GATTTAAATAGCAAGAGCTT A T - CC GA--- GACC GTG GTT GA- G-
TGTTCGGAATGATGTGTGGA GATTTAAA
ACCCAGAATCACAGACCCTG
CGATACATGA

GAM6858 9933 CAAGCAGTGAAGGGTGCAGA - T A-- G A- T T- TTCA GTTTG
TCATGGATAGAGCTTTCAAG CAAGC AG GA GGGT CAG TCA GGA AGAGCT AGAA
AAGTTTGTTCTAGTTCTTCT GTTCG TC CT TCCA GTC AGT CCT TCTTGA TCTT
CCTGAAACTGGACCTCCCTC A - CCC G AA - CT ---- -----
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GAM6978 9973 CAGGTATGACATGTGCCACT A A T- ACT AT-- GAGCACCG
GTGTCTGAAATTCCTGAGCA CAGGT TG CA GTGCC GTGTCTGAA TCCT
CCGAGGGCCGCTTCAGGCAC GTCCA AC GT CACGG CACGGACTT GGGA
CAGGCACTTTGCCAACCTG - C TT AC- CGCC --------
GAM6982 9985 CATGGGGTCGTGTCACTGGG AT G C TCA CCTCA A-- C ATA A TTCCGA
CTCCTCAGGGAAGGCAGTAG C G GGT GTG CTGGGCT GGG AGG AGTAGGTTGT GTT TC
GGGGCA
GTTGTATAGTTATCTTCCGA G C TCA CGT GGCCCGG CCC TCC TCATCCAACA CAA AG
TCCCGT
GGGGCAACATCACTGCCCTG -- G - TCC ACCG- CAC A CAC - ------
AAACCACACAACCTACTACC ACATCAC
TCACCCCGCCAGGCCCGGCC

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        TTGCACTGCG
                  -------
GAM6994 11149 TGCTCTGTTGCCTAGGCTGG    C TT     C--    --      T AATTTTG
        AGTGCAGTGATGCAATTTTG TGCT TG  GCCTAGG   TGGAG  TGCAGTGA GC
        GCTCACTGCAACCTCCACCT ACGA AC  TGGGTCC   ACCTC  ACGTCACT CG
        CCTGGGTTCAAGCA       - T-     TCC    CA      - -------
GAM6996 10970 TCCCAGATTCTTCCTGGTGG      TT- -   G  GA  C       GCAACACCC  GCCTTAA
        AGGCATTCGGAGAGCAACAC TCCCAGA   CT TCCT GTG  GG ATTCGGAGA       TG
        CCTGGCCTTAACACACTACA AGGGTCT   GA GGGG CAC  CT TAAGTTTCT       AC
        TATCTTTGAATTTCACACGG      TCC  C   G   A- T       ATACATCAC -------
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GAM7017 10244 GAATAAATAAGCTGCTCTAA     ----   C  C   A TG CA-    T     TG TT     AG  TTACTGGGAA
        TTGCCAAGAATTCACATGTG GAATAA    ATAAG TG TCTA T  C   AGAAT CACATG  G  GTATGC  CA

        GTTGTATGCAGCATTACTGG CTTGTT    TGTTC AC AGGT A  G   TCTTA GTGTAC  C  TATGTG  GT

        GAAATTGAAGTGTATCTGCA     TGAA    - -    - GT TCG    -     GT --     AA ----------
        TGTGATTCTGCTGTGATGGA AT
        CACTTGTAAGTTTGTTC

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GAM7022 10767 GGGTGCATGGACTAGGACCC     CA  A    AC  G    AGAAA   T    --    AG    GGCCTGAG
        TGGAGGCAGAAATAGTTACC GGGTG  TGG CTAGG  CCT GAGGC    TAGT ACCGA  GGGGA  TTACA

        GAGGGGAAGTTACAGGCCTG CTCAC  ACC GGTTC  GGA TTTCG    GTCG TGGTT  TCCCT  AGTGT

        AGTGTGAGTCCCTGTTTGGT    AG  -    CT   G    AGTA-   T    TG    G-    --------
        TGCTGATGAGCTTTGAGGTC
        CTTGGCCAGACACTC
GAM7067 10053 CCTCAGCAGACATCAGAAAA   - G-- - C     AAATTCA     AAGAATG     GA  GAAAACTTA

        TTCATGCTCGGAAGAATGCC CCT CA   CA GA ATCAGA      TGCTCGG      CCTACAG  AT
        TACAGGAATGAAAACTTAAT GGA GT   GT CT TGGTCT      ACGAGTT      GGGTGTT  TA
        AATTGTGGGAAATACTTGAG   T  ATG  A  T     ATAAA--      CATAAA-      AA ---------
        CAAAATATCTGGTTTCATGG
        TATGTAGG
GAM7078 10852 GTGCTAGGGGGTCACCTATG   -        CCTA      CCAG    CCTCCT  CCCGAA
        TGGGAGCCAGCTCTGCCTCC GTG CTAGGGGGTCA   TGTGGGAG   CTCTG    GC
        TGCCCCGAAGCTCCAGAGAC CAC GGTCTCTCAGT   ACATCCTC   GAGAC    CG
        TTCTCCTACAACTGACTCTC   A        CA--      TTCA    CT----  ------
        TGGACAC
GAM7080 10009 CCATTTTTTTGTAGGTCAGA   T      A  -  A   ---      AAAC   TTTTT   CTCTTCC   G  GGTC
        AGTGGTTGCAAACTGGATTT CCA TTTTTTGT GG TC GAAG   TGGTTGC    TGGA    AGA      TGTT GG

        TTAGACTCTTCCTGTTGGGG GGT AAGAAACA CC AG CTTC   ACCGGCG    ACCT    TCT      ACAG
CT
        GTCTCGGACATTTGCTCTTT   C      - G  A   TTA      AC--    TT---   CGTTT--   G  ----
        TCCACAGCGGCCAATTCTTC
        AGAGCCACAAAGAACTGG
GAM7095 10960 TCATCTATCCCCTAGGCCAG    CTA---   CTAG-   GATTA    CAGCT    CCAGTT   TTTCCT-
CAC
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ATTATCTTATCAGCTACTGA TCAT TCCC GCCA TCTTAT ACTGAC AGC ACTT
CCCAGTTAGCTTTCCTACTT AGTG AGGG CGGT AGAGTG TGACTG TCG TGGA
CACAACAGGTTTCTAATGCT TTTAAA TTGAA AAAG- ----- TATT-- TAATCTT ---
TTATGTCAGTGTGAGAGAAA AAC
TGGCAAGTTGGGAAAATTTG
TGA

GAM7102 10939 TCACTCTGTCGCCCAGGCTG C TC --- C -- GTAC CTCA
GAGTGCAGTGGTACAGCCTC TCACT TG GCCC AGG TGGAG TGCAGTG AGC
AGCTCACTGCAACCTCCACC AGTGA AC CGGG TCC ACCTC ACGTCAC TCG
TCCCGGGCTCAAGTGA - T- CCC - CA ---- ----
GAM7124 9762 AGTGTCTCCAGATTGCACGA T C- ATTG AAC TTTTTCACAC ------ A- TCAA
ACATTTCATTTTTCACACAG AG GTCT CAG CACG ATTTCA AGGGTCAC CAG ATACCA
GGTCACCAGAATACCATCAA TC TAGA GTC GTGC TAAAGT TCCTAGTG GTC TATGGT
TTTTTTGGTATCACTGTCAA T CC GA-- AA- CTTCCACGA- AAAACT AC ----
AAGTGATCCTAGCACCTTCT TTTTT
GAAATAACGTGAGCTGCCAG
ATTCT

GAM7135 11161 TGGACTAGGACCCTGGAGGC A AC G AGAAA T -- AG GGCCTGAG
AGAAATAGTTACCGAGGGGA TGG CTAGG CCT GAGGC TAGT ACCGA GGGGA TTACA

AGTTACAGGCCTGAGTGTGA ACC GGTTC GGA TTTCG GTCG TGGTT TCCCT AGTGT
GTCCCTGTTTGGTTGCTGAT - CT G AGTA- T TG G- --------
GAGCTTTGAGGTCCTTGGCC
A
GAM7140 10443 GCAGGTCCATCTTCAGTGGC AG T A --- G------ T G GGA GTTA ACT
ATTGGGCCTTGGCTGGGATG GC G CCATCTTC GTGG CATTG GCCT G CTG TGCTGA TCC

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TCGGCAGTACAGGCAGGCAC GA - C TAG GGAGACA - G ATG ACG- ---
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AGGTGGCAGGT
GAM7146 9924 ATTATGTGCTGTAGTATGTA A -- T- --- TA TA AATA
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TAAATCATTTCTACATTGCA A TT TT TAA TC TA ----
CAAAAT
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TCTGGGTGGCCTTCAGTCCA AGTTTA AGGATGT GGGTGGCCT CAG CC TGA AGAACA

TGAAAGAGAACACATCTGTT TCGAAT TCCTACG TCTACTGGA GTC GG ACT TCTTGT
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CTGCATCCTCATCAATAAGC
T
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GTTTTCTAATGGAGCCATTA GCTGG G GGGAGT ATGTTT CTAATGGA
TCTGTTGGAGGCATTCATTC CGACC C CCCTTA TACGGA GGTTGTCT
CCCTCACCAGC A TC CT-- - -------

GAM7169 9622 AATGTAAACCCCTTAAAGCA TA - TAAA ATGTGTGT TG-- A- A - TGTC
GATGTGTGTGGGGCCTTATG AATG AAC CCCT GCAG GGGGCCTTA AAGACC GG TTCTG
CGGG
AAGACCAGGATTCTGCGGGT TTAC TTG GGGA CGTC CTTCGGAGT TTTTGG TC GAGAC
GTTC
GTCAGGGGATTGCCCCTCTT GC T ---- -------- CAGA GA A A ----
GACAGAGACTAGGGTTTTAG ATTG
ACTGAGGCTTCCTGCAGGGT AGGGG
GTTCGCATT TCCCC

GAM7199 10669 GGATTTGGCAAAGAAGGCAG ATT GAA--- A- ATCC
TACAGTTAATCCTGGCTGCA GG TGGCAAA GGCAGT CAGTTA
ACTGCTGGAAAATTTGCTAC CC ATCGTTT TCGTCA GTCGGT
ACCC CAC AAAAGG AC ----
GAM7201 9649 ACTCTATTTTATTCAAATGG TT- T ATGATATGAG AAT
CACTATGATATGAGTTCAAA ACTCTATTTTA CAAA GGCACT TTCAAAA
AAATTTTTGAAACAGTGTCC TGAGGTAGAGT GTTT CTGTGA AAGTTTT
TTTGTTTTGAGATGGAGT TTT C CA-------- ---
GAM7212 10691 GGCCAGGACTCTTGCAGAAC - - AGAA AGA G AG T C CACC
TGAGACCTGGGAGCTCCTCC GGC CAG GACTCTTGC CTG CCT GG C CCT CCT
CTCACCAGGAAGGGACCCGA CCG GTC CTGGGGGCG GAC GGA CC G GGA GGA
GGCAGGCGGCGGGGGTCTCT A T GCG- --- G CA - A ----
GAGCC
GAM7241 9910 ATGACTGTGCTGCAGGAGGC AC T C CGGC AAGAACTAC CTGATGTT
GGCTCAGTGTGAAGAACTAC ATG TG GCTG AGGAGG TCAGTGTG GGGTTTC
GGGTTTCCTGATGTTGAAGC TAC AC TGAC TCTTCC AGTCACAC CTCGAAG
TCAGAATTAGCCACACTGAC GT - - ---- CGATTAAGA --------
CTTCTCAGTCATGCAT
GAM7250 9971 CAGGGAGAAGAGCTGTGTGC -------- A - AT---------- TTATAAATT
TGTGATGTGGTTTATAAATT CAGGGAGA AG GCTG TGTGCTGTG GTGGT
ACCATTTGGAAGGAGCTGCA GTCCTTCT TC CGAC ACACGACAC TACCA
CAGCACAGCAGCCTGCAACT CATCAACG - G GTCGAGGAAGGTT ---------
ACTCTTCCTG
GAM7255 10218 CTTTGAGATGACTGGTATTG G T TG A AAT AG G AG C A CT CTAACT
AATGGAGCAGTCTTTGAAAG CTTT AGA GAC GT TTG GGAGC TCTTT AA G ACCA CC TC
GCACCAACCCTTCCTAACTG GAAA TCT CTG TA AAC TCTCG AGAAA TT C TGGT GG AG
ATGGTGGTCTCTTGAAAGAG G T TT - CT- G- G CT - - T- ------
GCTCTTCCAAATTTGTCTTC
TGAAAG
GAM7257 10808 GTAGAGGTGGGGTTTCTCCA A - T T A TT CT CTTTA
TGTTGGTCAGGCTGGTCTTT GT GAGGTGGG GT TC CC TG GGTCAGG GGT
AACTCCTGACCTCAGGTGAT CG TTCCGCCC CA AG GG AC CCAGTCC TCA
ACGCCCGCCTTGGC G G T T - T- -- -----
GAM7260 10138 CTGAATCATGCAGTGTATAC A CA ACAGGAT -- - CT GGAA
AGGATGTCAGTGAAGAGGTC CTG ATCATG GTGTAT GTCAGT GAAGAG GT GGCA
TGGCAGGAATGCCTCACTCT GAC TAGTAT TACATG CAGTCA CTTCTC CA CCGT
CTTCCTACTGACTGGTACAT G TG GT----- TC T CT ----
GTTATGATGCAG
GAM7264 10497 GCTGTCTATTATGAGTCTGA ---------- - - C C CTG GAAGGA
CTGGCACAGACATCTGTCAA GCT GTCTAT TATG AGT TGACTGGCACAGA AT TCAAGGAA

GGAAGAAGGATTCTTTGAGC CGA CAGGTA ATAC TCA ACTGACTGTGTTT TG AGTTTCTT

GTATTTGTGTCAGTCAACTG AAGACAACAC T G - A CG- ------
CATATATGGACCACAACAGA
AAGC

GAM7272 10040 CCCTTTCAAAACAAAGCTTT A- AA TT GATAG T CAGAAC
CCCAGGATAGCCCTGGGCAG CCCTTTCAA ACA GCT CCCAG CCC GGG
AACTCCTGGGATTGACTGGG GGGAGAGTT TGT TGA GGGTC GGG CCT
CAGTAATGTAGTTGAGAGGG GA AA C- AGTTA T ------

GAM7302 10059 CCTCCTGTGTCCCAAAACGA G AAACGAAA CCTATA A G TTCCAGAAT
AAACACTCCTATATTTTGTA CCTCCT TGTCCCA ACACT TTTTGT GC CC
GCGCCTTCCAGAATGGGGCA GGAGGA ACAGGGT TGTGA AAGGCG CG GG
GCGGAAACTAGTGTTGGGAC A -------- TCA--- A G ---------
AAAGGAGG

GAM7320 10130 CTCTTGACCAGAGGTTCTCA CT - - AG C T TA TGCC
AATGAGGGACATTTTACCTG CT TGACCAGA G GTTCTCAAATG GGA AT T CC
CCGGGGACATTTCCAATGTT GA ATTGGTTT C CAGGGGTTTGT CCT TA A GG
TGGGGACACTTTTGGTTATC CT T A AA T C GG ----
AG

GAM7331 10397 GAGGTAGGAGAACTGCTTGA A AAC GAA GG G C A A GAGATCA
ACTCAGGAGGCGGGGGCTGC GAGGT GGAG TGCTT CTCA AGGC GGGG TGCA TG GCT

AATGAGCTGAGATCAAGCCA CTCTA CCTT GTGAG GGGT TCCG CCTC ACGT AC CGA

CTGCACTCCAGCCTATGGGA - AGA ATA A- A - C - -------
TAGAGTGAGATTCCATCTC

GAM7345 10245 GAATAAATAAGCTGCTCTAA AA C C A TG CA- T TG TTGT G ACT GAGA
TTGCCAAGAATTCACATGTG GAAT ATAAG TG TCTA T C AGAAT CACATG G ATGCA CTTT GG

GTTGTATGCAGCTTTACTGG TTTG TGTTC AC AGGT A G TCTTA GTGTAC C TATGT GAAG TC

GAGACTGAAGTGTATCTGCA AA - - - GT TCG - GT ---- - --- ----
TGTGATTCTGCTGTGATGGA
CACTTGTAAGTTT

GAM7349 10185 CTGTCTCTGGGCCCTGTCTG GG-- CT---- CT T A TG G ATAATCTACTA
AGGCTTCTTAAGATGTTGTT CTGTCTCT GCC GT GAGGC TCTT AGA TT TTACA
ACAATAATCTACTATGTGGA GACAGAGA CGG CA CTCTG GGAG TCT GA GGTGT
GTGTCTGGAGGTGTCTCTTA ATTA TCTCTT TT T G GT - ----------
CTTCTCTGGCATTAAGAGAC
AG

GAM7350 10828 GTCCTTTAGTCTCTATTTTT AG- TC T CC--- - GCAG - G ACATG
GCTCCTAATTGTTCCTGCAG GTCCTTT TC TATTT TGCT TAATTGTT CCT GTA GTA GTTA

GTAGTAGGTTAACATGTAAC CGGGAAA AG ATAGA ACGG GTTAACGA GGA CAT CAT CAAT

GTACTTACAGAAGGAAGCAA GAA TC T TACAA A AGA- T G -----
TTGAACATGGCATAGATACT
GAAAGAAAGGGC

GAM7363 9686 AGCAAGGACAAGTTGTGACC GA T ---- CCA - AT A T CAAGCTT
TTCCCAGTCCTCTCTCCATT AGCAAG CAAGTTG GACCT TC GTCC TCTCTCC TTGC GA CAG

TGCAGATCAGCAAGCTTCTG TTGTTT GTTCGAC TTGGG AG CAGG GGGGAGG AACG CT GTC

TCAGCAAGGAGGGGTGGACA A- - TCAA TAA T -- A - -------
ATGAAACTGGGTTCAGCTTG
ATTTGTT

GAM7366 10635 GGAGAATTGCTTGAACCCGG AA TG GAA--- GGC - T - GAAG
GTGGCGGAGGTTGTGGTGAG GGAG T CTT CCCGGGT GGAG GT GTGGTG AGT
TGAAGATTGCACTATTGCAC CCTC A GAG GGGTCCG CCTC CG TATCAC TTA
TCCAGCCTGGGCAACAAGAG AA GT AACAAC A-- A T G ----
TGAAACTCC

GAM7369 11010 TCTCTCTTCCCTCTCATCAT C CTCTCATCA TT T ----- - T TTAAC
AGATTAATCACTTAGTTGCA TCTCT TTCC TAGA AATCACT AGTT GCAAGGG ACCAG AAA
AGAA
AGGGACCAGTAAATTAACAG AGAGA AAGG GTCT TTGGTGA TCAG CGTTTTC TGGTT TTT
TTTT
AATGGTGAACATTTTCCTTT C TC------- -- - TAGGT G C TCC--
TCTTGGTGCTTTTGCTGGAT GTGAA
GACTAGTGGTTTCTGCTGGA TG
ACAGAGA AC

GAM7371 10718 GGGAAAGCAGAAGGTTGGGG AA- - GG TG G GGCAGGCA
CTGGAGGTCTGCTGGCAGGC GGG AGCAG AAGGTTGG C GA GTCTGCT
AGGCAGACATTTGGAGCCAA CCC TCGTC TTTCAACC G TT CAGACGG
CTTTCCTGCTCAGCCC GAC C GA GT A --------

GAM7374 10056 CCTCATTGGTTCATTCGGCA GG AT- G TTA AC G TGC
GCTGTTTATTTAGAACCTGC CCTCATT TTC TC GCAGCTGT TTTAGA CTGCC TG
CGTGTGCTAGGGCAGATCTG GGAGTAG GGG AG TGTCGACA GGGTCT GACGG AT
GGATACAGCTGTGGACAAGG GA AAC G TA- A- G ---
GAGGATGAGG

GAM7400 10658 GGAGGGGAGGATACAAGAGG G CAA GA T -- AAACCACTCAC
AATGATAAATGGCAAGGAAA GGA GGGAGGATA GAG ATGATAAA GGCA AGGA
ACCACTCACTCTTAATGCTT CCT TTCTCCTGT CTC TACTGTTT TCGT TTCT
TTTGTCATACTCATGTCCTC G A-- A- T AA ----------
TTGTCC

GAM7415 10006 CCATCTTCAGTGGCATTGGG A --- G------ T G GGA GTTA ACT
CCTTGGCTGGGATGCTGAGT CCATCTTC GTGG CATTG GCCT G CTG TGCTGA TCC
TATCCACTGGAGCATCGGCA GGTGGAGG TACC GTGAC CGGA C GAC ACGGCT AGG

GTACAGGCAGGCACAGAGGC C TAG GGAGACA - G ATG ACG- ---
AGTGGATCCATCGGAGGTGG

GAM7440 10107 CTCAGGTCCTTTAGTGCTTC GTC - T A ACA GAG
TCAGTCAACAGACAGGGAGG CTCAG CTTTA GTGC TCTCAGTCA CAG GGGAGG
GAGCTTCCCCTGTGACTGAG GAGTC GAAAT CGCG GGAGTCAGT GTC CCCTTC
GTGCGCATAAAGACTGAG A-- A T - --- ---

GAM7446 9680 AGAGTCTCATTCTGTTGCCC TCATT GTT G ---- ATGGT TCA
AGGCAGGAGTGCAATGGTGT AGAGTC CT GCCCAGGCAG AG TGCA GTGACC
GACCTCAGGTCACTGCAACC TCTTAG GA TGGGTCCGTC TC ACGT CACTGG
TCTGCTGCCTGGGTTCAAGC C---- ACT G TCCA ----- ---
GATTCT

GAM7449 11162 TGGAGACTGGTAGCTTATTA CT--- A TAA GTGTT ATTCCTG

AAGAAACTCCGTGTTACTCA TGGAGA GGT GCTTAT AGAAACTCC ACTC
TTCCTGGAGTTGGGGGTTTC ACCTCT TCA CGGATG TCTTTGGGG TGAG
TGTAGGCACTTTATTTCTCC TTATT - --- GT--- -------
A
GAM7464 10499 GCTTACAATTGCTGGTACCT CAATT TACC--- -- CAAGT A- ACCT
GGTAGCATTTATTTTCCCTC GCTTA GCTGG TGGT AGCATTTATTTTCCCT ACCT GTA
AAGTACCTAGTAACCTTATG TGAGT CGACT ACCA TCGTAGATGGGAGGGA TGGA TAT

AAGGTAGGGAGGGTAGATGC TATGT TCCTTAC TC ----- AG ----
TCTACCACATTCCTTCAGCT
GTATTGAGT
GAM7473 10168 CTGGAGGATTTGGGGTGCCC ATTT CCCCT C A AA AAG AA-- AGGG
CTCTCGGCAGGGAACAGGAA CTGGAGG GGGGTG CT GGC GGG CAGG TAGG TCCCAGA

GTAGGAATCCCAGAAGGGTC GACCTCC CCCCAC GA CTG CTC GTCC ATCC GGGGTCT

TGGGGGAACCCTAACCCTGA ACT- TT--- C A GA CA- CAAG ----
GCTCAGTCCAGTTCACCCCT
CACCTCCAG
GAM7477 9962 CAGCGCGGCTCCCGCCACCC CG ---- G AC- ---- TTG A - GA ----
TCAATAAATGTTGCTTGGAG CAGCG GCTC CC CC CCTCAAT AAATG CTTGG GTGGA CC
GGCT CT
TGGACCGAGGCTCTGCAGGA GTCGT TGAG GG GG GGAGTTG TTTAT GGACC CGCCT GG
CCGG GA
ATGCAGGGAGGGCCGGGCTC CT TGTT A ACA AATC TG- C C G- GAGG
CGCCCCAGGGTTATTTCTAA GGAA
GTTGAGGACAGGAGGTTGTG GCA
AGTTCTGCTG CGT

GAM7520 10937 TCACCCTGTTGCCTAGGCAG CC TT C GA AA- GTCATCATAG
GACGGAATGCAGTGAAGTCA TCAC TG GCCTAGG AG CGG TGCAGTGAA
TCATAGTTTACTGTAACACT AGTG AC CGGGTCC TC GTC ATGTCATTT
GAACTCCTGGGCTCAAGTGA A- T- - AA ACA ----------
GAM7530 10502 GCTTCCTCACCACCTTGTGC CC-- CC - CAC CC- ACCACA
ACTGCTGCTCCCACACCACA GCTT TCA ACC TTGTG TGCTGCT CAC
GTGACTAGCAGCACATAATG CGAA AGT TGG AATAC ACGACGA GTG
GTTTGAATTAAAGC ATTA T- T --- TCA ------
GAM7542 10697 GGCGCTGGTGTCAAACAGTT T - AAACA GA TT - - C CTGTAGA
ATGTGATGCTTTGAAGCACC GGCGC GGTG TC GTTATGT TGC TG AAG CAC CTCA
CTCACTGTAGATGAGAGTGT CCGTG CCAC AG CGATACA ACG AC TTC GTG GAGT
CTTGCACTGCAAACATAGCC C T C---- A- TC G T A -------
GATCACCCGTGCC
GAM7546 10064 CCTGCTGTATGCTAGGCATT - -- CT- C A- GGGC
GTGCAAGGTGTTAGGGCTGA CC TGCTGT ATG AGG ATTGTGC AGGTGTTA
TGCTTGAGCACAGTACCTCC GG ATGACG TAC TCC TGACACG TTCGTAGT
ACATCTGCAGTATGG T TC ACC A AG ----
GAM7553 9603 AACTGGTCGGTGATTTAGGT TC TT T C TCCACCTTTC
AGTTTCCTGTTGTTGGGATC AACTGG GGTGAT AGGTAGT TC TGTTGTTGGGA
CACCTTTCTCTCGACAGCAC TTGACT TCATTA TCCGTCA AG ACGACAGCTCT
GACACTGCCTTCATTACTTC -- CT C C ----------

AGTT
GAM7559 11219 TGTGGCTCTGCCTCCCTGTC TG CTGCCT ----- - CTATAA-- - CTCTCCCT
TCACTCTCCCTATAACTGGC TG GCT CCCTGTCTCA CTC TCC CTG GC
CTCTCCCTGCTCAGACCTTC AC CGA GGGACAGAGT GAG AGG GAC CG
CTGGACGAGCTGCATGAGAC GT C----- ACGTC C TCCTTCCA T --------
AGGGCAGCTGCA
GAM7591 11291 TTTGGAGTAATTCAGTATAG AATTCAG --- GTTTAAAA
GTTCGTTTAAAAGAGATTTT TTTGGAGT TATAGG TTC
TATAACTTCAGA AGACTTCA ATATTT GAG
------- TTA --------
GAM7592 9988 CATTAGATTCTCATAAGAGC - C AAC TTGTGAGC ACAT
CCAAACCCTATTGTGAGCTG CATTAGATTCTCATAAG AGC CA CCTA TGC
CACATGCAAGGGATCTAGGT GTAATCTAAGAGTATTC TCG GT GGAT ACG
TGTGCGCTCCTTATGAGAAT C C GTT CTAGGGA- ----
CTAATG
GAM7601 9925 ATTATTCTGATGAAAATCCA TTC A- ---- T T TG TGTGTAAT
CAATGTCTTTGAGCTTCTGG ATTA TGATG AAATCCACAA TG CTTTGAGCT C GT
TTGTGTAATGCTGGGGTTTA TAAT ACTAC TTTGGGTGTT AC GAAATTTGG G CG
AAGTCACCATTTGTGGGTTT TA- GG TACC T - GT --------
GGCATCAATTAAT
GAM7636 10163 CTGCCTATATTACATTCATT ATATTACA CA GA TT C- G ACAGTGAACGAA
TTGATGGTTTGTATCTCAAA CTGCCT TT TTTT TGGT GTATCT AAA GAGT
GGAGTACAGTGAACGAAACT GACGGA AA AGAA GCCA CATAGA TTT TTCA
TGTTTAAAGATACACCGGAA GAAGAG-- AA AG -- AA G ----------
AGAAAAAGAGAAGAGGCAG
GAM7654 10171 CTGGATTCCCCAAAGCTCAC - TC--- AAA CACA -- AA- AT - GTAGTTTG
AGTTTGGCACTGAATCATAT CTG GAT CCC GCT GTTTGGCA CTG TCATATACA C TC
ACAATCTCGTAGTTTGGATG GAC CTA GGG CGA CAGATCGT GAC AGTGTGTGT G AG

GCTGTGTGTGACTGCAGACT A CACCC A-- ---- CA GTC CG T --------
GCTAGACAGCAGGGCCCACA
TCACAG
GAM7663 10023 CCCCGAGGGTGTGACTGAGA GA T TG ---- - T ---------- - - AGATGG
GCCAGTCCCCAGCACCCTTG CCCC GGG G ACTG AGAGC CAG CCCCAG CACC CTTG TCC

TCCAGATGGGGACCAGGAGG GGGG CCC C TGGT TCTCG GTC GGGGTT GTGG GGAC
AGG
TGGGTGAAGATATTTGGGGT AG C GT CGTG A T TATAGAAGTGG A C ------
CTGAGCTCTGTGCTGGTTGC
CCCCGAGGGG
GAM7700 9895 ATACTTACTAGCATATTATA - AGAGTG
TAGCTCTAAGAGTGTAGAGT ATACT TACTAGCATATTATATAGCTCTA
TATATGATGTGCTAGTGAAG TGTGA GTGATCGTGTAGTATATTGAGAT
TGT A ------
GAM7707 10136 CTGAAAGTCTATCTGCTGCC CTGCTGC C G CT TCA-- AAAC
ACGCCTGGGCACATACTGCA CTGAAAGTCTAT CACG CTG GCACATA GCA TTTACA
TCATTTACAAAACTGTAGAG GATTTTTAGATA GTGT GAC TGTGTGT TGT AGATGT
CACCTGTTGTGTGTGCAGTT TTCTTTA T G -- CCACG ----
GTGATTTCTTATAGATTTTT
AG

GAM7729 11171 TGGCCTCTCTGTGCTTCCAT CCATTTCCCCAT A AGGAATAACAC
TTCCCCATCTGTAAGATAGG TGGCCTCTCTGTGCTT CTGT AGAT
AATAACACATCTCACAGGAG ATCGGAGAGGTACGAG GACA TCTA
CATGGAGAGGCTA ---------- C ----------
GAM7776 10338 GAGGCAGGAGAATCGCTTGA G AATC GAA--- AGGC - T GA AAGAT
ACCCAGGAGGCGGAGGTTGT GAGGCAG AG GCTT CCCAGG GGAG GT GTGGT GCG

GGTGAGCGAAGATCGTGCCA CTCTGTC TC CGAG GGGTCC CCTC CG TACCG TGC
TTGCACTCCAGCCTGGGCAA - AAAA AACAAC GA-- A T -- -----
CAAGAGCAAAACTCTGTCTC
GAM7777 9688 AGCAGACTGCCCTGTTGACC AGAC TGT--- AGAATT -- TAC CTGATTA
AGAATTTGTTAGATTGCTAT AGC TGCCC TGACC TGTTAG ATTGCTAT AATG
TACAATGCTGATTATATTTT TCG ACGGG ATTGG ACAGTC TAACGATA TTAT
ATAGCAATTACTGACATAAG GTA- TTTCAT AAT--- AT TT- -------
GTTATACTTTGGGCAATGGC
T
GAM7784 10812 GTAGTTACCATTGCCTTTTC AC T - --- A A TT G AAACTAGTCCAAAA
TGTGAGCTATTTGTTTTGGT GTAGTT CAT GC CTTTT CTGTG GCT TTTGTT GGTTT CTG
TTGCTGAAACTAGTCCAAAA CATTAA GTA TG GAGAA GACAC CGA AGACAA TTAAA GAC

CAGGAAATTTAACAGACAGC GT C T ACC - C T- G ----------
CACAGCCAAAGAGTGTCATG
TGAATTAC
GAM7817 10084 CGCTCTTTCACCCAGGCTGG CTTTC C-- -- - A ATCT
AGTGCAGTGGCATGATCTCA CGCT ACCCAGG TGGAG TGCAGTG GC TG
GCTCACTGCAACCTCCATCT GCGA TGGGTCC ACCTC ACGTCAC CG AC
CCTGGGTTCAAGCG ACT-- TCT CA T - ----
GAM7837 11248 TTCTATGTTATACCCTGGAG --------- C- GGAG GG GGAATC-- AG
TCCTGGTTGAGGGGTGGGGG TTCTATG TTATAC CT TCCT TTGAGGGGTGGG
AGAAAAGT GT
AATCAGAAAAGTAGGTTTAC GAGATAT AATGTG GA AGGA AATTCTTCACTT TCTTTTTA
CA
ATTTAACATTTTTCTTAACT GTATGAATA AA ACA- AA ACATCAAT --
ACATTCACTTCTTAAAAAGG TACATTT
AACAAGAAGTGTAAATAAGT T
ATGTATAGAG A

GAM7845 9677 AGAGGTGTTCCTTAGGCCAC A TG TT ----- C CCT G--- - CGCTCCA
ACCCTGCCCTCCCTGGACTG AG GG TTCC AGGC CACACC TGCCCTC GGACT CCTGA CCT

CCTGACCTCGCTCCAAGGCT TC CT AAGG TTCG GTGTGG ACGGGAG CTTGG GGACT GGA

CAGGGGAAGGTTCTGAGGGC C GT -- TAAAA - T-- AAGG C -------
AGGTGTGAAAATGCTTGGAA
TGTCCCT
GAM7854 11177 TGGGATTACAGACATGAGCC ATTA A AG- ACT G CC GTTATG CAGC
ACTGTGCCCAGCCAGGGCTG TGGG CAGAC TG CC GT CCCAG AGGGCTGTGT TAGTGA

TGTGTTATGTAGTGACAGCT ACCC GTTTG AC GG CA GGGTC TCTCGACATA GTCACT

CACTGATACAGCTCTCTCTG CA-- A CAA ATT G TC ------ ----
GGGACTTAGGAACCAAGTTT
GACCCCA
GAM7865 10071 CCTTCAAAAAGTTTGTAGCC AAAAAG G A G G TAA---- AAG - GATAACCA
TATCGGGGTGGAGAGATAAG CCTTC TTTGTA CCT TCG GGTG AGAGA GCC TAT CCA
CCAAGTATCCAGATAACCAT GGAGG AAACAT GGA AGT TCAT TCTTT CGG ATA GGT
GGCATAAGGCAGAATATTTT GG---- - G A G TATAAGA A-- C --------
CTGTACTATGAGAGGTACAA
AGGGGAGG
GAM7884 10879 GTGTTTTGCACTGTAATACC ------ C G -- AAAGT
TCGGTCGTAGCAAAGTGCCG GTGTT TTGCACTGTAATAC TCGGTC TA GC
TGGGACCGAAGTATTATGGT CGCAG GACGTGGTATTATG AGCCAG GT CG
GCAGTGACTTGACGC TTCAGT A G GC -----
GAM7889 10195 CTTACCCCAGTATCCTATTA - GTAT - A TAC CAGTGAT TCTCA
TCTCATACCTAAGGCAGTGA CTTAC CCCA CC TATT TCTCA CTAAGG GGTT
TGGTTTCTCAGACCTCTTAG GAATG GGGT GG GTAG AGAGT GATTCT CCAG
ATTGAGAAGATGTGGCATGG T AC-- T A TA- ------- -----
GTGTAAG
GAM7898 11292 TTTTAGCATGGCTTGTAATA CA GC A A - GC CGTG
GCAAACAGTTTGTAATAGCA TTTTAG TG TTGT AT GCAAACAGT TTGTAATA AATGA
ATGACGTGTTATTTATTGCA AAGGTC AT AACG TA TGTTTGTTA GACGTTAT TTATT
GCATTGTTTGTAATAGCAAA -- AA A A C -- ----
ATACTGGAA
GAM7902 11246 TTCCCTGAGACTCTTTAACT AGA- TC CT- AAAAAG- TG TGCTGTTTTAT
TCTTGAAAAAAGTTGATGCT TTCCCTG C TTTAA TCTTGA T A
GTTTTATTTGAAAAATCGTC AGGGGAT G AAATT AGAACT A T
AAGACTATTAAAAGGCAAAT AAAC GA ATC GCTAAAA GT ----------
AGGGGA
GAM7911 10241 GAAGCTACCTGAGGTTTAGA ----- CT T AA C- AG G ATTC C TTATTT
ATTCCTTCAGCCCTAGCTGC GAAGCT AC GAGG TTAG TTCCTTCAG CCT CT CTTTT TG TTT

TTTTATTCTGCTTTTTATTT TTTCGG TG CTTT GATC AAGGAAGTC GGA GG GAGAA AC AAA

AAACAAAAAGAGGGGGAGGA AAACA T- T A- TA G- G AA-- - ------
TCTGAAGGAAACTAGTTTTC
TGTACAAAGGCTTT
GAM7915 9767 AGTTCAGACATTCTAGACTG CA TTCT CG G TCAG AAAA
TTCCGTCAGACTCAGTTTCA AGTT GACA AGACTGTTC TCA AC TTTC
AAAGAGAATGTGTGGGAGAA TCAG CTGT TCTGACAAG GGT TG AGAG
CAGTCTTTGTCCGACT C- T--- AG G TA-- ----
GAM7933 10714 GGCTTCCTCACCACCTTGTG CC-- CC - CAC CC- ACCACA
CACTGCTGCTCCCACACCAC GGCTT TCA ACC TTGTG TGCTGCT CAC
AGTGACTAGCAGCACATAAT TCGAA AGT TGG AATAC ACGACGA GTG
GGTTTGAATTAAAGCT ATTA T- T --- TCA ------
GAM7954 10654 GGAGGACCTGGCCAAAGTGG CCT - AAA TGCAG- GT TAGGAG - TGAA
GTGGTGCAGGGGTGGTCTTA GGAGGA GG CC GTGGGTGG GGGTG CT GGCT TTCC

GGAGGGCTTTCCTGAAGGAG TCTCCT CC GG CACCCACC CCCAC GG CCGG GAGG

TGGCCAGGGTTCACCCATCT AC- A --- TTTCTA TT GA---- T ----

TTCCACCCACGGACCCATCC
TCT
GAM7966 10015 CCCAGAACAAAGACCTCTAG - G C -- C A CCTAGACC- TTTC
CCAACATGTAAGCACCTAGA CC CA AACAAAGA C TCTAGCCAA ATGT AGCA ATGG
CCATGGTTTCCCATCCTTAT GG GT TTGTTTCT G AGATCGGTT TACA TTGT TACC
CATTGTTAACATTTTGGCTA T G T AT T A TACTATTCC ----
GATAGTTCTTTGTTGTGTGG
GAM7980 9944 CACGCGTCTTTGTGGTCACC CTTTGT ACCT T AA A T---- ATCATTTG
TGGCTTAGGAAGCTCACAAG CACGCGT GGTC GGCT AGG GCTCACA GG CCTC
GTCCTCATCATTTGGAGGTG GTGTGCA TCGG CCGA TCC TGAGTGT CC GGAG
TTTCCCTGTGAGTGCCCTCA TTCTT- ATC- C CG C TTTGT --------
GCCCTAGGCTTTCTTACGTG
TG
GAM8013 10484 GCTCTTGTTGCCCAGGCTGG T- TT C - ---- - A ATCT
AGTGCAGTGGCATGATCTCA GC CTTG GCCCAGG TGG AG TGCAGTG GC TG
GCTCACTGCAACCTCTGCCA TG GAAC TGGGTCC ACC TC ACGTCAC CG AC
CCTGGGTTCAAGCTGT TC T- - G TCCA T - ----
GAM8026 11200 TGGTTCATAATATTCCTTGC T TATTCCTT -------- - GGA TT CTT
AGATGTTGAACGATGGGCTG TGGT CATAA GCAGATGT TGAACG ATGGGCT TTGT
TGGAAC
GATTGTTTTGGAACCTTGTT ATCA GTATT CGTTTACA ACTTGT TACCCGA GACG ACCTTG

CCAGCAGAGCCCATGTGTTC - CGACATT- AAAGAAGT G --- -- ---
ATGAAGAAAACATTTGCTTA
CAGCTTATGACTA
GAM8031 10474 GCTATCAGTTCTTGCTATTC ------ C A TC - GTTTTTAG
TCAGAGCACTCTATCATGTT GCTATCAGTTCT TGCTATTCT AG GCAC TAT CAT
TTTAGGTGTATATTGTGTAT CGGTAGTCAAGA ACGATAGGA TT TGTG ATA GTG
TCAGGATAGCATTAAAAAGA AAAATT C A TT T --------
ACTGATGGC
GAM8047 9650 ACTCTTAAACCTTTAGAAAT AAAC GAAATGCTA CT- CTA CAATA
GCTACAGCATCTAGCTTCTC ACTCTT CTTTA CAGCAT AGCTTCT GAT
TAGATCAATAATCACAGAGG TGAGAA GAAAT GTCGTG TCGGAGA CTA
CTTAAGTGCTGACCTCATAA ATA- ACTCCA--- AAT CA- -----
AGATAAAGAGT
GAM8100 10927 TATGAGGGACATGAACACCT A C AACA- TG- GA TG GG TCCTGGAATTAAT

GCAGATTTTGGGGTCCACAG TATG GGGA ATG CC CA TTT G TCCACAGGGG
GGGTCCTGGAATTAATTCCC GTAC CTCT TAC GG GT AGA C AGGTGTCCCT
TGTGGATACTGAGAGATGAC - - CTACA TCA AG GT AT ----------
TGGACATCCATTCTCCATG
GAM8109 10255 GACAGGATTCCAGTACAGGT ATTC CTTCAT T GAATA
CTCTCATTTCCTTCATGATT GACAGG CAGTACAGGTCTCTCATTTC GA TAG
AGGAATACTACTTTGAAATG TTGTCT GTCATGTCCAGAGAGTAAAG TT ATC
AGAGACCTGTACTGTATCTG AT-- T----- C -----
TT
GAM8145 10534 GGACCAGACTATTGTGACAT - GA TT CAT -- A G--- TATTCAAT
GGAGAATGTAGAGGAATTAT GGA CCA CTA GTGA GGAGA ATGT GA GAAT
TCAATGTTCAGGATCAACAT CCT GGT GAT CACT CCTCT TACA CT CTTG
GATCTCCTCACTCTAGGATG A AG CT --- AG A AGGA --------

GATCC
GAM8164 10756 GGGGCAGAGCGGATGGAAGC CA-- C --- - AT GTTC ATAC
CGGAGATCCCAGGTTCCCGG GGGG GAG GGAT GGAAGCC GGAG CCCAG CCGGA

AATACTCCGGCTGGGGCCTT CCCC CTC CCTG TCTTCGG CTTC GGGTC GGCCT
CGGGCTTCTCCTGTCCCCTC ATCC C TCC G CG ---- ----
CCTACCCC
GAM8206 10265 GAGAATCACTTGAACCCAGG AA GA-- AGG GT A CAAGATCGT
AGGTGGAGGTTGCAGTGAGC GAG TCACTT ACCCAGG TGGAG TGCAGTG GC
CAAGATCGTGCCATTGCACT CTC GGTGAG TGGGTCC ACCTC ACGTTAC CG
CCAGCCTGGGTAACAGAGTG AG ACAA G-- -- - ---------
GGACTC
GAM8276 9662 AGAATCGCTTGAACCCAGGA AA GAA-- AG C GT A CAGGATCAC
GGCGGAGGTTGCAGTGAGCC AG TCGCTT CCCAGG G GGAG TGCAGTG GC
AGGATCACGCCACTGTACTC TC AGCGAG GGGTCC C CCTC ATGTCAC CG
CACCCTGGGCGACAGAGCGA AG ACAGC -- A -- - ---------
GACT
GAM8285 9996 CCAGAGGCTGTGACCATGGC AG-- TG CTA- - --- ACA--- T CCCAA
TAGTAGACAGTGGCAACATA CCAG GC TGACCATGG GTA GACAGT GGCA TAG CATC

GTCATCCCCAAGATGCTAAT GGTC TG ACTGGTACT CAT CTGTCA TCGT ATC GTAG
CTTCTGCTGGAACTGTCATA CAAA TA ATTG A AGG CTTCTA - -----
CGTTATCATGGTCAATGTAA
ACCTGG
GAM8288 11188 TGGGGTGCTCATCTTCTGTA G -- C G T GG - - CGGT
ACTGTTGGGAAGGCTCGGTG TGGG TG CTCAT TTCT TAACTG TG AA GG CT
GTCCATTTTCACCAGTTAAA ACCC AC GAGTA AAGA ATTGAC AC TT CC GG
GAATATGAGGCCAGCCCA G CG T A C TT A T ----
GAM8311 10567 GGAGAATCACTTTAACCAGA AA A A-- AG A GT - A C AGAT
GAGTTGGAGGTTGCAGGGAG GGAG TC CTTT ACC AG GTTGGAG TGCAG GG GC G
CCGAGATCGCACCACTGCAC CCTC AG GAAA TGG TC CGACCTC ACGTC CC CG C
TCCAGCCTGGGTGACAAAGC AG C CAG G- - -- A A - ----
GAGACTCC
GAM8339 10047 CCTAAAACATAAGTGAAGAT AAAC A GAT T T --- TCAT
CAGGCTACAGTGCTTTTCTC CCTA AT AGTGAA CAGGC ACAG GCTTT TC
ATGACATGGAGCCTTGTTGT GGAT TA TCACTT GTTTG TGTT CGAGG AG
TTGTTCACTCATTCTAGG CT-- C --- T C TAC ----
GAM8349 10804 GTAAATCTCCCTGATACCAT TCCCT TACCATC AAAC GAAATGCTA CT- CTA
C
CACTCTTAAACCTTTAGAAA GTAAATC GA ACTCTT CTTTA CAGCAT AGCTTCT GAT
TGCTACAGCATCTAGCTTCT CATTTAG CT TGAGAA GAAAT GTCGTG TCGGAGA CTA
CTAGATCAATAATCACAGAG TACC- ------- ATA- ACTCCA--- AAT CA- -
GCTTAAGTGCTGACCTCATA AATA
AAGATAAAGAGTTCCCATGA
TTTAC

GAM8362 10477 GCTCACACAGCAAGTCTTTG C A CT TG AA TTAGGAATG - CCCTCC CA--
TCAAAGCTTAGGAATGGAAG GCTCACA AGCA GT T TCA GC GAAGTA GGTTGTC TAGT
TGGG
TAGGTTGTCCCCTCCTAGTC CGAGTGT TCGT CA A AGT CG TTTCGT CTAACAG ATCA
ACCT

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        ATGGGATCTCTCCAACTCAC      C   A  -- GT  --  TGCA-----    T     ------   CTCA
        TAGACAATCTTGCTTTACGT ATCTC
        GCTGATGAACATGCTCTGTG
        AGC
                    -----
GAM8380 11178 TGGGCAAAAAGTGAGAAAGT   CAAAAAG      AAG   - GG--     C  TTACA     AAAC
        AAGACTGTGGGAGGTGACTG TGGG     TGAGAAAGT   ACTG T   GAGGTGA TG    GATCGGA

        TTACAGATCGGAAAACTCTG ACCC     ACTCTTTCA   TGAC G   TTTCACT AC    TTAGTCT
        ATTGAACCATTCACTTTATT    CA-----       AA-   C ATTA     T  CAAG-     ----
        AGCCAGTAAACTTTCTCAAC
        CCCA
GAM8386 10715 GGCTTGGGCCGACCCCAGAG    T  G  --          CCCATCACC
        AGAGCCCATCACCTTCTTTT GGCT GG CC  GACCCCAGAGAGAG
        TGGGGTTTGGGGCTTGGCC  CCGG TC GG  TTGGGGTTTTTCTT
                     T  G  GT          ---------
GAM8396 10963 TCCACAGTTTGATCTCTTCT    C     A  --    C  T  CCTCCA     TCTTT   TCCTCTTCCT
        CTGTTCCCTCCACACTCTTC TCCA AGTTTG TCT  CTTCT TG TC     CACTCT     TGC
        TTTTGCTCCTCTTCCTGTAT GGGT TCGAAC AGA  GAAGG AC AG     GTGAGA     ATG
        TTCAGAGTGGTTAAGATCAT    A    -  CT    T  T  AATTG-     CTTT-  ----------
        GGAAGTCAGACAAGCTATGG
        G
GAM8439 11244 TTCCATGGGCAGGGGCCATG     GG    GG   GACA    AT   CCACA
        ACAGGGAGATAGGCCACACC TTCCAT  GCAGG  CCAT   GGGAG  AGG
        TTTCCCAGGTGGAACCTGCA GAGGTA  CGTCC  GGTG   CCCTT  TCC
        GATGGAG               GA    AA   GA--    --  -----
GAM8447 11197 TGGTGGCATATGCGTGTAAT    G   TA---  G---      -  G  A     ---   TGAGGCAGGAGAATT
        CCCAGCTACTTGGGAGGCTG TGGT GCA    TGC    TGTAATC CCA CT CTTGGG   AGGC
        AGGCAGGAGAATTGCTTGAA ACCA CGT    ACG    ACATTGG GGT GA GGACCC   TTCG
        CCCAGGAGGTGGAGGTTACA    -  TAGAG   AGTG      A   G  -     AAG   ---------------
        GTGAGCAGAGATTGCACCA
GAM8452 10018 CCCAGCCCAAGATTGAATTC      C   GA------      C   T        GAATTGCAG
        TGATTAAAGGAGGCTGAATT CCCAGC CAA       TTGAATT TGAT AAAGGAGGCT
        GCAGAGCCTCCTTTCATCAA GGGTCG GTT       AGCTTAA ACTA TTTCCTCCGA
        ATTCGAGTTTTGAATTGAGC      A   AAGTTTTG      -   C        ---------
        TGGG
GAM8473 10257 GACCAGCCATCCTGGTTTAC       -  T  TG    ACA      -   GAA
        ATGGGACGCAGGAACTGCCG GACCAGC CA CC  GTTT   TGGGACG CAG
        TTTTAAAGCTGGGCTGAGTT CTGGTTG GT GG  CGAA   ATTTTGC GTC
        GGTC                  A  C  GT    ---      C   ---
GAM8489 10498 GCTGTTGGTGAGTATGGAGA   G   TGA      G   ---    C   CA-     GGC
        TCTCTGCCCTTGTCAGAGGA GCT TTGG   GTATGGA ATCT   CTGCC TTGT   GAGGAA
        AGGCTTCCTCATCACAAGGC CGA AACC   CGTGTCT TGGA   GACGG AACA   CTCCTT
        AGGGCAGGTGTCTGTGCCCA   G   ---      G   CGG    -   CTA     ---
        AGAGC
GAM8506 11282 TTGGTTAGGTAGTGGAACCT         TA--      C    A       CTATGTGATTCC
        TCTAAATGACGCACTATGTG TTGGTTAGG    GTGGAAC TTCTA ATGACGCA
        ATTCCTGTGTCATATAGAAT GACCGATTC    TATCTTG AAGAT TACTGTGT
        GTTCTATGATTCTTAGCCAG         TTAG      T    A       ------------
GAM8531 11133 TGATAGCAACTCTGCTTCCT   T     -    ----       T   ACAGG
```

TGCCTCAGGACAGGTTTGTG TGA AGCAACT CTGCT TCCTTGCC CAGG
GCAAGGAAGAAAGCAGAAGT ACT TCGTTGA GACGA AGGAACGG GTTT
TGCTTTCA T A AAGA T -----
GAM8539 10907 TACTTGGGATCAGTTAGTCT A- -- TTA CCT A-- A TTGGAGA G TTA--
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AT G
CTTGGAGAGATAGTGATTTA A GAATT TTAGTC CGGGTCTT CGT TTGT CACCG TTGTCA TG
T
GCTCAAGAGGGAGTGAGATG GG TA --- TT- AAA A ------- G TAGAG
TGACTGTTGCCACATGTTAA AAGAGG
ATGCTTTTCTGGGCCTGATT CTC
ATTTAAGGGA GAG

GAM8542 10858 GTGGCGTTTATTCCCTTAGT GTTTA A AT-- - G CAG
ATGTAGGTGACCCAGGGTGG GTGGC TTCCCTT GT GTAG GT ACC
CTTTGCTTTGGCAAGGGAGA CACTG GAGGGAA CG CGTT CG TGG
AGTCAC AA--- - GTTT T G ---
GAM8563 9636 ACATGTCATATTGAGCCTCC T A CCT -- CAG CATA
TACTGAACTCAGCCACATAT ACATG CAT TTGAG CCTACT GAACT CCA
GGAAGTTTGAAGTGGGTCCT TGTAC GTA AGCTC GGGTGA TTTGA GGT
CGAAATGCATGT - A CT- AG A-- ----
GAM8598 11295 TTTTGGCCCTGTGCTCTTGA C------- - G- AGAGT GA C TCACATTT
TAACAGAGTGTTTGAGGGAC TTTTGGC CTGTG CTCTT ATAAC GTTT GGGA AACTT
AACTTTCACATTTGAGTTTT AAAACTG GACAC GAGAA TGTTG TAAA CCTT TTGAG
TCCAAAATTAAAGGTTGTAG TTATCTAT T GA GAAAT A- T --------
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TCAAAA
GAM8601 10899 TAAATTGGAATGACAGAAGA AATTGGA GA AAGA G G TATAT
TGAGAGCTAGGAAGTGGTAT TA AT CAG TGAGA CTAGGAA TGG
ATTTAATTTCTAGATTTCAG AT TG GTC ACTTT GATCTTT ATT
GGCTGGAGTGGTGGAGTA GAGGTGG AG GGG- A A -----
GAM8631 10973 TCCCGGAGTTTATGGTCTGG GAG-- TCT- TG A C T TGCCA TCTA
TGAGAAGATCCCTGCTCTGA TCCCG TTTATGG GG AGAAG TCCCTG TC GAGTCAC AGC

GTCACTGCCAAGCTCTAGCT GGGGC AAATATC CC TCTTT AGGGAC AG TTCAGTG TCG

ATGTGACTTTGAACAGGGAA AAATA TATC TG A A T TA--- ----
TTTCTGTCCCTATCTATAAA
ATAAACGGGG
GAM8636 10398 GAGGTAGGTGCTTTAACTGT ----- TG TA--- T CCTG- AGGT
GTGCACCCTGTGAGGTAGGT GAGGTAG G CTT AC GTGTGCAC TGAGGT
GCTTTAACTGTGTGCACATT CTTCGTC C GGA TG TACACGTG ATTTCG
GTGAGGTAGGTGCTGAAACT AAAGT GT TGGAG T TGTCA ----
GCTTC
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CCTTCAGAGAAGACTGCAGC ATCGT GGG CG ACACAGG ACC TC CGTC GAAG
TCCCAAGGACACAAGCTGTT A TTGT A- A C-- GA A -------
GGGATGCTA
GAM8665 11079 TGAGGCAGGAGAATCACTTG GAGAA A GA-- GGG A GT AGC AGAT

AACCTGGGAGGCAAGAGGTT TGAGGCAG TC CTT ACCT AGGC AGAG TGCAGTG TG

GCAGTGAGCTGAGATCATAC ACTCTGTC AG GAG TGGG TCCG TCTC ACGTCAC AC
CACTGCACTCTGGCCTGGGT AG--- C ACAA --- G -- CAT ----
AACAGAGCGAGACTGTCTCA
GAM8678 10842 GTGAGATGTGTTCCAGGAAG AG CC C- ---------- CCCAT
TCGTCTTGAGCACCCATTGC GTG ATGTGTT AGGAAGT GTCT TGAGCA
TCAGAGTTTATATTGGACTT CAC TACACGA TCTTTCG CAGG ACTCGT
GCTTTCTAGCACATACCAC CA -- TT TTATATTTGAG -----
GAM8693 9740 AGGTGGCAGAGAGGCAATAT TG- A TATCAA T CATCACA
CAATCCTTCTGCATCACACA AGG GCAG GAGGCAA TCCT CTG
GTGGGAAAAGTTTGTCTCAT TCT CGTT CTCTGTT AGGG GAC
TGCAGTTCT TGA A TGAAA- T -------
GAM33612 9627 ACACACGTGAGATGTGTTCC CAC AG CC C- ---------- CCCAT
1 AGGAAGTCGTCTTGAGCACC ACA GTG ATGTGTT AGGAAGT GTCT TGAGCA
CATTGCTCAGAGTTTATATT TGT CAC TACACGA TCTTTCG CAGG ACTCGT
GGACTTGCTTTCTAGCACAT TAA CA -- TT TTATATTTGAG -----
ACCACAATTGT
GAM33612 9713 AGGCAGGAGAATTGCTTGAA CA AA GAA--- AGG GT - AGT AGAT
2 CCCAGGAGGTGGAGGTTGCA AGG GGAG TTGCTT CCCAGG TGGAG TGCAG GG CG

GGGAGTCGAGATCGTGCCAC TCT CCTC AACGAG GGGTCC ACCTC ACGTC CC GC
TGCACTCCAGCCTGGGCAAT A- AA AGTAAC G-- -- A GT- ----
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GAM33612 9714 AGGCAGGAGAATTGCTTGAA G AA - AA- GGA - GT A - AGAT
3 CCTGGAAGGCGGAGGTTGCA AGGCAG AG TTGCT TG CCT AGGC GGAG TGCAGTG GC CA

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TGCACTCCAGCCTGGGCAAC - AG C AAC --- A -- - T ----
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GAM33612 9716 AGGCAGGAGAGTCGCTGGAA A AG GAA-- GAG - CT A - AGAT
4 CCTGAGAGGCGGAGCTTGCA AGGC GGAG TCGCTG CCT AGGC GGAG TGCAGTG GC CG

GTGAGCCGAGATCGCGCCAC TCTG CCTC AGCGAC GGG TCCG CCTC ACGTCAC CG GC

TGCACTCCAGCCTGGGCAAC - AG ACAAC --- A -- - C ----
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GAM33612 9918 ATGGCGTGAACCCGGGAGGC G G- AA- AGGC CT A - AGAT
5 GGAGCTTGCAGTGAGCCGAG AT GC TG CCCGGG GGAG TGCAGTG GC CG
ATCGAGCCACTGCACTCCAG TA CG AC GGGTCC CCTC ACGTCAC CG GC
CCTGGGCAACAGAGCGAT G AG AAC GA-- -- - A ----
GAM33612 10095 CTACTCTGGAGGCTGAGGCA A GGAGGC---- GAA AA--- AGGCA GT TG A
6 GGAGAATCGCTTTAACCCGG CT CTCT TGAGGCAGGA TCGCTTT CCCGGG GAG TG
GTG GC
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TAC CG
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TCCAGCCTGGGCAACAAGAG - AGAT
CGGAATTCTGTCTCAAAAAA CG

AAAAAAGAGAG GC
C ----
GAM33612 10105 CTCAGGAGGCTGAGGCAGGA AG A AGGA TGAGC GGAG C AGCCG
ACGATG
7 GGATCACTTGAGCCTGGGAG CTCAGG GCTG GGCAGG TCACT CTG GTCTAGGCTG AGTG
GG
GTCTAGGCTGCAGTGAGCCG GGGTCT CGAC CTGTCC AGTGA GAC CGGGTCCGAC TCAC
CC
GGACGATGCCACTGCACTCC CA C CAG- ----- AA-- C GTCA- ------
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ACCCTGTCCCAGCACTCTGG
G

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8 AACCTGGGAGGTGGAGGTTG CTGAGGCAGAG CTCT CC GG TGGAG TGCAGTG C
CAGTGAGCCGAGATTGTCCA GACTCTGTCTC GAGA GG CC ACCTC ACGTCAC G
CTGCACTCCAGCCTGGGCAA AGAAT CAAC GT G-- -- CT -------
CAGAGTAAGACTCTGTCTCA
G
GAM33612 10149 CTGAGGCAGGAGAATCACTT G AA GAA--- TG AAA GT A - AGAT
9 GAACCTGGGAAATGGAGGTT CTGAGGCAG AG TCACTT CC GG TGGAG TGCAGTG GC CA

GCAGTGAGCCAAGATTGAGC GACTCTGTC TC AGTGAG GG CC ACCTC ACGTCAC CG GT

CACTGCACTCCAGCCTGGGC - AA AACAAC GT G-- -- - A ----
AACAAGAGTGAAACTCTGTC
TCAG
GAM33613 10167 CTGGAACCCAGGAGGAGGAG GAA AGGA - T -- GCCAAGA
0 GTTGTGGTGAGCCAAGATCG CTG CCCAGG GGAG GT GTGGT GA
TGCCACTGCACTCCAGCCTG GAC GGGTCC CCTC CG CACCG CT
GGCAACAG AAC GA-- A T TG -------
GAM33613 10203 CTTGAACCCAGGAGGTGGAG AA- AGG AT A CGAGACCAC
1 ATTGCAGTGAGCCGAGACCA CTTG CCCAGG TGGAG TGCAGTG GC
CGCCACTGCACTCCAGCCTG GAAC GGGTCC ACCTC ACGTCAC CG
GGCAACAAG AAC G-- -- - ---------
GAM33613 10206 CTTGAACCCGGGAGGTGGAG AA- AGG GC AACC ACC
2 GCTGCAGTGAACCCAGACCC CTTG CCCGGG TGGAG TGCAGTG CAG
TGCCACTGCACTCCAGCCTG GAAC GGGTCC ACCTC ACGTCAC GTC
GGCAACAAG AAC G-- -- C--- ---
GAM33613 10208 CTTGAACCTGGGAGGTGGAG AA TG AGG GCTA A - AGAT
3 GCTACAGTGAGCTGAGATCA CTTG CC GG TGGAG CAGTG GC TG
TGCCACTGCACTCCAGCCTG GAAC GG CC ACCTC GTCAC CG AC
GGCAAG -- GT G-- AC-- - T ----
GAM33613 10249 GAATCGCTTGAACCTGGGAG -- GAA-- TG AGGAA GT A- GAGAT
4 GAAGAGGTTGCAGTGAGCCG GAATC GCTT CC GG GAG TGCAGTG GCC
AGATGGCACCACTGCACTCC CTTAG CGAG GG CC CTC ACGTCAC CGG
AGCCTGGGCAACAGAGCAAG AA ACAAC GT GAC-- -- CA -----
ATTC
GAM33613 10254 GACAGCTGGAATGTTCTGAA AGC AA - -- A TC GAAATCTG- A ACATTG T
5 GAACTGGGTGATCTTGTGAA GAC TGG TGTT CTG AAG ACTGGGTGA TTGT TGG CCCT
GCAC

ATCTGTGGACCCTACATTGG CTG ACT ACAA GAC TTC TGACTTACT AATA ATC GGGA
TGTG
CACTTAGTGTGTACCTAAGG A-- GG A GT G GA AACCCTGCA - ATCCA- -
GCTAACGTCCCAAATAAAGT TAGT
CATTCAGTGCTTTGCAGAAA
CAGGTCAAGTC

GAM33613 10266 GAGAATCGCTGGAACCCAGG AATCG-- GAA AGGA - T -- GCCAAGA
6 AGGAGGAGGTTGTGGTGAGC GAG CTG CCCAGG GGAG GT GTGGT GA
CAAGATCGTGCCACTGCACT CTC GAC GGGTCC CCTC CG CACCG CT
CCAGCCTGGGCAACAGAACA AGAACAA AAC GA-- A T TG -------
AGACTC
GAM33613 10267 GAGAATCGCTGGAACCCAGG ATCG-------- GAA AGGA - T -- GCCAAGA
7 AGGAGGAGGTTGTGGTGAGC GAGA CTG CCCAGG GGAG GT GTGGT GA
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CCAGCCTGGGCAACAGAACA GCCTCAGAACAA AAC GA-- A T TG -------
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8 AGGCAGAGATTGCAGTGAGC GAG TCGCTT CCC AGGC GAG TGCAGTG GC
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CCAGCCTGGGCAACAAGAGC AA AACAAC -- AC -- - ---------
GAAACTC
GAM33613 10276 GAGAATTGCTTGAACCCGGG AA TG GAA-- AGG GT A - AGAT
9 AGGTGGAGGTTGTAGTGAGC GAG T CTT CCCGGG TGGAG TGTAGTG GC CG
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0 ACCCTAGAGGCAGAGGTTGC GAGAC GGAG TCGCT CCC AGGC GAG TGCAGTG GCA

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CTGCACTCCAGCCTGGGCAA - AA GAACAAC --- AC -- - -------
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GAM33614 10290 GAGACAGGAGAATTGCATGA A AA A- AA- AGGCA GT A - AGCT
1 ACCCAGGAGGCAGAGGTTGC GAGAC GGAG TTGC TG CCCAGG GAG TGCAGTG GC TG

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CTGCACTCCAGCCTGGGCAA - AG AA AAC GAC-- -- - T ----
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GAM33614 10291 GAGACAGGAGAATTGCTTGA G AA - AA- TGG - GTTA A- AAGAT
2 ACCTGGCAGGCGGAGGTTAC GAGACAG AG TTGCT TG CC CAGGC GGAG CAGTG GCC

AGTGAGCCAAGATGGTACCA CTCTGTC TC AACGA AC GG GTCCG CCTC GTCAC TGG

CTGCACTCCAGCCTGGGCAA - AC T AAC --- A AC-- CA -----
CATAGCAACACTCTGTCTC
GAM33614 10302 GAGATGGGAGGTTCACTTGA AT- A-- AC AA AGG - T G CCAACATC
3 ACCCAGGAGGTGGAGGCTGT GAG GGG GGTTC TTG CCCAGG TGGAG GC GTGGT AG

GGTGAGCCAACATCCTGCCA CTC CTC CCGAG AAC GGGTCC ACCTC CG CACCG TC

CTGCACTCCAGCCTGGGCAA AGT AAA AC -- G-- A T - --------
CAGAGCCAAACTCTGACTC

GAM33614 10312 GAGGATCCCTGAGTGGGGGT GATCC G GGG G ----- A CATGATCAA
4 TGAGGCTGCAGTGAGCCATG GAG CT AGTG GTT AGGCT GCAGTG GC
ATCAAGCCACTGCACTCCAG CTC GA TCAC CGG TCCGA CGTCAC CG
CCTGGGCAACACTGAGACAC ACA-- G AA- G CCTCA - ---------
TC

GAM33614 10313 GAGGATCCCTGAGTGGGGGT - TCC- G GGG G ----- A CATGATCAA
5 TGAGGCTGCAGTGAGCCATG GAG GA CT AGTG GTT AGGCT GCAGTG GC
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CCTGGGCAACACTGAGACAC T CACA G AA- G CCTCA - ---------
TCTCTC

GAM33614 10318 GAGGCAGAAGAATCACTTCA A AA A AA--- TG AGG GT A- TGACATT
6 ACCTGGGAGGTGGAGGTTGC GAGGCAGA G TC CTTC CC GG TGGAG TGCAGTG GC

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CTGCACTCCAGCCTGGGCAA - AC - ACAAC GT G-- -- CG -------
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GAM33614 10319 GAGGCAGAAGAATGGCCTGA AGAATG - AA- AGGC CT A - AGAT
7 ACCCAGGAGGCGGAGCTTGC GAGGCAGA GC CTG CCCAGG GGAG TGCAGTG GC TG

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CTGCACTCCAGCCTGGGCAA CAGAA- A AAC GA-- -- - C ----
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GAM33614 10320 GAGGCAGAGAATTGCTCGAA G AGAA GAA-- AGACA GT A - AGAT
8 CCCGGGAGACAGAGGTTGCA GA GCAG TTGCTC CCCGGG GAG TGCAGTG GC CG

GTGAGCCGAGATTGTGCCAC CT CGTC AGCGAG GGGTCC CTC ACGTCAC CG GT
TGCACTCCAGCCTGGGCAAC G AG-- ACAAC GAC-- -- - T ----
AGAGCGAGACTGCGTC

GAM33614 10326 GAGGCAGGAGAACAGCTTGA A AACA GAA--- GGCA GT A - AGAT
9 ACCCAGGTGGCAGAGGTTGC GAGGC GGAG GCTT CCCAGGT GAG TGCAGTG GC TG

AGTGAGCTGAGATCATGCCA CTCTG CCTC CGAG GGGTCCG CTC ACGTCAC CG AC

CTGCACTCCAGCCTGGGCAA - AGAG AACAAC AC-- -- - T ----
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GAM33615 10331 GAGGCAGGAGAATCACTTGA G AA GAA--- TG AAA GT A - AGAT
0 ACCTGGGAAATGGAGGTTGC GAGGCAG AG TCACTT CC GG TGGAG TGCAGTG GC CA

AGTGAGCCAAGATTGAGCCA CTCTGTC TC AGTGAG GG CC ACCTC ACGTCAC CG GT

CTGCACTCCAGCCTGGGCAA - AA AACAAC GT G-- -- - A ----
CAAGAGTGAAACTCTGTCTC

GAM33615 10332 GAGGCAGGAGAATCACTTGA G AA A GAA--- TG AGA GT GC AGAT
1 ACCTGGGAGATGGAGGTTGC GAGGCAG AG TC CTT CC GG TGGAG TGCGGTGA CG

GGTGAGCCGAGATCGCATCA CTCTGTC TC AG GAG GG CC ACCTC ACGTCACT GC

CTGCACTCCAGCCTGGGCAA - AA C AACAAC GT G-- -- AC ----
CAAGAGCGAAACTCTGTCTC
GAM33615 10333 GAGGCAGGAGAATCACTTGA A AA GAA--- TG AGG GT A- GAGAT
2 ACCTGGGAGGTGGAGGTTGC GAGGC GGAG TCACTT CC GG TGGAG TGCAGTG GTC

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CTGCACTCCAGCCTGGGCAA - AA AACAAC GT G-- -- CG -----
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3 ACCCAGGAGATGGAGGTTGC GAGGC GGAG TCGCTT CCCAGG TGGAG TGCAGTG GC TG

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CTGCACTCCAGCCTGGGCAA - AG ACAAC G-- -- - C ----
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AGTGAGCCAAGATTGCGCCA CTCTG CTTC CGAA GGGTCC CCTC ACGTCAC CG GT
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5 ACCCAGGAGGTGGAGGTTGC GAGGCAGGA TCGCTT CCCAGG TGGAG TGCAGTGT CG

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CTGCACTCCAGCCTGGGCAA AA- GCAAC G-- -- GC ----
CGGAGTGAAATTCTGTCTC
GAM33615 10343 GAGGCAGGAGAATCGCTTGA GAGAA GAA--- G- GAGGTTA A - AGAT
6 ACCCGGGGGGGAGGAGGTTAC GAGGCAG TCGCTT CCCGGG GGAG CAGTG GC TG

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CTGCACTCCAGCCTGGGCAA AA--- AACAAC GA AC----- - C ----
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GAM33615 10346 GAGGCAGGAGAATCGCTTGA A AA GAA-- TG AGG GT A CGAGATCAT
7 ACCTGGGAGGTGGAGGTTGC GAGGC GGAG TCGCTT CC GG TGGAG TGCAGTG GC

AGTGAGCCGAGATCATGCCA CTCTG CTTC AGCGAG GG CC ACCTC ACGTCAC CG
CTGCACTCCAGCCTGGGCAA - AG ACAAC GT G-- -- - ---------
CAGAGCGAGACTTCGTCTC
GAM33615 10353 GAGGCAGGAGAATGGCATGA CA AATG A- AA- AGGC CT A - AGAT
8 ACCCAGGAGGCGGAGCTTGC GAGG GGAG GC TG CCCAGG GGAG TGCAGTG GC CG

AGTGAGCCGAGATTGCGCCA CTCT CCTC CG GC GGGTCC CCTC ACGTCAC CG GT
CTGCACTCCAGCCTGGGCAA A- AGAA AG AAC GA-- -- - C ----
CGGAGCAAGACTCCATCTC
GAM33615 10354 GAGGCAGGAGAATGGCCTGA G AATG - AA- AGG CT A- CGAGATA
9 ACCTAGGAGGTGGAGCTTGC GAGGCAG AG GC CTG CCTAGG TGGAG TGCAGTG GC

AGTGAGCCGAGATAGCGCCA CTCTGTC TC CG GAC GGGTCC ACCTC ACGTCAC CG

CTGCACTCCAGCCTGGGCAA - AGAG A AAC G-- -- CG -------
CAGAGCGAGACTCTGTCTC
GAM33616 10358 GAGGCAGGAGAATTACTTGA A AATTA-- AAA- AGG GT A - AGAT
0 AACCAGGAGGTGGAGGTTGC GAGGC GGAG CTTG CCAGG TGGAG TGCGGTG GT CG

GGTGAGTCGAGATCGTGCCA CTCTG CCTC GAAC GGTCC ACCTC ACGTCAC CG GC

CTGCACTCCAGCCTGGGCAA - AAAACGA AACG G-- -- - T ----
CAAGAGCAAAACTCCGTCTC
GAM33616 10362 GAGGCAGGAGAATTGCTTGA A AA GAA-- A- C AAGC A CAAGATAGT
1 ACCCAGGAGGCAGAAGCTGC GAGGC GGAG TTGCTT CCCAGG GG AG TGCAGTG GC

AGTGAGCCAAGATAGTGCCA CTCTG CCTC AGCGAG GGGTCC CC TC ACGTCAC CG

CTGCACTCCAGCCTGGGCAA - AG ACAAC GA - ---- - ---------
CAGAGCGAGACTCCGTCTC
GAM33616 10364 GAGGCAGGAGAATTGCTTGA GAGAA GAA-- AGGC GT A - AGAT
2 ACCCAGGAGGCGGAGGTTGT GAGGCAG TTGCTT CCCAGG GGAG TGTAGTG GC TG

AGTGAGCTGAGATCACGCCA CTCTGTC AACGAG GGGTCC CCTC ACGTCAC CG AC
CTGCACTCCAGCCTGGGCAA AG--- ACAAC GA-- -- - C ----
CAGAGCAAGACTGTCTC
GAM33616 10367 GAGGCAGGAGAATTGCTTGA A AA GAA-- TG AGGCA GT A - AAAT
3 ACCTGGGAGGCAGAGGTTGC GAGGC GGAG TTGCTT CC GG GAG TGCAGTG GC TG

AGTGAGCTGAAATCGCGCCA CTCTG CCTC AACGGG GG CC CTC ACGTCAC CG GC
CTGCACTCCAGCCTGGGCAA - AG ATAAC GT GAC-- -- - C ----
TAGGGCAAGACTCCGTCTC
GAM33616 10369 GAGGCAGGAGAATTGCTTGA A AA GAA-- TG A- TGAA T A - AGAC
4 ACCTGGGAGGTGAAGGTTGC GAGGC GGAG TTGCTT CC GG GG GGT GCAGTG GC TG

AGTGAGCTGAGACCATGCCA CTCTG CCTC AACGAG GG CC CC TCA CGTCAC CG AC

CTGCACTCCAGCCTGGGCAA - AA ACAAC GT GA ---- - - T ----
CAGAGCAAAACTCCGTCTC
GAM33616 10371 GAGGCAGGAGAATTGCTTGA G A TG GAA-- GTCA GTC AGCC ATCC
5 ACTCAGGGTCAGAGGTCGCA GAGGCAG AGA T CTT CTCAGG GAG GCAGTG GAG
GTGAGCCGAGATCCCTCCAC CTCTGTC TCT A GAG GGGTCC CTC CGTCAC CTC
TGCACTCCAGCCTGGGCAAC - G GT ACAAC GAC- A-- ---- ----
AGAGTGAGTCTCTGTCTC
GAM33616 10376 GAGGCAGGAGGATCACTTGA C GGA A GAG GGA AG C A- CATGATT
6 GTGTGGAAGGTTGAGGCTGT GAGG AGGA TC CTT TGT AGGTTG G TGTAGTG GC
AGTGAGCCATGATTGCACCA CTCT TCCT AG GAG ACG TCCGAC C ACGTCAC CG
CTGCACTCCAGCCTGGGCAA T AC- A ACA GG- CT - CA -------
CAGAGAGACATCCTTTCTC
GAM33616 10378 GAGGCAGGGAAATCGCTTGA AAA GAA-- AGACA GTTT A - AGAT
7 ACCCAGGAGACAGAGGTTTC GAGGCAGGG TCGCTT CCCAGG GAG CAGTG GC CG

AGTGAGCCGAGATCGTGCCA CTCTGTCTC AGTGAG GGGTCC CTC GTCAC CG GC
CTGCACTCCAGCCTGGGCAA AG- ACAAC GAC-- AC-- - T ----
CAGAGTGAGACTCTGTCTC
GAM33616 10383 GAGGCTGAGACAGGAGAATT TGAGACA AA GAA-- AGG GTTT AGC AGAT

8 GCTTGAACCCAGGAGGTGGA GAGGC GGAG TTGCTT CCCAGG TGGAG CAGTG CA

GGTTTCAGTGAGCCAAGATT CTCCG CCTC AGCGAG GGGTCC ACCTC GTCAC GT
GTACCACTGCACTCCAGCCT ------- AG ACAAC G-- AC-- CAT ----
GGGCAACAGAGCGAGACTCC
GCCTC
GAM33616 10444 GCAGTCTGCGGGACCAGACT C C-- ---------- GA TT CAT -- A GAAATT TCA
9 ATTGTGACATGGAGAATGTA GCAGT TG GGGA CCA CTA GTGA GGAGA ATGT GA AT
GAGAAATTATTCAATGTTCA CGTCA AC CCCT GGT GAT CACT CCTCT TACA CT TG
GGATCAACATGATCTCCTCA A TCA ACACATACCTA AG CT --- AG A AGGACT ---
CTCTAGGATGGATCCATACA AT
CATCCCACTCAAACTGC

--
GAM33617 10464 GCGTGAACCTGGGAGGCGGA G- AA- TG AGGC CT A - AGAT
0 GCTTGCAGTGAGCCGAGATC GC TG CC GG GGAG TGCAGTG GC CG
GTGCCACTGCACTCCAGCCT CG AC GG CC CCTC ACGTCAC CG GC
GGGCAACAGAGC AG AAC GT GA-- -- - T ----
GAM33617 10466 GCTACTCAGGAGGCTGAGGC A AG A AGGA TGAGC GGAG C AGCCG
AC
1 AGGAGGATCACTTGAGCCTG GCT CTCAGG GCTG GGCAGG TCACT CTG GTCTAGGCTG
AGTG GG
GGAGGTCTAGGCTGCAGTGA CGG GGGTCT CGAC CTGTCC AGTGA GAC CGGGTCCGAC
TCAC CC
GCCGGGACGATGCCACTGCA A CA C CAG- ----- AA-- C GTCA- --
CTCCAGCCTGGGCAACAGAG GATG
TGAGACCCTGTCCCAGCACT
CTGGGAGGC

GAM33617 10479 GCTCGAACCCAGAAGGTGGA CGAA-- AAGG TT A - AGAT
2 GTTTGCAGTGAGCCGAGATC GCT CCCAG TGGAGT GCAGTG GC CG
GTGCCACTGCACTCCAGCCT CGA GGGTC ACCTCA CGTCAC CG GC
GGGCAACACAGC CACAAC CG-- -- - T ----
GAM33617 10503 GCTTGAACCCAGGAAGTGGA GAA-- AAG GT - A CATGATC
3 GGTTGCAGGGAGCCATGATC GCTT CCCAGG TGGAG TGCAG GG GC
GCACCACTGCACTCCAGCCT CGAG GGGTCC ACCTC ACGTC CC CG
GGGCAACAGAGC ACAAC G-- -- A A -------
GAM33617 10505 GCTTGAACCCAGGAGGCGGA GAA--- AGGC GT A - AGAT
4 GGTTGCAGTGAGCCAAGATT GCTT CCCAGG GGAG TGCAGTG GC CA
GCGCCACTGCACTCCAGCCT CGAA GGGTCC CCTC ACGTCAC CG GT
GGGCAACAAAAGC AACAAC GA-- -- - C ----
GAM33617 10508 GCTTGAACTCGGGGTGGAGG - AA- G GT A- CAAGATC
5 TTGCAGTGAGCCAAGATCGC GC TTG CTCGGG TGGAG TGCAGTG GC
CCCACTGCACTCCAGCCTGG CG AAC GGGTCC ACCTC ACGTCAC CG
GCAACAATGC T AAC G -- CC -------

GAM33617 10530 GGAATGTTCTGAAGAACTGG AA - -- A TC GAAATCTG- A ACATTG TTAGT
6 GTGATCTTGTGAAATCTGTG GG TGTT CTG AAG ACTGGGTGA TTGT TGG CCCT GCAC

GACCCTACATTGGCACTTAG CT ACAA GAC TTC TGACTTACT AATA ATC GGGA TGTG
TGTGTACCTAAGGGCTAACG GG A GT G GA AACCCTGCA - ATCCA- -----
TCCCAAATAAAGTCATTCAG
TGCTTTGCAGAAACAGGTC
GAM33617 10533 GGACCAGACTATTGTGACAT - GA TT CAT -- A GAAATT TCAAT
7 GGAGAATGTAGAGAAATTAT GGA CCA CTA GTGA GGAGA ATGT GA AT
TCAATGTTCAGGATCAACAT CCT GGT GAT CACT CCTCT TACA CT TG
GATCTCCTCACTCTAGGATG A AG CT --- AG A AGGACT -----
GATCC
GAM33617 10547 GGAGAATCACTAGAACCTGG A A AGAA-- GGA GAA T A- GAGAT
8 AAGGCGAAGGTTGCAGTGAG GGAG ATC CT CCT AGGC GGT GCAGTG GCG
CGGAGATCGTGCCACTGCAC CCTC TAG GA GGG TCCG TCA CGTCAC TGC
TCCAGCCTGGGCAACAGAGC A C GACAAC --- ACC - CG -----
GATACTCC
GAM33617 10557 GGAGAATCACTTGAACCCGG AATCA GAA-- AGG CT A - AGAT
9 GAGGTGGAGCTTGCAGTGAG GGAG CTT CCCGGG TGGAG TGCAGTG GC TG
CTGAGATCACGCCACTGCAC CCTC GAG GGGTCC ACCTC ACGTCAC CG AC
TCCAGCCTGGGCAACAGAGC AGACC ACAAC G-- -- - C ----
CAGACTCC
GAM33618 10570 GGAGAATCGCTTGAACCCAG AA GAA-- GAA A- GT A- AAGAT
0 AAGGCAGAGGTTGCAGTGAG GGAG TCGCTT CCCA GGC GAG TGCAGTG GCC
CCAAGATGGTGCCACTGCAC TCTC AGCGAG GGGT CCG CTC ACGTCAC TGG
TCCAGCCTGGGCAACAGAGC AG ACAAC --- AC -- CG -----
GAGACTCT
GAM33618 10571 GGAGAATCGCTTGAACCCAG AATC GAA-- AAG GT - A CATGATC
1 GAAGTGGAGGTTGCAGGGAG GGAG GCTT CCCAGG TGGAG TGCAG GG GC
CCATGATCGCACCACTGCAC CCTC CGAG GGGTCC ACCTC ACGTC CC CG
TCCAGCCTGGGCAACAGAGC AGAA ACAAC G-- -- A A -------
AAGACTCC
GAM33618 10573 GGAGAATCGCTTGAACCCAG AA GAA-- AGA GT A - AGAT
2 GAGATGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG GC TG
CTGAGATCACGCCACTGCAC CCTC AGTGAG GGGTCC ACCTC ACGTCAC CG AC
TCCAGCCTGGGCAACAGAGT AG ACAAC G-- -- - C ----
GAGACTCC
GAM33618 10576 GGAGAATCGCTTGAACCCAG AATC GAA--- AGG AGGT -
AGCCGAGATCACACACA
3 GAGGTGGAGAGGTTGCAGGG GGAG GCTT CCCAGG TGGAG TGCAG GG
AGCCGAGATCACACACACCA CCTC CGAG GGGTCC ACCTC ACGTC CC
CTGCACTCCAGCCTGGGCAA AAAA AACAAC G-- ---- A ----------
CAAGAGCAAAACTCC
GAM33618 10584 GGAGAATCGCTTGAACCCAG AA GAA-- AGG - T AGC AGAT
4 GAGGTGGAGGTTGTGGCGAG GGAG TCGCTT CCCAGG TGGAG GT GTGGCG TG
CTGAGATCATGCCACTGCAC CCTC AGTGAG GGGTCC ACCTC CG CACCGT AC
TCCAGCCTGGGCAACAGAGT AG ACAAC G-- A T --- ----
GAGACTCC
GAM33618 10601 GGAGAATCGCTTGAACCTGG AA C- AA- TG AGG GT TG A TGAGATTGT
5 GAGGTGGAGGTTGTGGTGAG GGAG TCG TTG CC GG TGGAG TG GTG GC

CTGAGATTGTGCCACTGCAC CCTC AGC GAC GG CC ACCTC AC CAC CG
TCCAGCCTGGGCAACAGATC AG TA AAC GT G-- -- GT - ---------
GAGACTCC
GAM33618 10608 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

6 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG CAG- ACAAC GA- -- ----------
TGAGACCC
GAM33618 10615 GGAGAATGGCATGAACCTGG AA A- AA- TG AGG CT A- CCAGATT
7 GAGGTGGAGCTTGCAGTGAG GGAG TGGC TG CC GG TGGAG TGCAGTG GC
CCCAGATTGCAACACTGCAC TCTC ACCG AC GG CC ACCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGC AG AG AAC GT G-- -- AA -------
CAGACTCT
GAM33618 10616 GGAGAATGGCGTGAACCCAG AATG G- AA- AGG CT A - AGAT
8 GAGGTGGAGCTTGCAGTGAG GGAG GC TG CCCAGG TGGAG TGCAGTG GC CG
CCGAGATCGCGCCACTGCAC CCTC CG AC GGGTCC ACCTC ACGTCAC CG GC
TCCAGCCTGGGCAACAGAGC AGAA AG AAC G-- -- - C ----
AAGACTCC
GAM33618 10619 GGAGAATTGCCTGAACCCAG AA - AA- - --- - A TTGCA
9 CAGGCAGAGGTTGCACCACT GGAG TTGC CTG CCCAG C AG GCAG GG
GCACTCCAGCCTGGGCAACA CCTC AACG GAC GGGTC G TC CGTC CC
GAGCAAGACTCC AG A AAC C ACC A A -----
GAM33619 10621 GGAGAATTGCTTGAACCCAA AA GAA-- AGA - GC A - AGAT
0 GAGGTGGAGGCTGCAGTGAG GGAG TTGCTT CCCA GG TGGAG TGCAGTG GC TG
CTGAGATCATGCCACTGCAC CCTC AACGAG GGGT CC ACCTC ACGTCAC CG AC
TCCAGCCTGGGCAACAGAGC AG ACAAC --- G -- - T ----
AAGACTCC
GAM33619 10628 GGAGAATTGCTTGAACCCAG AA GAA-- A- C AAGC A CAAGATAGT
1 GAGGCAGAAGCTGCAGTGAG GGAG TTGCTT CCCAGG GG AG TGCAGTG GC
CCAAGATAGTGCCACTGCAC CCTC AGCGAG GGGTCC CC TC ACGTCAC CG
TCCAGCCTGGGCAACAGAGC AG ACAAC GA - ---- - ---------
GAGACTCC
GAM33619 10630 GGAGAATTGCTTGAACCCAG AA GAA--- AGG GT A - AGAT
2 GAGGTGGAGGTTGCAGTGAG GGAG TTGCTT CCCAGG TGGAG TGCAGTG GC CG
CCGAGATTGAGCCACTGCAC CCTC AACGAG GGGTCC ACCTC ACGTCAC CG GT
TCCAGCCTGGGCAACAAGAG AA AACAAC G-- -- - A ----
CAAAACTCC
GAM33619 10631 GGAGAATTGCTTGAACCCAG AA GAA-- AGG GTTT AGC AGAT
3 GAGGTGGAGGTTTCAGTGAG GGAG TTGCTT CCCAGG TGGAG CAGTG CA
CCAAGATTGTACCACTGCAC CCTC AGCGAG GGGTCC ACCTC GTCAC GT
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- AC-- CAT ----
GAGACTCC
GAM33619 10636 GGAGAATTGCTTGAACCCTG AA - AA- TGG A- GT A - AGAT
4 GAGGCAGAGGTTGCAGTGAG GGAG TTGC TTG CCC AGGC GAG TGCAGTG GC CG

CCGAGATCGTGCCACTGCAC CCTC AGCG GAC GGG TCCG CTC ACGTCAC CG GC
TCCAGCCTGGGCAACAGTGC AG T AAC --- AC -- - T ----
GAGACTCC
GAM33619 10638 GGAGAATTGCTTGAACCTGG AA TG GAA-- TG AAG GT AGC AGAC

5 GAAGTGGAGGTTGCAGTGAG GGAG T CTT CC GG TGGAG TGCAGTG CG
CCGAGACTGAGCACTGCACT TCTC A GAG GG CC ACCTC ACGTCAC GT
CCAGCCTGGGCAACAGAGTG AG GT ACAAC GT G-- -- GA- ----
AGACTCT
GAM33619 10641 GGAGAATTGCTTGAACCTGG AA GAA-- TG A- TGAA T A - AGAC
6 GAGGTGAAGGTTGCAGTGAG GGAG TTGCTT CC GG GG GGT GCAGTG GC TG
CTGAGACCATGCCACTGCAC CCTC AACGAG GG CC CC TCA CGTCAC CG AC
TCCAGCCTGGGCAACAGAGC AA ACAAC GT GA ---- - - T ----
AAAACTCC
GAM33619 10656 GGAGGATCACTTGAACCTGG GA C- AA- TG AGA GTCT - TGAGATT
7 GAGATGGAGGTCTCAGTGAG GGAG TCA TTG CC GG TGGAG CAGTGA GC
CTGAGATTGCGTCACTGCAC CCTC AGT AAC GG CC ACCTC GTCACT CG
TCCAGCCTGGGCAACAAAAT AG AA AAC GT G-- AC-- G -------
GAGACTCC
GAM33619 10657 GGAGGCTGAGATGGGAGGTT GCT ATGGGA AC AA AGG - T G CCAACATC

8 CACTTGAACCCAGGAGGTGG GGAG GAG GGTTC TTG CCCAGG TGGAG GC GTGGT AG

AGGCTGTGGTGAGCCAACAT CCTC CTC CCGAG AAC GGGTCC ACCTC CG CACCG TC

CCTGCCACTGCACTCCAGCC AGT AAA--- AC -- G-- A T - --------
TGGGCAACAGAGCCAAACTC
TGACTCC
GAM33619 10663 GGATCACTTGAGCCCAGGAG A- GA-- GGA AG C A CATGTTCCT
9 GTTGAGGCTGCAGTGAGCCA GG TCACTT GCCCA GGTTG G TGCAGTG GC
TGTTCCTGCCACTGCACTCC CC AGTGAG CGGGT CCGAC C ACGTCAC CG
AGCCTGGGCAACAGAGTGAG AG ACAA --- CT - - ---------
ACC
GAM33620 10676 GGCAGGAGAATCACCTGAAC GAGAA - AA- GGCA GT - AG AGAT
0 CCGGGTGGCAGAGGTTGCAG GGCAG TCAC CTG CCCGGGT GAG TGCAG GG GCG

GGAGGCGAGATCGTGCCACT CTGTC AGTG GAC GGGTCCG CTC ACGTC CC TGC
GCACTCCAGCCTGGGCAACA AG--- A AAC AC-- -- A G- ----
GAGTGAGACTGTC
GAM33620 10679 GGCAGGAGAATCGCTTGAAC G AA GAA-- TG AGACA GT - CAAGATC
1 CTGGGAGACAGAGGTTGCAG GGCA GAG TCGCTT CC GG GAG TGCAGTGA GC
TGAGCCAAGATCGTGTCACT CTGT CTC AGTGAG GG CC CTC ACGTCACT TG
GCACTCCAGCCTGGGCAACA - AG ACAAC GT GAC-- -- G -------
GAGTGAGACTCTGTC
GAM33620 10681 GGCAGGAGAATTGCTTGAAC G AA TG GAA-- TG AGG GT AGC AGAT
2 CTGGGAGGTGGAGGTTGCAG GGCAG AG T CTT CC GG TGGAG TGCAGTG CG
TGAGCCGAGATCGCACCACT CTGTC TC A GAG GG CC ACCTC ACGTCAC GC
GCACTCCAGCCTGGGCAACA - GG GT ACAAC GT G-- -- CAC ----
GAGTGAGGCTCTGTC
GAM33620 10755 GGGGATGTGACTCCTGATAT - C- - AAA A--- AG---- CT G ACGC
3 GAAATCCATTGCCAAGGCTG GGGGAT GTGACT CTGA TATG TCC TTGCCA GCTGAC TATC
TCACT
ACCTTATCGTCACTACGCCA CTCTTA CACTGA GACT GTAT AGG AACGGT CGACTG GTAG
GGTGA
GAGAAGTGGGATGGAGTCAG T AC T CA- ATAA CGAAGA AG - ----

CAGAAGCTGGCAAAATAGGA CAGAGA
ACTATGTTCAGCAAGTCACT
ATTCTC

GAM33620 10838 GTGAACCCGGGAGACGGAGC GAA AGAC CT A - AGAT
4 TTGCAGTGAGCTGAGATCGT GT CCCGGG GGAG TGCAGTG GC TG
GCCACTGCACTCCAGCCTGG CA GGGTCC CCTC ACGTCAC CG GC
GCAAC AC- GA-- -- - T ----
GAM33620 10942 TCACTGGAACCCAGGAGGTG -- GAA AGG GT A T AGATAG
5 GAGGTTGCAGTGAGTCAAGA TCACT G CCCAGG TGGAG TGCAGTG G CA
TAGTGCCACTGCACTCCAGC AGTGA C GGGTCC ACCTC ACGTCAC C GT
CTGGGCAACAGAGTGA GA AAC G-- -- - - ------
GAM33620 10943 TCACTGGAACCTGGGAGGTG A---- GAA TG AGG GT A TGAGACTGT
6 GAGGTTGCAGTGAGCTGAGA TC CTG CC GG TGGAG TGCAGTG GC
CTGTGCCACTGCACTCCAGC AG GAC GG CC ACCTC ACGTCAC CG
CTGGGCAACAGAGCAAGA AACGA AAC GT G-- -- - ---------
GAM33620 10948 TCACTTGAACCCTGGAGGCA - AA- TGG A- GT A CGATATCAT
7 GAGGTTGCAGTGAGCCGATA TCACT TG CCC AGGC GAG TGCAGTG GC
TCATGCCACTGCACTCCAGC AGTGA AC GGG TCCG CTC ACGTCAC CG
CTGGGCAACACAGTGA C AAC --- AC -- - ---------
GAM33620 10968 TCCATTGCCAAGGCTGACCT A--- AG---- CT G ACGCCAGAGA
8 TATCGTCACTACGCCAGAGA TCC TTGCCA GCTGAC TATC TCACT
AGTGGGATGGAGTCAGCAGA AGG AACGGT CGACTG GTAG GGTGA
AGCTGGCAAAATAGGA ATAA CGAAGA AG - ----------
GAM33620 10996 TCGCTTGAACCCCGGAGGCA GAAC-- GG A- AT A CGAGATCAT
9 GAGATTGCAGTGAGCCGAGA TCGCTT CCC AGGC GAG TGCAGTG GC
TCATGCCACTGCACTCCAGC AGCGAG GGG TCCG CTC ACGTCAC CG
CTGGGCAACAAGAGCGA AACAAC -- AC -- - ---------
GAM33621 11040 TGAGACAAAAGAATTGCTTG AAA AA GAA-- TG AGG A T A - AGAT
0 AACCTGGGAGGTGGAAGTTG TGAGAC AG TTGCTT CC GG TGGA GT GCAGTG GC CA

CAGTGAGCCAAGATTGTGCC ACTCTG TC AACGGA GG CC ACCT CA CGTCAC CG GT
ACTGCACTCCAGCCTGGGCA CC- AG ATAAC GT G-- - - - T ----
ATAAGGCAAGACTCCGTCTC
A
GAM33621 11045 TGAGACAGGAGAATTGCTTG G AA - AA- TGG - GTTA A- AAGAT
1 AACCTGGCAGGCGGAGGTTA TGAGACAG AG TTGCT TG CC CAGGC GGAG CAGTG GCC

CAGTGAGCCAAGATGGTACC ACTCTGTC TC AACGA AC GG GTCCG CCTC GTCAC TGG

ACTGCACTCCAGCCTGGGCA - AC T AAC --- A AC-- CA -----
ACATAGCAACACTCTGTCTC
A
GAM33621 11046 TGAGACAGTATCACTTGAAC TA-- GAA-- GGG GT A - AGAT
2 CCAGGGGGTGGAGGTTGCGG TGAGACAG TCACTT CCCAGG TGGAG TGCGGTG GC CG

TGAGCCGAGATTGTGCCACT ACTTTGTC AGTGAG GGGTCC ACCTC ACGTCAC CG GT

GCACTCCAGCCTGGGCAACA TCAG ACAAC G-- -- - T ----
GAGTGAGACTCTGTTTCA

GAM33621 11048 TGAGAGGACTGCTTGAACTC A A - - AA- G GT A- CAAGATC
3 GGGGTGGAGGTTGCAGTGAG TGAG GG CT GC TTG CTCGGG TGGAG TGCAGTG GC

CCAAGATCGCCCCACTGCAC ACTC CC GA CG AAC GGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGCAACAATGC C A A T AAC G -- CC -------
AAGACCCCTCA
GAM33621 11055 TGAGGCACAAGAATTGCTTG CA AA TG GAA-- TG AGGG GTTT GC GCCGAGA

4 AACCTGGGAGGGGGAGGTTT TGAGGCA AG T CTT CC GG GGAG CAGTGA CGA
CAGTGAGCCGAGCCGAGATT ACTCTGT TC A GAG GG CC CCTC GTCACT GTT
GTGTCACTGCACTCCAGCCT C- AG GT ACAAC GT GA-- AC-- GT -------
GGGCAACAGAGTGAGACTCT
GTCTCA
GAM33621 11058 TGAGGCAGGAAAATCACTTG AAAA - AA- TGG A- GT A CGATATCAT
5 AACCCTGGAGGCAGAGGTTG TGAGGCAGG TCACT TG CCC AGGC GAG TGCAGTG GC

CAGTGAGCCGATATCATGCC ATTCTGTCT AGTGA AC GGG TCCG CTC ACGTCAC CG

ACTGCACTCCAGCCTGGGCA CAG- C AAC --- AC -- - ---------
ACACAGTGAGACTCTGTCTT
A
GAM33621 11069 TGAGGCAGGAGAACCGCTTG CA AAC GAA-- AGGA GAGGT GC AGAT
6 AACCCAGGAGGAGGAGGAGG TGAGG GGAG CGCTT CCCAGG GGAG TGCAGTGG CG

TTGCAGTGGGCCGAGATCGA ACTCT CCTC GTGAG GGGTCC CCTC ACGTCACC GC

GCCACTGCACTCCAGCCTGG A- AGA ACAAC GA-- ----- GA ----
GCAACAGAGTGAGACTCCAT
CTCA
GAM33621 11072 TGAGGCAGGAGAATAGGGTG A AATAGG--- GAA AGG CT A - AGAT
7 AACCCAGGAGGTGGAGCTTG TGAGGC GGAG GT CCCAGG TGGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC CA GGGTCC ACCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AGAGCGAGA AC- G-- -- - C ----
ACAGAGCGAGACTCCGTCTC
A
GAM33621 11073 TGAGGCAGGAGAATCACTTG A AATCA-- AA- AGA - GT A - AGAT
8 AACCCAAGAGGCGGAGGTTG TGAGGC GGAG CTTG CCCA GGC GGAG TGCAGTG GC TG

CAGTGAGCTGAGATCGCGCC ACTCTG CCTC GAAC GGGT CCG CCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AAAACGA AAC --- A -- - C ----
ACAAGAGCAAAACTCCGTCT
CA
GAM33621 11081 TGAGGCAGGAGAATCGCTTG CA AA GAA-- GAA A- GT A- AAGAT
9 AACCCAGAAGGCAGAGGTTG TGAGG GGAG TCGCTT CCCA GGC GAG TGCAGTG GCC

CAGTGAGCCAAGATGGTGCC ACTCT TCTC AGCGAG GGGT CCG CTC ACGTCAC TGG

ACTGCACTCCAGCCTGGGCA A- AG ACAAC --- AC -- CG -----
ACAGAGCGAGACTCTATCTC
A
GAM33622 11089 TGAGGCAGGAGAATCGCTTG A AA GAA-- AGGC - T CCGAGAT
0 AACCCGGGAGGCGGAGGTTG TGAGGC GGAG TCGCTT CCCGGG GGAG GT GTGGTGAG

TGGTGAGCCGAGATCTCGCC ACTCTG CCTC AGTGAG GGGTCC CCTC CG CACCGCTC

ACTGCACTCCAGCCTGGGCA - AG ACAAC GA-- A T -------
ACAGAGTGAGACTCCGTCTC
A
GAM33622 11090 TGAGGCAGGAGAATCGCTTG GAGAA GAA--- G- GAGGTTA A - AGAT
1 AACCCGGGGGGAGGAGGTTA TGAGGCAG TCGCTT CCCGGG GGAG CAGTG GC TG

CAGTGAGCTGAGATCGCGCC ACTCTGTC AGTGAG GGGTCC CCTC GTCAC CG GC
ACTGCACTCCAGCCTGGGCA AA--- AACAAC GA AC----- - C ----
ACAAGAGTGAAACTGTCTCA
GAM33622 11097 TGAGGCAGGAGAATCGTTTG GAGAA - AA- AGGC GTTC A- GAGAT
2 AACCTAGGAGGCGGAGGTTC TGAGGCAG TCG TTTG CCTAGG GGAG CAGTG GCT

CAGTGAGCTGAGATGGCGCC ACTCTGTC AGT AGAC GGGTCC CCTC GTCAC CGG
ACTGCACTCCAGCCTGGGCA AG--- G AAC GA-- AC-- CG -----
ACAGAGTGAGACTGTCTCA
GAM33622 11099 TGAGGCAGGAGAATGGCCTG G AATG - AA- AGG CT A- CGAGATA
3 AACCTAGGAGGTGGAGCTTG TGAGGCAG AG GC CTG CCTAGG TGGAG TGCAGTG GC

CAGTGAGCCGAGATAGCGCC ACTCTGTC TC CG GAC GGGTCC ACCTC ACGTCAC CG

ACTGCACTCCAGCCTGGGCA - AGAG A AAC G-- -- CG -------
ACAGAGCGAGACTCTGTCTC
A
GAM33622 11106 TGAGGCAGGAGAATTGCTTG A AA GAA-- A- C AAGC A CAAGATAGT
4 AACCCAGGAGGCAGAAGCTG TGAGGC GGAG TTGCTT CCCAGG GG AG TGCAGTG GC

CAGTGAGCCAAGATAGTGCC ACTCTG CCTC AGCGAG GGGTCC CC TC ACGTCAC CG

ACTGCACTCCAGCCTGGGCA - AG ACAAC GA - ---- - ---------
ACAGAGCGAGACTCCGTCTC
A
GAM33622 11107 TGAGGCAGGAGAATTGCTTG G AA GAA--- AGG GT A - AGAT
5 AACCCGGGAGGTGGAGGTTG TGAGGCAG AG TTGCTT CCCGGG TGGAG TGCAGTG GC CA

CAGTGAGCCAAGATTGCGCC ACTCTGTC TC AACGAG GGGTCC ACCTC ACGTCAC CG GT

ACTGCACTCCAGCCTGGGCA - AA AACAAC G-- -- - C ----
ACAAGAGCAAAACTCTGTCT
CA
GAM33622 11109 TGAGGCAGGAGAATTGCTTG A AA GAA-- TG AGGCA GT A - AAAT
6 AACCTGGGAGGCAGAGGTTG TGAGGC GGAG TTGCTT CC GG GAG TGCAGTG GC TG

```
          CAGTGAGCTGAAATCGCGCC ACTCTG CCTC  AACGGG    GG  CC    CTC  ACGTCAC CG GC

          ACTGCACTCCAGCCTGGGCA     -   AG     ATAAC  GT  GAC--  --      - C ----
          ATAGGGCAAGACTCCGTCTC
          A
GAM33622 11112  TGAGGCAGGAGAGTCGCTGG     A   AG     GAA--  GAG   -   CT     A  -  AGAT
7         AACCTGAGAGGCGGAGCTTG TGAGGC GGAG  TCGCTG    CCT   AGGC GGAG  TGCAGTG GC CG

          CAGTGAGCCGAGATCGCGCC ACTCTG CCTC  AGCGAC    GGG   TCCG CCTC  ACGTCAC CG GC

          ACTGCACTCCAGCCTGGGCA     -   AG     ACAAC  ---   A   --      - C ----
          ACACAGCGAGACTCCGTCTC
          A
GAM33622 11113  TGAGGCAGGAGGATTGCTTC         GG   C   AA---    GA     GC      A  TATGATCAT
8         AACCCAGGAGCTGGAGGCTG TGAGGCAGGA  ATTG TTC    CCCAG  GCTGGAG  TGCAGTG GC

          CAGTGAGCTATGATCATGCC ACTCCGTCCT  TAAT AAG    GGGTC  CGACCTC  ACGTCAC CG

          ACTGCACTCCAGCCTGGGCA         A-   -   ACAAC    --      --      - ---------
          ACAGAATAATATCCTGCCTC
          A
GAM33622 11114  TGAGGCAGGGAAATCGCTTG         AAA     GAA--     AGACA   GTTT     A  -  AGAT
9         AACCCAGGAGACAGAGGTTT TGAGGCAGGG   TCGCTT    CCCAGG    GAG    CAGTG GC CG

          CAGTGAGCCGAGATCGTGCC ACTCTGTCTC   AGTGAG    GGGTCC    CTC    GTCAC CG GC

          ACTGCACTCCAGCCTGGGCA         AG-     ACAAC     GAC--   AC--    -  T ----
          ACAGAGTGAGACTCTGTCTC
          A
GAM33623 11118  TGAGGCGGGAGAATGGCGTG       G  AATG  G-  AA-     AGG    CT      A    AGATC
0         AACCCAGGAGGTGGAGCTTG TGAGGCGG AG    GC  TG   CCCAGG   TGGAG  TGCAGTG GCGG

          CAGTGAGCGGAGATCTTGCC ACTCTGTC TC    CG  AC   GGGTCC   ACCTC  ACGTCAC CGTT

          ACTGCACTCCAGCCTGGGCA       -  AGAG  AG  AAC     G--    --      -    -----
          ACAGAGCGAGACTCTGTCTC
          A
GAM33623 11119  TGAGGGAGGAGAATGGCATG     GA    AA    A-  AA-  TG  AGG     CT      A-  CCAGATT
1         AACCTGGGAGGTGGAGCTTG TGAGG  GGAG  TGGC  TG   CC  GG   TGGAG  TGCAGTG  GC

          CAGTGAGCCCAGATTGCAAC ACTCT  TCTC  ACCG  AC   GG  CC   ACCTC  ACGTCAC  CG
          ACTGCACTCCAGCCTGGGCA     G-    AG    AG  AAC  GT  G--    --      AA -------
          ACAGAGCCAGACTCTGTCTC
          A
GAM33623 11121  TGAGGTACGACAATTGCTTG       CGACAA TG   GAA--     AGG    GC      A   AGATCA
2         AACCCAGGAGGTGGAGGCTG TGAGGTA     T  CTT     CCCAGG    TGGAG  TGCAGTG GTG
          CAGTGAGTGAGATCACACCA ACTCTAT     A  GAG     GGGTCC    ACCTC  ACGTCAC CAC
          CTGCACTCCAGCCTGGGCAA       CCCAG- GT   ACAAC     G--     --      -  ------
          CAGAGTGAGACCCTATCTCA
GAM33623 11157  TGCTTGAACCCAAAAGGCGG     GAA--    AAA   -   GT      A  -  AGAT
```

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3          AGGTTGCAGTGAGCCAAGAT TGCTT    CCCA   GGC GGAG  TGCAGTG GC CA
           TGTGCCACTGCACTCCAGCC ACGAG    GGGT   CCG CCTC  ACGTCAC CG GT
           TGGGCAACAGAGCA         ACAAC   ---  A   --      - T ----
GAM33623 11158  TGCTTGAACTCGGGGTGGAG   -  AA-     G    GT      A-  CAAGATC
4          GTTGCAGTGAGCCAAGATCG TGC TTG   CTCGGG TGGAG  TGCAGTG  GC
           CCCCACTGCACTCCAGCCTG ACG AAC   GGGTCC ACCTC  ACGTCAC  CG
           GGCAACAATGCA          T  AAC     G    --      CC -------
GAM33623 11160  TGGAATGTTCTGAAGAACTG    ATG-------    --  A       TC    GAAATCTG-  A   ACATTG   T
5          GGTGATCTTGTGAAATCTGT TGGA        TTCTG  AAG ACTGGGTGA  TTGT        TGG CCCT
GCAC
           GGACCCTACATTGGCACTTA ACCT        AAGAC  TTC TGACTTACT  AATA        ATC GGGA     TGTG
           GTGTGTACCTAAGGGCTAAC    GAACTGGACA    GT   G       GA    AACCCTGCA   -   ATCCA-   -
           GTCCCAAATAAAGTCATTCA TAGT
           GTGCTTTGCAGAAACAGGTC
           AAGTCCA
                        ----
GAM33623 11184  TGGGGCAGGACGATTGCTTG        ACGA     GA--     GAGCTTAAA   C  A-     GACTT
6          AGCCCAGGAGCTTAAAGCTG TGGGGCAGG    TTGCTT    GCCCAG        GCTG AGT  AGTGGT

           CAGTAAGTGGTGACTTGCCA ACTCTGTCT    AACGAA    CGGGTC        CGAC TCA  TCACCG
           CTGCACTCCAGCCTGGGCAA        CAG-     ACAA     ---------   C   CG     -----
           CAAAGCAAGACTCTGTCTCA
GAM33623 11254  TTGAACCCTGGAGGCGGAGG    AA-   TGG    -   GT      A-   GAGAT
7          TTGCAGTGAGCCGAGATGGC TTG   CCC   AGGC GGAG  TGCAGTG  GCC
           ACCACTGCACTCCAGCCTGG AAC   GGG   TCCG CCTC  ACGTCAC  CGG
           GCAACAA              AAC   ---   A    --      CA   -----
GAM33623 11259  TTGCTTGAACCCAGGAGGCA  TG   GAA--     AGGCA   GT      A  -  AGAT
8          GAGGTTGCAGTGAGCCAAGA T  CTT     CCCAGG     GAG  TGCAGTG  GC  CA
           TTGTGCCACTGCACTCCAGC A  GAG     GGGTCC     CTC  ACGTCAC  CG  GT
           CTGGGCAACAGAGTGA     GT   ACAAC     GAC--   --      -  T  ----
GAM33623 11261  TTGCTTGAACCCAGGAGGTG  TG   GAA--     AGG    GT      A  -  AGAC
9          GAGGTTGCAGTGAGCTGAGA T  CTT     CCCAGG   TGGAG  TGCAGTG  GC  TG
           CCATGCCATTGCACTCCAGC A  GAG     GGGTCC   ACCTC  ACGTTAC  CG  AC
           CTGGGCAACAGAGTGA     GT   ACAAC     G--     --      -  T  ----
GAM33624 11267  TTGCTTGAACCTGGGAGGGG  TG   GAA--  TG  AGGG    GTTT     GC   GCCGAGA

0          GAGGTTTCAGTGAGCCGAGC T  CTT     CC  GG    GGAG    CAGTGA  CGA
           CGAGATTGTGTCACTGCACT A  GAG     GG  CC    CCTC    GTCACT  GTT
           CCAGCCTGGGCAACAGAGTG  GT   ACAAC  GT  GA--    AC--     GT   -------
           A
GAM33624 11268  TTGCTTGAACCTGGGAGGTG      GAA--  TG  AGG    A  T     A  -  AGAT
1          GAAGTTGCAGTGAGCCAAGA TTGCTT     CC  GG   TGGA GT GCAGTG  GC  CA
           TTGTGCCACTGCACTCCAGC AACGGA     GG  CC   ACCT CA CGTCAC  CG  GT
           CTGGGCAATAAGGCAA          ATAAC  GT  G--    -  -     -  T  ----
GAM33624 11270  TTGCTTGAGCCCAGGAGCTT      GA--     GAGCTTAAA   C  A-     GACTT
2          AAAGCTGCAGTAAGTGGTGA TTGCTT    GCCCAG        GCTG AGT  AGTGGT
           CTTGCCACTGCACTCCAGCC AACGAA    CGGGTC        CGAC TCA  TCACCG
           TGGGCAACAAAGCAA          ACAA     ---------   C   CG     -----
GAM33624 11271  TTGCTTGAGCCCCAGAGTTT  TG   GAGC-    A   T   GC      AGC   GATC
3          GAGGCTGCAGTGAGCTGTGA T  CTT     CCCAG GTT GAG  TGCAGTG   TGT
```

TCACACCACTGCACTCCAGC A GAG GGGTC CGA CTC ACGTCAC ACA
CTGGGCAACAGAGTGA GT ACAAC - C -- C-- ----
GAM33624 11274 TTGGAGCCCAGAAGGTTGAA GA GAA A C A - TGAT
4 GCTGCAGTGAGCTGTGATCA TTG GCCCA GGTTG AG TGCAGTG GC TG
TGCCACTGCACTCCAGCCTG GAC CGGGT CCGAC TC ACGTCAC CG AC
GGCAACAG AA --- C - - T ----
GAM33624 10781 GGTCCAGATGTGGCCATGGG - A TGGCCAT - C C TG CCTG
5 AGACTGAGGGGCGGACGTGT GGTC CAG TG GGGAGACTGAGG GG GGA G TT
TCCTGGGTGCTTCCTTCATC CCAG GTC AC TCCTCTGACTCT CT CCT C GG
TCAGTCTCCTCACTGAGACC A - ------- A T T GT ----
GAM33624 9748 AGTCACCAGAGTCCATTGTA C CATT TA C TTT A TG CGTAC
6 TTAGTCTTATTTTCATCACC AGTCA CAGAGTC GTAT GT TTA TCATC CCG GG
GTGGGCGTACCCTGTGGGAT TCGGT GTCTCAG CATG CA AAT AGTAG GGT CC
GATGTTAAACGTACTCTAGA T ATCT -- - TGT - GT -----
CTCTGTTGGCT
GAM33624 10587 GGAGAATCGCTTGAACCCGA AATC GA-- GAG - GT GCCAAGATCACA
7 GAGGTGGAGGTTGCAGTGAG GGAG GCTT ACCC AGG TGGAG TGCAGTGA
CCAAGATCACATCACTGCAC CCTC CGAG TGGG TCC ACCTC ACGTCACT
TCCAGCCTGGGTGACAGAGC AGAA ACAG --- G -- ----------
AAGACTCC
GAM33625 10995 TCGCTTGAACCCAGGAGGTG GAA-- AGG GT A- AAGAT
1 GAGGTTGCAGTGAATGAAGA TCGCTT CCCAGG TGGAG TGCAGTG ATG
TCGTGCCACTGCACTCCAGC AGCGAG GGGTCC ACCTC ACGTCAC TGC
CTGGGCGATAGAGCGA ATAGC G-- -- CG -----
GAM33625 10145 CTGAGCTTAGCTATCTTTGT A TTA A TT TG A- AC A AAACCT C TTAT
2 GGTTCAATTCACCGGAGTCT CTG GC GCT TCT G GTTC ATTC CGG GTCTCA GG AGGTG

CAAAACCTGGCAGGTGTTAT GAC CG CGG AGA C CAGG TGAG GCC CGGAGT CC TCTAC

CATCTTCCTGAGGCACCGAG A TC- - C- GT GC A- A ------ T ----
AGTCGGGACTGCCAGAGGCC
TGCACAG
GAM33625 10866 GTGTAGCATGCATCAGTACT T ATG A CA C T ATACTATGCTTTAAAA
5 TCACCTACTGTATGGATATA GTG AGC CATC GTACTT CCTA TG ATGGAT
CTATGCTTTAAAAATCCATT CAC TCG GTGG CGTGGA GGAT AC TACCTA
CATTAGGCCAGGTGCGGTGG - --- - CC T T ----------
CTCAC
GAM33625 10867 GTGTAGCATGCATCAGTACT - ATG A CA C T ATACTATGCTTTAAAA
6 TCACCTACTGTATGGATATA GTGT AGC CATC GTACTT CCTA TG ATGGAT
CTATGCTTTAAAAATCCATT CGCA TCG GTGG CGTGGA GGAT AC TACCTA
CATTAGGCCAGGTGCGGTGG C --- - CC T T ----------
CTCACGC
GAM33625 10441 GCAGGGATTCATGGACTAGG TT A --- G - T AC AGCTAGAC
7 TTTGCACCTTCTGAACCATG GCAGGGA C TGG ACTAGGTTT CA CCTTC GA CATG
AGCTAGACCATGTCTGGAGG CGTCCCT G ACC TGGTCCAAG GT GGAGG CT GTAC
CTGGAACCTGGTGACCCAGG CG - CAG - C T -- --------
CTCCCTGC
GAM33625 10493 GCTGTAACACAGAGCAGGTT CACAGA GG CCCACA CCACAAGAAACAAA

9 TGGAATGGCTCCACCCACAG GCTGTAA GCAGGTTTGGAAT CTCCA GGG

GGCCACAAGAAACAAACCCA CGACGTT TGTCTAGACCTTG GAGGT CCC
TGGAGAGTTCCAGATCTGTT ------ A- A----- ----------
TGCAGC
GAM33626 10408 GAGTCAGGAGAATCGCTTGA TCA AA GAA--- AGG - T AGCTAAGATCA
0 ACTCGGGAGGTGGAGGTTGT GAG GGAG TCGCTT CTCGGG TGGAG GT GTGGTG
GGTGAGCTAAGATCACACCA CTC CCTC AGCGAG GGGTCC ACCTC CG TACCAC
TTGCACTCCAGCCTGGGCAA TA- AA AACAAC G-- A T ----------
CAAGAGCGAAACTCCATCTC
GAM33626 10705 GGCTCCGGTGGTTGCAGTCA CC T TG A- A T C GAG - -- - ATGT
1 GATGGCAGCTGGAGGTGGAG GGCT GG GGT C GTC GA GG AGCTG GTGGA GCA ACC TG

CAACCTGATGTCGTGGTTTT CCGA TC CTA G CAG CT TC TCGAC CACCT CGT TGG GC
GCATCCACGACAGCTTCTCT -- - GT AA A C T AG- A TT T ----
CAGACAAGTGATCCTAGCC
GAM33626 10915 TAGGAATGGGATGGTTGTTT A - T-- TA GAG
4 TAGGTAGGCTTGGGAGCCAG TAGGA TG GGATGGTTG TTTAGG GGCTTGG
GCTGCCCTGAACTCTGGCCA ATCTT AC CCTACCGGT AAGTCC TCGGACC
TCCACACTTCTA C A CTC CG ---
GAM33626 10238 GAAGAATCGCTTGAATCCCA A- A -- GAA - AA - GT A - AGAT
7 AAGGTGGAGGTTGCAGTGAG GA GA TC GCTT TC CCA GG TGGAG TGCAGTG GC CG

CCGAGATCGCGCCACTGCAC CT CT AG CGAG AG GGT CC ACCTC ACGTCAC CG GC
TCCAGCCTGGCGACAGAGCA GC C AA AC- C -- G -- - C ----
AGACTCCGTC
GAM33627 9940 CACCCGTGCCTGGGATTCTC C T A ACAAAGGAG T AG - TTACA
0 TAAGACAAAGGAGAAGTCTT CACC GTGCC GGG TTCTCTAAG AAG CTTAA C C
AAAGCCTTACAGCGTCTTAA GTGG CATGG CCC GAGAGATTT TTC GAATT G G
GTCTTAGATCACATTTAGAG A - A ACACTAGA- T CT C -----
AGACCCGGTACAGGTG
GAM33627 9721 AGGCGCTAAACCTAAGGCTT AAACCTAA-- C A T AAGATTA
1 TTCTGGGAAGAGCTGTTAAG AGGCGCT GGCTTTT TGGGA GAGC GTT
ATTAGACTGTTCTCCCAAAA TCTGTGA CCGAAAA ACCCT CTTG CAG
AGCCAATAATTCTGAGTGTC GTCTTAATAA - - T -------
T
GAM33627 11194 TGGTAGGGAATTAGATGTCT T C-- C- -- T A- GATG AGAGAAAA
2 CTCAGAATCTTTTGTCTCTG TGGTAGGGAA TAGATGT TCT AGAAT CTTTTGTC CTG GAA CCT

AGAAGATGCCTAGAGAAAAG ACCATCCTTT ATTTACA AGA TCTTA GAAAATAG GAT CTT GGG

GGAATTCAATAGGATAAAAG T CTT CC CT - AA AA-- --------
TCATTCTCCAGATTCACATT
TATTTTCCTACCA
GAM33627 11273 TTGCTTTCTAATTGGAGTAA CTA AGTA CTTG T T TCAT
5 CTGGCCTTGGAACCTGTAGT TTGCTTT ATTGG ACTGGC GAACCTG AG CAG
CAGTCATTTGCCTCAGGTTT AACGAAA TGACC TGACCG TTTGGAC TC GTT
ACCTGCCAGTCCCACCAGTC TC- ACCC TCCA - C ----
TAAAGCAA
GAM33627 11012 TCTCTGAGCCTCTGCTGCTT - --- GTGTAACAAAATGAATAA C AGGGGC
9 TTCTTGTGTAACAAAATGAA TCTCTG AGCCTCTGCT GCTTTTCTT TACCTGCC TG
TAATACCTGCCCTGAGGGGC GGAGAC TTGGAGACGG TGAGAGGAA ATGGACGG AT

TATGGCAGGTAAAGGAGAGT G ACG ---------- T ------
GCAGGCAGAGGTTGCAGAGG
GAM33628 9777 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33628 9957 CAGAGTCTCGCTCTGTTGCT - TC CTGTT C-- -- T AATCTTG
2 CAGGCTGGAGTGCAGTGGTG CA GAG TCGCT GCTCAGG TGGAG TGCAGTGG GC

CAATCTTGGCTCACTGCAAC GT CTC AGCGA TGGGTCC ACCTC ACGTCACT CG
CTCCATCTCCTGGGTTTAAG A TT ATT-- TCT CA - -------
CGATTCTCATG
GAM33628 10409 GAGTCTCGCTCTGTTGCTCA TC CTGTT C-- -- T AATCTTG
3 GGCTGGAGTGCAGTGGTGCA GAG TCGCT GCTCAGG TGGAG TGCAGTGG GC
ATCTTGGCTCACTGCAACCT CTC AGCGA TGGGTCC ACCTC ACGTCACT CG
CCATCTCCTGGGTTTAAGCG TT ATT-- TCT CA - -------
ATTCTC
GAM33628 9778 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33628 9779 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
5 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33628 11021 TCTGTGGTTGAAGGAATGGA - G GAATGGA GTGA AGAT ACAGATA
9 TGGAAGTGTGTGAGCTAGAT TCTGTG GTT AAG TGGAAGTGT GCT TGC
TGCACAGATAGCAAGCAGAA AGACAC CAG TTC GTCTTTACA CGA ACG
CATTTCTGGTGAACTTGGAC A G AAGTG-- AGA- ---- -------
ACACAGA
GAM33629 10190 CTGTGGTTGAAGGAATGGAT - G GAATGGA GTGA AGAT ACAGATA
0 GGAAGTGTGTGAGCTAGATT CTGTG GTT AAG TGGAAGTGT GCT TGC
GCACAGATAGCAAGCAGAAC GACAC CAG TTC GTCTTTACA CGA ACG
ATTTCTGGTGAACTTGGACA A G AAGTG-- AGA- ---- -------
CACAG
GAM33629 10094 CGTCTAGGTGAAATGAGCTG - TG ATGAG GTA T CCT CAG TAATGC
1 TGTAGTCCTTTAGAGCCTCT CGTCTAG G AA CTGT GTCCTT AGAG CTGGA AAGG
GGACAGAAGGTAATGCTCTT GTAGATC C TT GGTA CGGGAG TCTT GACCT TTCT
AATCCAGTGATTCTCGAGGG A GT AGGA- AGA C AGT AA- ------
CAGAATGGAGGATTTGCACT
AGATG
GAM33629 9780 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33629 10768 GGGTGCCTGGAAGCTACTGC GCCT- CTA- C- -- AA AA TTTCAAT

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3          TTCTTCTAGTCAAATGGAAA GGGT    GGAAG   CTGCTTCTT  TAGT  CA  TGG  ATC
           TCTTTCAATGATGCCAGGTG CCCG    CCTTC   GACGAAGAA  GTCG  GT  ACC  TAG
           GTGCTGTTAAGAAGCAGAAT    AATCC    TTAA       TT   TG  GG   G-  -------
           TCTTCCCCTAAGCCC
GAM33629 10806  GTAGAGATGGAGTTTTACTA  A     -  TT    A  TT     TTGATCTTGAACT
4          TGTTGCCCAGGTTGATCTTG GT GAGATGG AG  TTACT TG  GCCCAGG
           AACTCCTGGGCTCAAGTGAT CA TTCTACC TC  AGTGA AC  CGGGTCC
           CCTCCCATCTTGAC       G      C  CT    -  T-      -------------
GAM33629 11049  TGAGATGGAGTTTTGCTCTT    AT-   TTT  CT   TT     CT   T-  AA   G --  AATCTTG
7          GTTGCCCAGGCTGTAGTGTA TGAG   GGAG   TG  CTTG  GCCCAGG  GTAG  GT  TGTA T  GC

           ATGTAGTGCAATCTTGGCTT ACTC   CCTC   AC  GAAC  TGGGTCC  CGTC  CA  ACAT A  CG
           AGTACAACCTCTGCCTCCTG    CGT    TT-  C-    T-      TC    TC  --   G TT  -------
           GGTTCAAGCCATTCTCCTGC
           CTCA
GAM33629 10299  GAGATGGAGTTTTGCTCTTG   AT-   TTT  CT   TT     CT   T-  AA   G --  AATCTTG
8          TTGCCCAGGCTGTAGTGTAA GAG   GGAG   TG  CTTG  GCCCAGG  GTAG  GT  TGTA T  GC
           TGTAGTGCAATCTTGGCTTA CTC   CCTC   AC  GAAC  TGGGTCC  CGTC  CA  ACAT A  CG
           GTACAACCTCTGCCTCCTGG    CGT    TT-  C-    T-      TC    TC  --   G TT  -------
           GTTCAAGCCATTCTCCTGCC
           TC
GAM33629 10787  GGTGACAAGAGTCTCACTCT    ACAA   TC   T  T      C---     A-   --  ATCAG
9          GTGGTCCAGACTGGAGTATA GGTG    GAG   TCAC CTG GGTCCAGA    TGGAGT  TAGT  GCT

           GTGCTATCAGAGCTTACTAC CCAC    CTC  AGTG GAC TCGGGTCT    ATTTCA  ATCA  CGA
           AACTTTAAACTTCTGGGCTC    C---   CT   -  -      TCAA     AC    TT  -----
           AGGTGATCCTCCCACC
GAM33630 10940  TCACTCTGTGGTCCAGACTG    T  T      C---     A-   --  ATCAG
0          GAGTATAGTGCTATCAGAGC TCAC CTG GGTCCAGA    TGGAGT  TAGT  GCT
           TTACTACAACTTTAAACTTC AGTG GAC TCGGGTCT    ATTTCA  ATCA  CGA
           TGGGCTCAGGTGA          -  -      TCAA     AC    TT  -----
GAM33630 9722   AGGCGTGAGAATCGCTTGAA    T  AA     AA--  GGA   GG  T-     A  CGAGATCCT
3          CCTGGAAGGTGGTGGTTGCA AGGCG GAG  TCGCTTG   CCT   AGGT  TGG  TGCAGTG GC

           GTGAGCCGAGATCCTGCCAC TCCGT CTC  AGCGAAC   GGG   TCCG  ACC  ACGTCAC CG

           TGCACTCCAGCCTGGGCAAC    -  AG     CAAC  ---   --  TC     - ---------
           CAAGCGAGACTCTGCCT
GAM33630 10294  GAGACGTGAGAATCGTTTGA     T  AATC   GAA--    AGG   GT     GCCCAAAT   CCA
4          ACCTGGGAGGTGGAGGTTGT GAGACG GAG   GTTT    CCTGGG  TGGAG  TGTAGTGA     CATG

           AGTGAGCCCAAATCATGCCA CTCTGT CTC   CGAG    GGATCC   ACCTC  ACGTCACT     GTAC

           CATGTCACTGCACTCCAGCC    -  AGAA   ACAAC    G--   --      --------  ---
           TAGGCAACAGAGCAAGACTC
           TGTCTC
GAM33630 9730   AGGCTTTAGAGTAGCAAAGG   CTTTA    AAA    ---   AT  GCT      CA  TGTCTTT
6          CCCCAGGGAATGGGCTCTGT AGG    GAGTAGC   GGCCCC   AGGGA  GG   CTGTTGGGA  GCT

           TGGGACAGCTTGTCTTTGGT TCC    TTCGTTG   CTGGGG   TCCCT  TC   GATGACCTT  TGG
```

TTCCAGTAGTTACTCCTCCC ----- GAA AAG CC ATT -- -------
TGAAGGGGTCAAGGTTGCTT
CCT
GAM33630 10405 GAGTAGCAAAGGCCCCAGGG AAA --- AT GCT CA TGTCTTT
7 AATGGGCTCTGTTGGGACAG GAGTAGC GGCCCC AGGGA GG CTGTTGGGA GCT
CTTGTCTTTGGTTTCCAGTA TTCGTTG CTGGGG TCCCT TC GATGACCTT TGG
GTTACTCCTCCCTGAAGGGG GAA AAG CC ATT -- -------
TCAAGGTTGCTT
GAM33630 9690 AGCAGCACAGAAATATTGGC A- CAG AAGCGAG
8 ACAGGGAAGCGAGTCTGCCA AGCAGCACAG AATATTGGCA GG
ATATTGGCTGTGCTGCT TCGTCGTGTC TTATAACCGT CT
GG --- -------
GAM33630 10826 GTCCTGGAAGACATGGTAGA - A T ---- A GA CCAACT
9 GCTGAAGGATCAGCCAACTT GTC CTGGA GACA GGT AGAGCTGA G TCAG
TGAGACTCAGCTCTAGCTGC CGG GACCT CTGT CCG TCTCGACT C AGTT
CTGTCTCCAGTGGC T - - TCGA - AG ------
GAM33631 10359 GAGGCAGGAGAATTGCTTCA CA AA CAAA--- TG A- GT ---- CAAG
1 AACTGGGCAGAGGTTGCAGT GAGG GGAG TTGCTT C GGC GAG TGCAGTG AGC
GAGCCAAGGTTGACCCACTG CTCT CCTC AACGAG G CCG CTC ACGTCAC TTG
CACTCCAGCCTGGGCAACAA A- AA AACAACG GT AC -- CCAG ----
GAGCAAAACTCCATCTC
GAM33631 10610 GGAGAATCGCTTGAATCCAG AATC GA-- A- T- A - AGAT
3 GAGGTTGCAGTGAGCTGAGA GGAG GCTT ATCCAGG GG TGCAGTG GC TG
TCACGCCACTGCACTCCAGC CCTC CGAG TGGGTCC CC ACGTCAC CG AC
CTGGGTGACAGAGCAAGACT AGAA ACAG GA TC - C ----
CC
GAM33631 11043 TGAGACAGGAGAATCGCTTG CA AA GAA--- AGGCA GT AGA AGAT
5 AACCCGGGAGGCAGAGGTTG TGAGA GGAG TCGCTT CCCGGG GAG TGCAGTG TG

CAGTGAGATGAGATCACACC ACTCT CCTC AGCGAG GGGTCC CTC ACGTCAC AC
ACTGCACTCCAGCCTGGGCA A- AA AACAAC GAC-- -- CAC ----
ACAAGAGCGAAACTCCATCT
CA
GAM33631 10287 GAGACAGGAGAATCGCTTGA CA AA GAA--- AGGCA GT AGA AGAT
6 ACCCGGGAGGCAGAGGTTGC GAGA GGAG TCGCTT CCCGGG GAG TGCAGTG TG

AGTGAGATGAGATCACACCA CTCT CCTC AGCGAG GGGTCC CTC ACGTCAC AC
CTGCACTCCAGCCTGGGCAA A- AA AACAAC GAC-- -- CAC ----
CAAGAGCGAAACTCCATCTC
GAM33631 10591 GGAGAATCGCTTGAACCCGG AA GAA--- AGGCA GT AGA AGAT
7 GAGGCAGAGGTTGCAGTGAG GGAG TCGCTT CCCGGG GAG TGCAGTG TG
ATGAGATCACACCACTGCAC CCTC AGCGAG GGGTCC CTC ACGTCAC AC
TCCAGCCTGGGCAACAAGAG AA AACAAC GAC-- -- CAC ----
CGAAACTCC
GAM33631 10204 CTTGAACCCGGGAAGCAGAG AA- AAGCA GT A - ACAT
8 GTTGCAGTGAGCCGACATCG CTTG CCCGGG GAG TGCAGTG GC CG
TGCCACTGCACTCCAGCCTG GAAC GGGTCC CTC ACGTCAC CG GC
GGCAACAAG AAC GAC-- -- - T ----
GAM33632 11105 TGAGGCAGGAGAATTGCCTG G AA - AA- AAGC GTC AA - AGAT
0 AACTCAGGAAGCGGAGGTCG TGAGGCAG AG TTGC CTG CTCAGG GGAG GCAGT GC TG

CAGTAAGCTGAGATCATGCC ACTCTGTC TC AGCG GAC GGGTCC CCTC CGTCA CG AC

ACTGCACTCCAGCCTGGGCA - AG A AAC GA-- A-- C- T ----
ACAGAGCGAGACTCTGTCTC
A

GAM33632 10620 GGAGAATTGCCTGAACTCAG AA - AA- AAGC GTC AA - AGAT
1 GAAGCGGAGGTCGCAGTAAG GGAG TTGC CTG CTCAGG GGAG GCAGT GC TG
CTGAGATCATGCCACTGCAC TCTC AGCG GAC GGGTCC CCTC CGTCA CG AC
TCCAGCCTGGGCAACAGAGC AG A AAC GA-- A-- C- T ----
GAGACTCT
GAM33632 9781 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33632 9660 AGAATCACTTGAACGTGGGA AA GAACG GGAG AG ----- A - AGAT
3 GGCAGAGGCTGCAGTGAGCC AG TCACTT TG GC AGGCT GCAGTG GC CG
GAGATCGTGCCACTGCACTC TC AGTGAG AC CG TCCGA CGTCAC CG GC
CAGCCTGGGCAACAGAGTGA AG ----- AA-- GG CCTCA - T ----
GACT
GAM33632 10198 CTTCACCTGAACTCACTGGG AC-- C A --- ------- T A AC G TAA
4 GCTTCTCCAGGGATATTAAC CTTC CTGAA TC CTGG GGCT TC CCAGGGAT TTA CTG ACTT

CTGGACTTTAAGAGTCAGAG GAAG GACTT AG GACC CCGA AG GGTCCCTG AGT GAC TGAG

TGAGTCCCTGGGACTAGTTC GGCA - - TAC CTTGATC - - GA - ---
AGCCCATCCAGGATTCAGAC
GGGAAG
GAM33632 10684 GGCATGAGAATCGCTTGAAC T AA AA-- AGGC GC A CAAGATCGT
5 CCGGGAGGCGGAGGCTGCAG GGCA GAG TCGCTTG CCCGGG GGAG TGCAGTG GC

TGAGCCAAGATCGTGCCACT CTGT CTC AGTGAGC GGGTCC CCTC ACGTCAC CG
GCACTCCAGCCTGGGCAACC - AG CAAC GA-- -- - ---------
GAGTGAGACTCTGTC
GAM33632 9683 AGATGTATTATGTCTGTCCT A T ATGTC GCG CCTGTGTCAG ----
ATGAATA
6 TGCGGGGGTTCTGGTCCCTG AG TG ATT TGTCCTT GGGGTTCTGGTC TCTTAAC TCTC

TGTCAGTCTTAACTCTCATG TC AC TAA GCAGGGA TCCCAAGACCGG AGAATTG GGAG

AATATAGAGGTAGTGTTAAG - T ATTTC --- ---------- TGAT -------
AGGCCAGAACCCTAGGGACG TA
CTTTAAATTCACT

--
GAM33632 10880 GTTACCTTCCTCTGCCTCTG C TC - T-- TC C-- CGT G GAG
9 CTCCCTTGTCTAGGGCGTGG GTTA CT CTCTG CCTC GC CCTTGT TAGGG GGA AT
AGATGAGGTGTCCTTCCTAT CGGT GA GAGAC GGAG CG GGGACA ATCCT CCT TG
TCACAGGGTTGCTGCGAGGA T GT A CGT TT CTT T-- G ---
CAGAGTGAGTTGGC

GAM33633 9782 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33633 10172 CTGGCATACAAGAGCCCGGA ATA A - AACT CC CTGCAATCAACAATAC ---
GAAC
1 ACTTCTGCCGATTTGTCACT CTGGC CAAG GC CCGG TCTG GATTTGTCA TCC CCG
GCAATCAACAATACTCCCCG GACCG GTTC TG GGTC AGAC TTGAACGGT AGG GGC
GAACATCGGCAAGGATGGCA AGG G T GT-- T- ---------- AAC ----
AGTTTCAGATGCTGGTGTGC AT
TTGGGAGCCAG

--
GAM33633 10166 CTGCTTGAACCCAGGAGGCA C AA AGGCA AT A- AAGAT
2 GAGATTGCAGTGAGTCAAGA CTG TTG CCCAGG GAG TGCAGTG GTC
TGGCACTACTGCACTCCAGC GAC AAC GGGTCC CTC ACGTCAT CGG
CTGGGCAACAG - -- GAC-- -- CA -----
GAM33633 11108 TGAGGCAGGAGAATTGCTTG A AA GAA--- AGG GT A - AGGT
4 AACCCGGGAGGTGGAGGTTG TGAGGC GGAG TTGCTT CCCGGG TGGAG TGCGGTG GC CG

CGGTGAGCCGAGGTCGCGCC ACTCTG CCTC AGCGAG GGGTCC ACCTC ACGTTAC CG GC

ATTGCACTCCAGCCTGGGCA - AA AACAAC G-- -- - C ----
ACAAGAGCGAAACTCCGTCT
CA
GAM33633 10366 GAGGCAGGAGAATTGCTTGA A AA GAA--- AGG GT A - AGGT
5 ACCCGGGAGGTGGAGGTTGC GAGGC GGAG TTGCTT CCCGGG TGGAG TGCGGTG GC CG

GGTGAGCCGAGGTCGCGCCA CTCTG CCTC AGCGAG GGGTCC ACCTC ACGTTAC CG GC

TTGCACTCCAGCCTGGGCAA - AA AACAAC G-- -- - C ----
CAAGAGCGAAACTCCGTCTC
GAM33633 11084 TGAGGCAGGAGAATCGCTTG A AA - GAA--- AGG GT A - AGAT
6 AACCCAGGAGGTGGAGGTTG TGAGGC GGAG TC GCTT CCCAGG TGGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC AG CGAG GGGTCC ACCTC ACGTTAC CG GC

ATTGCACTCCAGCCTGGGCA - A- A AACAAC G-- -- - C ----
ACAAGAGCAGAACTCCGTCT
CA
GAM33633 10578 GGAGAATCGCTTGAACCCAG AA - GAA--- AGG GT A - AGAT
7 GAGGTGGAGGTTGCAGTGAG GGAG TC GCTT CCCAGG TGGAG TGCAGTG GC CG

CCGAGATCGCGCCATTGCAC CCTC AG CGAG GGGTCC ACCTC ACGTTAC CG GC
TCCAGCCTGGGCAACAAGAG A- A AACAAC G-- -- - C ----
CAGAACTCC
GAM33633 10872 GTGTGATATAGGTGGTCTGG ATA - - GGC ACAA AT A -- GCTG
8 GATCATGGCTGGACAAACAC GTGTGAT GGTGGT CT GGGATCAT TGG ACACA GCAGT GG
AAGAGT

AATGCAGTAGGAAGAGTGCT CATACTG CCACTA GA TTCTAGTA ACC TGTGT CGTCA CT
TTCTCG
GGCTCTTGGTCACTGCTGTG C-- C G --- CAG- -- - GG ----
TGACCCAATGATCTTGAGCA
TCACCCGTCATAC
GAM33633 10370 GAGGCAGGAGAATTGCTTGA A AA GAA--- T - CAGAGGT G CGAGATAAC
9 ACCTGGTGGGGCAGAGGTTG GAGGC GGAG TTGCTT CC GG TGGGG TGCAGT AGC

CAGTGAGCCGAGATAACGCT CTCTG CCTC AATGAG GG CC ACCTC ACGTCA TCG
ACTGCACTCCAGCCTGGGCA - AA ACAACG T G ------- - ---------
ACAGAGTAAAACTCCGTCTC
GAM33634 10351 GAGGCAGGAGAATCGTTTGA GCA AA GAA--- TG AAGC - -- C GTCGAGA
0 ACCTGGGAAGCGGAGGTTGC GAG GGAG TCGTTT CC GG GGAG GT TG CGTGA
CGTGAGTCGAGATCATGCCA CTC TCTC AGCGAG GG CC CCTC CG AC GTACT
TTGCACTCCAGCCTGGGCAA --- AA AACAAC GT GA-- A TT C -------
CAAGAGCGAAACTCTCTC
GAM33634 9663 AGAATTGCTCGAACCCGGGA AA GAA-- AGACA GT A - AGAT
1 GACAGAGGTTGCAGTGAGCC AG TTGCTC CCCGGG GAG TGCAGTG GC CG
GAGATTGTGCCACTGCACTC TC AGCGAG GGGTCC CTC ACGTCAC CG GT
CAGCCTGGGCAACAGAGCGA AG ACAAC GAC-- -- - T ----
GACT
GAM33634 11255 TTGCTCGAACCCGGGAGACA GAA-- AGACA GT A - AGAT
2 GAGGTTGCAGTGAGCCGAGA TTGCTC CCCGGG GAG TGCAGTG GC CG
TTGTGCCACTGCACTCCAGC AGCGAG GGGTCC CTC ACGTCAC CG GT
CTGGGCAACAGAGCGA ACAAC GAC-- -- - T ----
GAM33634 10480 GCTCGAACCCGGGAGACAGA GAA-- AGACA GT A - AGAT
3 GGTTGCAGTGAGCCGAGATT GCTC CCCGGG GAG TGCAGTG GC CG
GTGCCACTGCACTCCAGCCT CGAG GGGTCC CTC ACGTCAC CG GT
GGGCAACAGAGC ACAAC GAC-- -- - T ----
GAM33634 10748 GGGCGAGTCCTTAACCTTGG - GA ACCTT AAA- TCT TTTA CCTG
4 CAAAATAAACTTCTGAATTT GG GC GTCCTTA GGCA TAAACT GAA TTGAGA
ATTGAGACCTGTCTCAGGTA CC CG CGGGAGT TCGT ATTTGG TTT GACTCT
CTTTTTGGTTTACATGTGCT A GA GT--- GTAC TT- CATG ----
TGTGAGGGCAGGCACC
GAM33634 9671 AGAGATGCTAAGTTTAGATT A GCTA TA C G AC TTTTTAAT
7 CCAGGGGGCAGGACTGGATT AG GAT AGTT GATTC AGGGG CAGG TGGA
TTTAATTTCATCTGGCTCCT TC CTA TCGA CTGAG TCCTC GTCT ACTT
GAGTCCTAGCTCCTAATCCT - ATCC TC - G -- --------
GAM33634 9783 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33634 11033 TGAATTTGTGACTTGTCTGG TTG - GTT CGAA TCTCTACT
9 TTTGGCATCTCGAAGGGCTT TGAAT TGACTTGT CTG TGGCATCT GGGCTT
TCTCTACTGGGTCCAGGGTG ACTTA ACTGGACA GAC ACCGTGGG CCTGGG
CCACAGAACAGGTCAGCATT CG- A --- A--- --------
CA
GAM33635 10348 GAGGCAGGAGAATCGCTTGA GAGAA GA-- AATCA GT - A---- CAAG
0 ATCTAGGAATCAGAGGTTGC GAGGCAG TCGCTT ATCTAGG GAG TGCA GTG GC

AGTGAGCCAAGGTCACACCA CTCCGTC AGTGAG TGGGTCC CTC ACGT CAC TG
CTTGCACTCCACAGCCTGGG AG--- ACAG GACAC -- T CACAC ----
TGACAGAGTGAGACTGCCTC
GAM33635 9784 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33635 10355 GAGGCAGGAGAATGGCGCGA A AATGG GAA---- AAG CT A - AGAT
3 ACCCGGGAAGTGGAGCTTGC GAGGC GGAG CGC CCCGGG TGGAG TGCAGTG GC CG

AGTGAGCCGAGATCGCGCCA CTCTG CCTC GCG GGGTCC ACCTC ACGTCAC CG GC

CTGCACTCCAGCCTGGGCAA - AAA-- AGACAAC G-- -- - C ----
CAGAGCGAAACTCCGTCTC
GAM33635 11042 TGAGACAGGAGAATCACTTG CA AA A GAAC- GG AG TT GG - AGAC
4 AACTCCGGAGGTTGAGGTTT TGAGA GGAG TC CTT TCC AGGTTG GT CAGT GC CG
CAGTGGGCCGAGACCGAGCG ACTTT CCTC AG GAG GGG TCCGAC CA GTCA CG GC

ACTGCACTCCAGCCTGGGCA A- AG C ACAAC -- CT C- G- A ----
ACAGAGCGAGACTCCATTTC
A
GAM33635 10988 TCCTGCATGGCAGTTCCATA G CAG - - CCA CCATCCTT
7 TGCAGAGCCAGAATCCATCC TCCT CATGG TTC CATA TGCAGAG GAAT
TTGTTCCTTCTGCATTGTGA AGGA GTACC AAG GTGT ACGTCTT CTTG
GAAAATCCATGGAGGA G TAA A T C-- --------
GAM33635 11030 TGAACCCCGGAGACAGAGGT A - G-- TT GT A-- AC ATGT
9 TGCAGTGAGCCGAGATACAT TGA CCC CGGA ACAGAGG GCA GAGCCGAG TACAT ATATAT

ACATATATATGTATATATCA ATT GGG GTTT TGTTTCC CGT CTCGGTTC GTGTA TATATA

TGTGCAACTTGGCTCTGCTC C T GAA T- -- AAC C- ----
CTTTGTAAGTTTGTGGGCTT
A
GAM33636 9632 ACAGAGGTTGCAGTGAGCCG TT GT A-- AC ATGT
0 AGATACATACATATATATGT ACAGAGG GCA GAGCCGAG TACAT ATATAT
ATATATCATGTGCAACTTGG TGTTTCC CGT CTCGGTTC GTGTA TATATA
CTCTGCTCCTTTGT T- -- AAC C- ----
GAM33636 10629 GGAGAATTGCTTGAACCCAG AA TG GAA-- AGGC GT A- CGAGATA
1 GAGGCGGAGGTTGCAGTGAG GGAG T CTT CCCAGG GGAG TGCAGTG GC
CCGAGATAGCACCACTGCAC CCTC A GAG GGGTCC CCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGT AG GT ACAAC GA-- -- CA -------
GAGACTCC
GAM33636 10061 CCTGACTCTGATCACAGGCA GA - CAA- ATA T TTTCAATCC
2 AAGGAATAAAGTCTCATTTC CCT CTCTGATC ACAGG AGGA AAG CTCA
AATCCTGAGCTTCTCCTAAT GGG GAGACTAG TGTTC TCCT TTC GAGT
TCTTGTGGATCAGAGCTGGG TC G TTAA C-- - ---------
GAM33636 9687 AGCAGACTGAACTAAGACAC A ACTAAG A G G T AAA
3 CCTCTGCCTGTGGTTGTCTT AGCAG CTGA AC CCCTCT CCTGTG TTG CTTGGC
GGCAAAGCCAGGTAATGCAG TCGTC GACT TG GGGAGA GGACGT AAT GGACCG

GAGAGGGGTGGACTCAGCCT C CAGG-- - - - - ---
GCT
GAM33636 11272 TTGCTTTAGCCCAGGAATTC TA-- AATTC TT - ATGAT
4 GAGTTTGCAGTGAGCTATGA TTGCTT GCCCAGG GAGT GCAGTGA GCT
TGGTGTCATTGCACTCCAGC AACGAA CGGGTCC CTCA CGTTACT TGG
CTGGGCAATCAAGCAA CTAA GAC-- -- G -----
GAM33636 9965 CAGCTGGGACTGCAGGGGCA GC A G GCACAAC C C TT ATT- TAGGGC
5 CAACATCACGCCTGGCTAAT CA TGGG CT CAGGG ATCA GCCTGG TAAT TTGT TTCTG

TTTTGTATTTTCTGTAGGGC GT ACTC GG GTCCT TGGT CGGACC ATTG GACA AGGAT
TAGGATTTCACAGTGTTACC AA - - AAAACTC - C T- CTTT ------
CAGGCTGGTCTCAAAATCCT
GGGCTCAAATG
GAM33636 10187 CTGTGACTATTTCGCTGAAT ACTATT AATCT AAC- AGG AC T CCATTTT
8 CTTTGCAACTCTGAGAGGTC CTGTG TCGCTG TTGC TCTGAG TCAGT TTTTATTT AC
AGTACTTTTATTTTACCCAT GACAC AGTGAC AATG AGACTC AGTCA AGAGTGGA TG
TTTGTAGGTGAGAAAACTGA ------ AC--- GGAA GG- AA - -------
GGCTCAGAAAGGGTAACACA
GTGACACAG
GAM33636 10164 CTGCCTCCCCACTCAAGCTC C CC- CAA TCT A AAA - A CAC AGGAC
9 TGTAAGGACGCAAAGAGGGC CTG CTC CACT GC GTA GGACGC GA GGGC AGGC GA

AAGGCCACGAAGGACTCAGC GAC GAG GTGA CG CGT CCTGTG CT CCCG TCCG CT
CTGGCCCATCGTGTCCCTGC C ACC CCC TCT C --- A G A-- -----
TCTGCCCCAGTGCCAGAGCC
AG
GAM33637 10216 CTTTCTCTCGTGAATGGAGC CT AAT- - TTTTC CTTT
2 TGTTTTCTTCAGAGCCTTTG CTTT CTCGTG GGAGC TG TTCAGAGC
CTCTGAAACATCACGCTCCC GAAG GGGTAT CCTCG AC AAGTCTCG
CTGTATGGGGAGAAG AG GTCC C TACA- ----
GAM33637 11088 TGAGGCAGGAGAATCGCTTG G AA GAA--- AGGC - C AGCCAAAATCG
3 AACCCGGGAGGCGGAGGTCG TGAGGCAG AG TCGCTT CCCGGG GGAG GT GTGGTG

TGGTGAGCCAAAATCGCACC ACTCTGTC TC AGTGAG GGGTCC CCTC CG TACCAC
ATTGCACTCCAGCCTGGGCA - AA AACAAC GA-- A T ----------
ACAAGAGTGAAACTCTGTCT
CA
GAM33637 10341 GAGGCAGGAGAATCGCTTGA G AA GAA--- AGGC - C AGCCAAAATCG
4 ACCCGGGAGGCGGAGGTCGT GAGGCAG AG TCGCTT CCCGGG GGAG GT GTGGTG

GGTGAGCCAAAATCGCACCA CTCTGTC TC AGTGAG GGGTCC CCTC CG TACCAC
TTGCACTCCAGCCTGGGCAA - AA AACAAC GA-- A T ----------
CAAGAGTGAAACTCTGTCTC
GAM33637 9914 ATGCATGGGGGTACACAGGG G A-- G CACAATGCA - GAAATAG A C TCC
5 GACACAATGCAGTGTTGGTG ATGCATG GGGT CACA GGGA GTGT TGGTGG TC TTGAGCA
TTC
GGAAATAGTCATTGAGCACT TACGTAT TTTA GTGT CCCT CACA ACCACC AG GACTTGT
AAG
TCTCCTTTCCTCTCATGTGA G AAA G --------- G ACTA--- A A ---
AATGTTCAGAGAATCACCAC TTTCCTCTCATGT

```
          CAGACACTCCCGTGTGAAAA
          TTTGTATGCAT
                      ----------
GAM33637 10177  CTGGGATTACATGTGTGAGC   GG TT  TG--     C  CGC     C---    TTGTT
6         CACCGCGCCTGGCCTCAAAT CTG  A  ACA   TGTGAGC AC  GCCTGGC   TCAAA
          TGTTTTTGAAGTAGTTAGGT GAC  T  TGT   ATACTCG TG  TGGATTG   AGTTT
          TGTAGCTCATAAGACTGTCT   TT C-  CAGA     A  T--     ATGA    -----
          TTCAG
GAM33637 11214  TGTGAGCCACCGCGCCTGGC      C  CGC     C---    TTGTT
7         CTCAAATTGTTTTTGAAGTA TGTGAGC AC  GCCTGGC   TCAAA
          GTTAGGTTGTAGCTCATA  ATACTCG TG  TGGATTG   AGTTT
                              A  T--     ATGA    -----
GAM33637 9785   AGTTTTAGGGTACATGTGCA   TTA   A  T TG  -    - G  T   T  ATAT
8         CAACATGCAGGTTTGTTACA AGTT  GGGT CA G  CAC AACATG CA GT TGT AC
          TATGTATACATGTGCCATGT TCAA  CCCA GT C  GTG TTGTAC GT TA ATA TG
          TGGTGTGCTGCACCCATTAA    TTA   C - GT   G    C  G  C   -  ----
          CT
GAM33638 10175  CTGGGATGGGATGGAGCAAG   G   G AT    A  A        T  A-    GAAT
0         AGGTGAAGATCTTGGAGTCT CT GGAT GG  GGAGC AG GGTGAAGATCT GG  GTCTG
          GGAATCAGACCACCTGGATT GG TCTA CC  CCTTG TC CTACTTTTAGG CC  CAGAC
          TTCATCCTAGTTCCCCGATC   G   G --    A -        T  AC    ----
          TGGG
GAM33638 10419  GATGGGATGGAGCAAGAGGT   G  AT    A  A        T  A-    GAAT
1         GAAGATCTTGGAGTCTGGAA GAT GG  GGAGC AG GGTGAAGATCT GG  GTCTG
          TCAGACCACCTGGATTTTCA CTA CC  CCTTG TC CTACTTTTAGG CC  CAGAC
          TCCTAGTTCCCCGATC      G --    A -        T  AC    ----
GAM33638 10562  GGAGAATCACTTGAACTCGA    AA  A  GA--   GAG   -  GT     A  TGAGATCCC
2         GAGGCGGAGGTTGCAGTGAG GGAG  TC CTT   ACTC   AGGC GGAG  TGCAGTG GC
          CTGAGATCCCGCCACTGCAC CCTC  AG GAG   TGGG   TCCG CCTC  ACGTCAC CG
          TCCAGCCTGGGTGACAGAGC    AG  C   ACAG   ---   A   --     - ---------
          GAGACTCC
GAM33638 11286  TTGTTGATTCTGTTGAGGAT  TG    TC   G   ----      TAT   TCC     - GATGGG
4         ATATCCCTATGATGTCCCTG T  TTGAT  TGTT AGGA   TATATCCC   GATG   CTGGGAA GC
          GGAAGCGATGGGGCATTCCC G  AACTA  ATAA TCTT   GTGTAGGG   CTAC   GACCCTT CG

          AGTCATCTGGGATGTGCAGT  GT    TT   A   TGAC      T--   T--     A ------
          TTCTAAATATTATCAATGG
GAM33638 10423  GATTCTGTTGAGGATATATC   TC   G   ----      TAT   TCC     - GATGGG
5         CCTATGATGTCCCTGGGAAG GAT  TGTT AGGA   TATATCCC   GATG   CTGGGAA GC
          CGATGGGGCATTCCCAGTCA CTA  ATAA TCTT   GTGTAGGG   CTAC   GACCCTT CG
          TCTGGGATGTGCAGTTTCTA   TT   A   TGAC      T--   T--     A ------
          AATATTATC
GAM33638 9625   ACAAATGTCTTTGGCCTCTG   AA   --    --     CC    C  A    AG  CCATT
6         TGCCTTTCCTCAGACTTTCA ACA  TGTC  TTTGGC  CTCTGTG  TTTCCT AG CTTTC  GC
          GGCCCATTGTGAGAGAGCTA TGT  ACAG  GAACTG  GGGACAT  GAAGGA TC GAGAG  TG

          GGAAGATACAGGGTTGTCAA   AC   TT    TT     A-    -  -    AG -----
          GTTGACACATGT
GAM33638 11269  TTGCTTGAACCTTGGAGGCA  TG   GA--   T    AGA   T    A  CAAGATCAT
7         GAGGTTGCAGTGAGCCAAGA T  CTT   ACCT GGAGGC   GGT GCAGTG GC
```

TCATGCCACTGCACTGTAGC A GAG TGGG CCTCCG TCA CGTCAC CG
CTCCTGGGTGACAGAGTGA GT ACAG T ATG - - ---------
GAM33638 10883 GTTCCTCTTCTCATTGGCTG TCTTCTCATT---- - CT -- A--- GT AATTG
8 ATGTGCTCTGTGGCATCTGT GTTCC GGCTGATG TGCT GTGGC ATCTGTCAC G TTT
CACAGGTTTTAATTGAAGGT CAAGG TCGACTAC ACGA CACCG TGGACGGTG C GAA

CAGCAGTGGCAGGTAAGCCA TTTTCCGACTTTCT T C- AA ACGA TG -----
CCAGCATCATCAGCTTCTTT
CAGCCTTTTGGAAC
GAM33638 10708 GGCTGATGTGCTCTGTGGCA - CT -- A--- GT AATTG
9 TCTGTCACAGGTTTTAATTG GGCTGATG TGCT GTGGC ATCTGTCAC G TTT
AAGGTCAGCAGTGGCAGGTA TCGACTAC ACGA CACCG TGGACGGTG C GAA
AGCCACCAGCATCATCAGCT T C- AA ACGA TG -----
GAM33639 11057 TGAGGCAGAAGAATCTCTTA A AGAAT- TAAA AGGC GT - CGAGATT
0 AACCCGGGAGGCGGAGGTTG TGAGGC GA CTCT CCCGGG GGAG TGCAGTGA GC

CAGTGAGCCGAGATTGCGTC ACTTTG CT GAGA GGGTCC CCTC ACGTCACT CG
ACTGCACTCCAGCCTGGGCA C CAGAGC CAAC GA-- -- G -------
ACAGAGCGAGACTCCGTTTC
A
GAM33639 10239 GAAGAATCTCTTAAACCCGG --- A - AAA--- AGGC GT - CGAGATT
1 GAGGCGGAGGTTGCAGTGAG GAA GA TCTC TT CCCGGG GGAG TGCAGTGA GC
CCGAGATTGCGTCACTGCAC CTT CT AGAG GA GGGTCC CCTC ACGTCACT CG
TCCAGCCTGGGCAACAGAGC TGC C C GACAAC GA-- -- G -------
GAGACTCCGTTTC
GAM33639 10125 CTCTTAAACCCGGGAGGCGG TAAA AGGC GT - CGAGATT
2 AGGTTGCAGTGAGCCGAGAT CTCT CCCGGG GGAG TGCAGTGA GC
TGCGTCACTGCACTCCAGCC GAGA GGGTCC CCTC ACGTCACT CG
TGGGCAACAGAG CAAC GA-- -- G -------
GAM33639 11024 TCTTTCACTGGAATCACATC T T- T C --- TCCCC CC CTCCCTCA
3 TGCAGCTCCTCCCCCTCCGC TCTT CAC GGAA CA ATCTG CAGCTCC CT GCC
CCTCCCTCAGGCTTAGACCG AGAG GTG TCTT GT TAGAC GTCGAGG GA CGG
TGGAGCTGTAACAGATCTGT T CT - C AAT TGCCA TT --------
TCTTCGTGTGAGA
GAM33639 10159 CTGCCAGCCGTCTGTCTCTA C G G CT T CCAA- G C - GGCCGT
4 GTGTTTTTCCAAATGACATC CTGC AGCC TCT TCT AG GTTTTT AT ACATC AGGG CTCT
CAGGGCTCTGGCCGTGGAGT GACG TCGG GGA AGG TC CAGGAA TA TGTAG TCCC GAGG

CCCTGATGTGATCGCTAAAG C - G CC - ATCGC G - T ------
GACCTCCGGAGAGGGGCTCG
CAG
GAM33639 10836 GTCTGTCTCTAGTGTTTTTC G -- T CCAA- G C - GGCCGT
5 CAAATGACATCCAGGGCTCT GTCT TCTCT AG GTTTTT AT ACATC AGGG CTCT
GGCCGTGGAGTCCCTGATGT CGGG AGAGG TC CAGGAA TA TGTAG TCCC GAGG
GATCGCTAAAGGACCTCCGG G CC - ATCGC G - T ------
AGAGGGGC
GAM33639 10465 GCGTTCCTGGGAAAACCATT CT AAACC-- T TT CT TCT GA AAG
7 TAGATTTCATTCTCCTTCCT GCGTTC GGGA ATT AGA TCATT CCTTCCTT CT CAG
TTCTCTGACAGAAGCTGCTG CGTAAG CCCT TAG TCT AGTAA GGAAGGAG GG GTC
GTGAGGAAGGTAATGATCTT AC ACCAAAC T -- T- T-- TC ---

GATCAAACCATCCCCAGAAT
GC
GAM33639 9989 CATTTTAGTAATGCTCAGCT A A - T CC- - TA--- TT- CA GTT
9 GGACCAGTGTTAGTTATATT CATTTT GT ATGCT CAGC GGA AG TGT GTTATA TGAGT
GAAAAAT
TGAGTCAGAAAAATGTTGTT GTGGAA CA TACGA GTCG CCT TC ACG TAATAT GTTCA
CTTTTTG
TTTCAACTTGCTTTATAATC G C T T CTA T TCCTC TTC A- ---
TCCTGCATCTATCTCCTGCT
GTAGCATCACGAAGGTG
GAM33640 9786 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33640 10212 CTTGCCATGCAGCCCTTTTT CA A- TTTT CACAATACAGCA
3 ATGGAGCAAGTCACAATACA CTTGC TGC GCCCT ATGGAGCAAGT
GCAGCTTGCTTCATTAGGGC GAACG ACG CGGGA TACTTCGTTCG
AAGCAAGCAAG A- AA T--- ----------
GAM33640 10786 GGTGAAACTGCCCTTTCCTT AAC CC TT GTTCTATGA TG- AAA TGGGGC

4 TCTGTTCTATGAGTGTGATG GGTGA TGC TTTCC TCT GTGTGA GTGTTTGAG ATG
GTGTTTGAGAAAATGTGGGG CCACT ACG AGAGG AGA TACACT CGCGGACTT TAT
CTATGGTTCAGGCGCACTTC C-- AA T- AACGTG--- TCA GG- ------
ACATGTGCAAAGATGGAGAA
AGCACTCACC
GAM33640 11189 TGGGTACTTTATCTCACACT GG TT CTC C A TG TTC
5 CTGATTTCTTGCTTCGTGGG TG TAC TAT ACA TCTG TTTCT C
AAACAGACTGTAATATTGTA AC ATG ATA TGT AGAC AAAGG G
AGCA GA TT A-- C - GT ---
GAM33640 11216 TGTGCATTCCTTCCAGAGCA CC ------- C TG A G CA TGCT
6 TTTGTGAGGAGTGTTCAGCT TGTGCATT TTCCA GAG ATT TG GGA TGTT GC
GCTGCAAACATCCCATGAAT ACATGTGG AAGGT CTC TAA AC CCT ACAA CG
CCTCAGCTACTTGGAACAGG AC TCATCGA C GT - - A- ----
TGTACA
GAM33640 10733 GGGAGGACTGCTTGAGCCCA G AC-- GA-- AGG CT A TGTGATCCT
7 GGAGGTGGAGTCTGTAGTGA GG AGG TGCTT GCCCAGG TGGAGT GTAGTG GC
GCTGTGATCCTGCCACTGCA CC TCC ACGAG CGGGTCC ACCTCA CGTCAC CG
CTCCAGCCTGGGCAACAGAG G CAGA ACAA G-- -- - ---------
CAAGACCCTGCC
GAM33640 10793 GGTGGGAGGACTGCTTGAGC TG AGGAC GA-- AGG CT A TGTGATCCT

8 CCAGGAGGTGGAGTCTGTAG GG GG TGCTT GCCCAGG TGGAGT GTAGTG GC
TGAGCTGTGATCCTGCCACT CC CC ACGAG CGGGTCC ACCTCA CGTCAC CG
GCACTCCAGCCTGGGCAACA GT CAGA- ACAA G-- -- - ---------
GAGCAAGACCCTGCC
GAM33640 10543 GGACTGCTTGAGCCCAGGAG A - GA-- AGG CT A TGTGATCCT
9 GTGGAGTCTGTAGTGAGCTG GG CT GCTT GCCCAGG TGGAGT GTAGTG GC
TGATCCTGCCACTGCACTCC CC GA CGAG CGGGTCC ACCTCA CGTCAC CG
AGCCTGGGCAACAGAGCAAG A A ACAA G-- -- - ---------

ACC
GAM33641 10062 CCTGAGACAGAGTTTGCTCT A - T- CT TT CTGGAGTTTAAT C TC
GCTTACCA
2 TGTTGCCCAGGCTGGAGTTT CCTGAG CAG AG TTGCT TG GCCCAGG GGCA GA TTG

AATGGCACGATCTTGGCTTA GGACTC GTC TC AACGA AC TGGGTCC CCGT CT AAC
CCACAACCTCTGCCTCCTGG C C TT -- T- T---------- - CC --------
GTTCAAGCAATTCTCCTGCC
TCAGG
GAM33641 10328 GAGGCAGGAGAATCACTTGA G AA AC- AA- AGA GT GA- GAGAT
3 ACCCGGGAGATGGAGGTTGC GAGGCAG AG TC TTG CCCGGG TGGAG TGCAGT GCC

AGTGAGCCGAGATGGCGCAA CTCTGTC TC AG AAC GGGTCC ACCTC ACGTCA CGG

CTGCACTCCAGCCTGGGCAA - AG GTA AAC G-- -- ACG -----
CAAATGGAGACTCTGTCTC
GAM33641 9699 AGGAAGAGGCTGGCTGTGTG -- G GG - --- C CTT- TATTT
4 GATGAGAGCAACTTGCTTTT AGGA AGA GCT CTGTGTGG AT GAGAGCAA TTG TTTACAATAAT

TACAATAATTATTTGTTATT TCCT TTT TGA GGTATATT TG TTCTCGTT AAC AAATGTTATTG

GTAAATTAACAATTTGCTCT AG A A- A GTC T AATT -----
TCTGGTATTATATGGAAGTA
TTTGATCCT
GAM33642 9787 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33642 10278 GAGAATTGCTTGAACCTGGG AA GAA--- TG AGG GT TG A - AAAT
2 AGGTGGAGGTTGTGGTGAGC GAG TTGCTT CC GG TGGAG TG GTG GC CG
CGAAATTGTGCCATTGCACT CTC AGCGAG GG CC ACCTC AC TAC CG GT
CCAGCCTGGGCAACAAGAGC AA AACAAC GT G-- -- GT - T ----
GAAACTC
GAM33642 10406 GAGTAGCTGGGATTACAGGT G G ATT - TGT A G G TTTTTGTATTT
4 GTGTGCCACCATGTCTGGCT GA TAGCT GG ACA GGTG GCC CCAT TCTG CTGA
GATTTTTGTATTTTTAGTAG CT GTCGG CC TGT CCAC TGG GGTG AGAT GATT
AGGTGGGGTTTCACCATGTT G A GGT A TT- - G - ----------
GGCCAGGCTGGTC
GAM33642 9788 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33642 10876 GTGTTCGAGCACACACCTCC G ACACC G G AGC-- CCAG
8 TTGCAGTGGCTTCAGCACCC GTGTTC AGCAC TCCTT CA TGGCTTC AC
AGGTCTCCGGGAGCCAGTGA CATAGG TTGTG AGGAA GT ACCGAGG TG
AGGAACCAAGTGTTGGATAC - AACCA - G GCCTC ----
GAM33642 10536 GGACCTGGAGTGCATCAGGA - T--- T TGA---- G TTTTTGC
9 TCTGACCAGATAGGAGTTTT GGACCT GGAG GCA CAGGATC CCAGATA GAG

TGCCTCGTGTCTGGGTGCTA CCTGGA TCTC CGT GTTTTAG GGTCTGT CTC
CGATTTTGTGCCGTTCTCTG G TTGC - CATCGTG G -------
AGGTCC
GAM33643 10695 GGCCTCCTCCCAGCGTCACG CT --- CCA- G - ATCCCT-- TACT ATGCT
0 GAATGCTGTCCTGATCCCTA GGC CC TC GCGTCACGGAAT CTGTC CTG AGCATT CAC

GCATTTACTCACATGCTGTG CCG GG AG TGTAGTGTCTTA GACGG GGT TCGTGA GTG

CTTAGTGCTTGACCATGTGG TT TGC AATG - T GTACCAGT TTC- -----
TGGCAGATTCTGTGATGTGT
AAGACGTGGTTGCC
GAM33643 10109 CTCCCAGCGTCACGGAATGC CC G G - ATCCCT-- TACT ATGCT
1 TGTCCTGATCCCTAGCATTT CT CA CGTCACGGAAT CTGTC CTG AGCATT CAC
ACTCACATGCTGTGCTTAGT GA GT GTAGTGTCTTA GACGG GGT TCGTGA GTG
GCTTGACCATGTGGTGGCAG AT - - T GTACCAGT TTC- -----
ATTCTGTGATGTGTAAG
GAM33643 10463 GCGTCACGGAATGCTGTCCT G - ATCCCT-- TACT ATGCT
2 GATCCCTAGCATTTACTCAC GCGTCACGGAAT CTGTC CTG AGCATT CAC
ATGCTGTGCTTAGTGCTTGA TGTAGTGTCTTA GACGG GGT TCGTGA GTG
CCATGTGGTGGCAGATTCTG - T GTACCAGT TTC- -----
TGATGT
GAM33643 10093 CGTCACGGAATGCTGTCCTG G - ATCCCT-- TACT ATGCT
3 ATCCCTAGCATTTACTCACA CGTCACGGAAT CTGTC CTG AGCATT CAC
TGCTGTGCTTAGTGCTTGAC GTAGTGTCTTA GACGG GGT TCGTGA GTG
CATGTGGTGGCAGATTCTGT - T GTACCAGT TTC- -----
GATG
GAM33643 10262 GAGAACTGTAGTGCAAGGTT AA TGCCA TTTG - AATC
4 TTGCCAACTTTTTGACCAGA GAG CTGTAGTGCAAGGTTT ACTT ACC AG
ATCCTCGGTGAGTAATAAAT CTC GACGTCACGTTTTAAA TGAG TGG TC
TTTGCACTGCAGCTC -- TAA-- ---- C ----
GAM33643 10914 TAGCTGCACAACACAAGCCC ACAACACA CA AGGCAA A ------ TG T AGAGC

5 ACAGGCAAACACACAGACTC TAGCTGC AGCC C ACACACAG C TCC CAGTG CT
CTGCAGTGTCTAGAGCAGTC ATCGACG TCGG G TGTGTGTC G AGG GTCAC GA
ACTGGGATATGAAGACTGTG GG------ AG ------ A AAGTAT -- T -----
TGTGGAGGCTGGGCAGCTA
GAM33643 11280 TTGGGGGTTGTTACATGCAT GGTTG G G A T- A TGGA
9 GATGCTGAGGTTTGGGAATA TTGGG TTACATGCAT AT CTG GGT TGGGA TA
TGGATGGTCCCATCACCCAG AACCC GATGTATGTA TG GAC CCA ACCCT GT
GTGATGTATGTAGTACCCAA AT--- G - - CT G ----
GAM33644 10773 GGGTTGTTACATGCATGATG TGT G G A T- A TGGA
0 CTGAGGTTTGGGAATATGGA GGGT TACATGCAT AT CTG GGT TGGGA TA
TGGTCCCATCACCCAGGTGA CCCA ATGTATGTA TG GAC CCA ACCCT GT
TGTATGTAGTACCC TG- G - - CT G ----
GAM33644 10675 GGCAGGAAAATTCCTTCACC AAA-- TTCA - A T GAGCCAAG
1 TGGGAGGTGGAGGTTGCAGT GGCAGG ATTCC CCTGGGAG GTGG GGT GCAGT
GAGCCAAGATTGCACCACTA CTGTTC TGAGG GGATCCTC CATC CCA CGTTA
CACTCCTAGGCAATGGAGTG CAGAG TAAC A A - --------
AGACCTTGTC
GAM33644 10485 GCTCTTTAAGAAGTAAGCAG CT AA - - A TTTC G TTAGT

2 AACTGTTTTGTTTTCTGTGC GCT TTAAG GTA AGC AGA CTGTTTTGT TGT CTGC
TGCTTAGTGCAGGACAATAT CGA GATTC CGT TCG TCT GACGAGATA ACA GACG
AGAGCAGATCTGGCTCTGCC C- CC C G A TA-- G -----
CCTTAGCAGC
GAM33644 10103 CTCAGAGGGCTTGGTCACCT AG -- CTC GA- GACTG
5 CTGCCATGAGGCTGGACTGC CTCAG GGC TTGGTCAC TGCCAT GGCTG
AGCTGTGGTGGCAAGTGACC GAGTC CTG GACCAGTG ACGGTG TCGAC
AGATGTCACTGAG A- TA A-- GTG -----
GAM33644 9657 AGAAAAATTAGTTAATATTT A AT AATA AAAA- TGTGC GGC -- TT
7 AAAAAACTGTATTGTGCATT AGA AA TAGTT TTTA ACTGTAT ATTTT TTCA CATGT
AACTTTTTT
TTGGCTTCACATGTTTAACT TCT TT GTCAA AAAT TGACATA TAAAA AGGT GTACG
TTGAAAAAA
TTTTTTAAGAAAAAAGTTGC A CT ---- GTCTA TGTC- AAA AA --
ATGAATGGAAAAAAAATCTG TAAG
TATACAGTATCTGTAAAAAC
TGTCTTATCT

GAM33644 10407 GAGTAGCTGGGATTACAGGT G G ATT - TGT A G G TTTTTGTATTT
8 GTGTGCCACCATGTCTGGCT GA TAGCT GG ACA GGTG GCC CCAT TCTG CTGA
GATTTTTGTATTTTTAGTAG CT GTCGG CC TGT CCAC TGG GGTG AGAT GATT
AGGTGGGGTTTCACCATGTT G A GGT A TT- - G - ----------
GGCCAGGCTGGTC
GAM33645 10122 CTCTGTAGTTATGTGCGGTC A- TG G CA- - TAT TT TGTTTGTC
0 TTACACTATTTTACATGGTC CTCTGTAGTT TG CG TCTTA CTATTTTACA TGGTCAC CAGC AGT

ACTATCAGCTTAGTTGTTTG GAGACGTCAG AC GT AGAGT GATGGAATGT GTCAGTG GTTG TCA

TCACTTGTTGGTGACTGCTG GG CT - TTA C --- T- --------
TAAGGTAGATTTGAGATGTC
CAGGGACTGCAGAG
GAM33645 10451 GCCCTAAACGAAGGGGGCCT CTAAACGAAG - AAGT - CTCAA-- G A TT-
TCAATT
1 CAAGTTACGACTTCTCAAGG GCC GGGGC CTC TACG ACTT GGCAGT AC TC CC
CAGTGACATCTTCCTCAATT CGG CCCTG GAG ATGC TGAA CCGTCG TG AG GG
GGTATGAGTAGCTGCCAGGC TCTTATA--- T AAT- A CAACGGA A - TAT ------
AACAAGTACGTATAAGAGTG
TCCCATATTCTGGC
GAM33645 10757 GGGGCCTCAAGTTACGACTT - AAGT - CTCAA-- G A TT- TCAATT
2 CTCAAGGCAGTGACATCTTC GGGGC CTC TACG ACTT GGCAGT AC TC CC
CTCAATTGGTATGAGTAGCT CCCTG GAG ATGC TGAA CCGTCG TG AG GG
GCCAGGCAACAAGTACGTAT T AAT- A CAACGGA A - TAT ------
AAGAGTGTCCC
GAM33645 11140 TGCACCTTCCCTGGGACAAC --------- CT GG TCTTGTGT
3 TTTCTTATTGATGGGTCTTG TGCACCT TCCCTGGGACAA TTCTTATTGAT G
TGTTTAATTAATGAGAGTTT ACGTGGA GGGGATTTTGTT GAGAGTAATTA T
GTTTTAGGGGTATGGGCCCA CCCGGGTAT T- AT --------
GGTGCA
GAM33645 11070 TGAGGCAGGAGAAGGCGTGA A AAGG GAA---- AGGC CT A GAGATCG
4 ACCCAGGAGGCGGAGCTTGC TGAGGC GGAG CGT CCCAGG GGAG TGCAGTG GCA

AGTGAGCAGAGATCGTGCCA ACTCTG CCTC GCG GGGTCC CCTC ACGTCAC CGT
CTGCACTCCAGCCTGGGCAA - AGA- AGACAAC GA-- -- - -------
CAGAGCGAGACTCCGTCTCA
GAM33645 10421 GATGTGTTCAAGAAAATTTA T AGAAAAT-- CATTGT
5 TTGCAGCATTGTTTGCAATA GATG GTTCA TTATTGCAG
GTGAAAAAACTGAACTCATC CTAC CAAGT GATAACGTT
T CAAAAAAGT ------
GAM33645 10459 GCCTTGGCTTCCCAAAGTGC GC CCC --- ATA AGCCAA
6 TAGGAATACAGGTGTGAGCC GCCTTG TT AAAGTGCT AGGA CAGGTGTG
AACATGCCTGTCCTGTAAGT CGGAAC AA TTTTATGA TCCT GTCCGTAC
ATTTTTTAAAACAAGGC AA TT- ATG --- ------
GAM33645 10555 GGAGAATCACTTGAACCCAG AA GA-- A-- A GT AGCCCAAAATCACAC
8 GAGTTAGAGGTTGCAGTGAG GGAG TCACTT ACCCAGG GTT GAG TGCAGTG
CCCAAAATCACACCACTGTA CCTT AGTGAG TGGGTCC CGA CTC ATGTCAC
CTCCAGCCTGCCTGGGTAAT AG ATAA GTC C -- ----------
AGAGTGAGATTCC
GAM33646 9646 ACCTTGCTGACAGTGGTAAT ---- A T TG --- T- AAG TA-- CT CTTAAT
0 TGTAGTGTGAAAGGCATAGT ACCTT GCTG CAG GGTAAT T AG GTGA GCA GTGTCCT TG

GTCCTCTTGCTTAATCATGG TGGAG TGAC GTT CCATTG A TC CACT CGT CATAGGG AC

GATACAGACTGCTCACTTCT AATT - T GT AAT TT --- CAGA T- ------
TAAATGGTTACCTTTGCAGT
TTAAGAGGT
GAM33646 10458 GCCTTGCAGTGAAGGAGGCA -- -- - A- ACCA A CTTCT
1 TGTGATCACCATCAAAGTCT GCCTT GCAG TGAAGGA GGC TGTGATC TCA AGT
TCTGCTCTGGGAAGGATCAC CGGGG CGTC ACTTCCT CTG ACACTAG GGT TCG
ACAGTCGTCCTTCAGCCTGC TC CG G AC GAAG C -----
CTGGGGC
GAM33646 10799 GGTGTCTGCCTGGTTGATCT GC TGA T TGA - - A T AACTA ATGATTAA
2 TGAATGATGGCAAGTGGGCA GGTGTCT CTGGT TCT GAA TGGCAA GTG GGC CTTT CAGGT
TTG
CTTTTCAGGTAACTATTGAT CCATAGA GACCG AGA CTT ACTGTT CAC TCG GAAG GTCTA AAC

GATTAACTGACAAAGATCTG -- TG- - C-- T A - T GA--- --------
TGAAGGCTACACTTTGTCAC CTGA
TTCAGAGTGCCAGAGATACC

GAM33646 10550 GGAGAATCACTTGAACCCAG AATCAC- AA- AGAC GT A- CCAGATC
5 GAGACGGAGGTTGCAGTGAG GGAG TTG CCCAGG GGAG TGCAGTG GC
CCCAGATCGCGCCACTGCAC CCTC GAC GGGTCC CCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAAT AGAATAA AAC GA-- -- CG -------
AAGACTCC
GAM33646 10910 TAGAAATGAGAGATGAGAGG A - A CCTCT G TG GGAA
8 TCCTCTGGGTAAGTGGGGAA TAGA ATG AGAGATG GAGGT GG TAAG G
CTGTTTGGTCTCATCGCCTC ATCT TAC TCTTTAC CTCCG CT GTTT C
CATTTCTACATCTCTA C A - CTACT G GT ----
GAM33646 9737 AGGTCTCATTTTGTTGCCCA TC T TT CT A T - A ATGGCTC
9 GGCTGGGGTACAGTGGTGCA AGG TCATTT G GCCCAGG GGGGT CAG GG TGCA GT

AGTATGGCTCACTGCAGCCT TCC AGTGAA C CGGGTCT TCTCA GTT CC ACGT CA
TGAACTCTTTCTGGGCTCAA T- - T- T- A - G - -------
GTGATCCT
GAM33647 9738 AGGTCTCATTTTGTTGCCCA TC-- T TT CT A T - A ATGGCTC
0 GGCTGGGGTACAGTGGTGCA AGG TCA TTTG GCCCAGG GGGGT CAG GG TGCA GT

AGTATGGCTCACTGCAGCCT TCC AGT GAAC CGGGTCT TCTCA GTT CC ACGT CA
TGAACTCTTTCTGGGCTCAA TCCT - T- T- A - G - -------
GTGATCCTCCT
GAM33647 9959 CAGATGCCTCCTTCGGGAGC ATG CG AGCCACA G AA AGTAAAAC
2 CACAGGATCCAGAGAGTCAA CAG CCTCCTT GG GGATCCAGA AGTC TGAA
TGAAAGTAAAACTTCAGGAC GTT GGAGGGA CC TTTAGGTCT TCAG ACTT
TGTCTGGATTTATTACGCCA GAA -- GCATTA- G G- --------
GGGAGGAAGTTG
GAM33647 9979 CATAGCTGTCTGGAGGCGCA CT T TG CAG AACCATAGACA
4 GTTTTCAGAAACCATAGACA CATAG G C GAGGCG TTTTCAGA
TCTGAGAAATATGTTTCTGG GTATT C G CTTTGT AAGAGTCT
CTTTTATG TT - GT ATA ----------
GAM33647 10617 GGAGAATGGCGTGAACCCGG AATG G- AA- AGGC GT A - AGAT
5 GAGGCGGAGGTTGCAGTGAG GGAG GC TG CCCGGG GGAG TGCAGTG GC CG
CCGAGATTGTGCCACTGCAC CCTC CG AC GGGTCC CCTC ACGTCAC CG GT
TCCAGCCTGGGCAACAGAGC AGAG AG AAC GA-- -- - T ----
GAGACTCC
GAM33647 10847 GTGCACTACAGACTCCAGCC A- GA CAG C-- - AAGCC A TCCTCCCTTT
6 TCCCTTTGAAGCCAGGTTCC GTGCACT CA CTC CCT CCT TTG AGGTTCCAG GCT
AGAGCTTCCTCCCTTTGGCC CATGTGA GT GAG GGG GGA GAC TCCAAGGTC CGG
TGGAACCTCAACAGCAGGAT AG AG TA- TTA C AAC-- - ----------
TGGGATGAGGATGGAAGTGT
AC
GAM33647 10855 GTGGACTTTGATGTGTGTGT GACTT T G AAA AAG - -- CAGT
7 AGGAAAATATTAAGGTGGGA GTG TGATG GTGT TAGG ATATT GTGGGA TGTGT GGAT

TGTGTGGATCAGTGTCCTAG CAT ACTAT CACG GTCC TGTGG CGCCCT ACACG CCTG

CACATTCCCGCAGGGTGTAA ----- - - GAA GA- T AT ----
GCCTGGCACTATCATAC
GAM33647 11137 TGATGTGTGTGTAGGAAAAT T G AAA AAG - -- CAGT
8 ATTAAGGTGGGATGTGTGGA TGATG GTGT TAGG ATATT GTGGGA TGTGT GGAT
TCAGTGTCCTAGCACATTCC ACTAT CACG GTCC TGTGG CGCCCT ACACG CCTG
CGCAGGGTGTAAGCCTGGCA - - GAA GA- T AT ----
CTATCA
GAM33647 10856 GTGGACTTTGATGTGTGTGT GACTT T G AAA AAG - -- CAGT
9 AGGAAAATATTAAGGTGGGA GTG TGATG GTGT TAGG ATATT GTGGGA TGTGT GGAT

TGTGTGGATCAGTGTCCTAG CAT ACTAT CACG GTCC TGTGG CGCCCT ACACG CCTG

CACATTCCCGCAGGGTGTAA ----- - - GAA GA- T AT ----
GCCTGGCACTATCATAC
GAM33648 11138 TGATGTGTGTGTAGGAAAAT T G AAA AAG - -- CAGT
0 ATTAAGGTGGGATGTGTGGA TGATG GTGT TAGG ATATT GTGGGA TGTGT GGAT

TCAGTGTCCTAGCACATTCC ACTAT CACG GTCC TGTGG CGCCCT ACACG CCTG
CGCAGGGTGTAAGCCTGGCA - - GAA GA- T AT ----
CTATCA
GAM33648 11276 TTGGCCCTCTCTGAGTCTGA TG CTCT- - GA GT TAAGAGTTAACAT
3 GAGAGTAGGTGTGCAATAAG T GCCCT GAGTC TGAGA GTAGGT GCAA
AGTTAACATTTGCTAACTTG A CGGGA CTCGG ATTCT CGTTCA CGTT
CAGTCTTATGGCTCCTTACA GT CATTC T GA AT ----------
GGGCTGA
GAM33648 9682 AGATCCGTGGTCCTTGGAGG G GT TG TAG GAACAAATAG AGTATTAGGA

4 TTTTAGGGAATGAACAAATA AGATCC TG CCT GAGGTTT GGAAT AGGCC
GAGGCCAGTATTAGGAGGCT TCTAGG AC GGG TTCCAGA TCTTA TTCGG
TAGCTCCAGAGATTCTAGAC G TG -- --- GAGACCTCGA ----------
CTTGGGGTCAGGGATCT
GAM33648 9744 AGGTTGGTAAAAGTGGTTTC - TGGTTT AGT- TTTTAGG TC GAATCA
6 TAACACAGTATCTCTTCTTT AGGTT GGTAAAAG CTAACAC ATCTCTTC TGT AGTG
TAGGTGTTCAGTGGAATCAC TCTAA CCGTTTTC GGTTGTG TAGGGAGG ACA TCAC
ACTTACAAAATTTGGAGGGA A ------ GTGT TTTAAA- T- ------
TTGTGGTGTTGGCTTTTGCC
AAATCT
GAM33648 9621 AATGGCTAGGTAAGGGAAGA GC GTAAG- - CATT
7 TGCATTCATTTATTCATTCA AATG TAG GGA AGATG
ACTAATATT TTAT ATC CTT TTTAC
A- AACTTA A ----
GAM33648 9694 AGCCCTAATATCTATAATTT TAATA TAATTT T T - A- TAA- GAAA
8 GAACTGTACTGGACCCATAG AGCCC TCTA GAACTG AC GGAC CCAT GTTT CT
TTTTAACTGAAAAGGGCCAA TCGGG AGGT CTTGAC TG TCTG GGTG CAAA GA
ACAAGTGGTGTCTGTCCAGT TC--- C----- C - T AA CCGG ----
TCCTGGACTGGGCT
GAM33648 9789 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33649 10579 GGAGAATCGCTTGAACCCAG AA GAA-- AGG GT AGC AGGT
0 GAGGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG TG
CTGAGGTCACACCACTGCAC CCTC AGCGAG GGGTCC ACCTC ACGTCAC AC
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- CAC ----
GAGACTCC
GAM33649 10507 GCTTGAACCTGGGATGTGGA GAA--- TG ATG GT A GAGATTG
1 GGTTGTAGTGAGCTGAGATT GCTT CC GG TGGAG TGTAGTG GCT
GGGCCATTGCACTCCAGCCT CGAG GG CC ACCTC ACGTTAC CGG
GGGCAACAAGAGC AACAAC GT G-- -- - -------
GAM33649 10538 GGACTACAGGCACATGCAAC A CACA CA C C TTTCT T AGAG
2 CACGTCTGGCTAATTTTCTT GGACT CAGG TG ACCA GTCTGG TAAT TGAG TTTAGT
GAGTTTTAGTAGAGACTGGG CTTGA GTCC GC TGGT CGGACC GTTG GCTC GGGTCA

TCTCGTTATGTTGTCCAGGC - TCGA CC - T TATT- T ----
TGGTCCCGAGCTCCTGAGTT
C

GAM33649 10686 GGCATGGTGGTGCTCTGATA TG --- GCT A - C AGGCTGAG
3 GCCCTAGCTACTCAGGAGGC GGCA GT GGT CTG TAGCC CTAGCTACT AGG
TGAGCCTAGTAGTTAGAGGC CCGT TA TCA GAC GTCGG GATTGATGA TCC
TGCAGTGAACTATGATTGTG GT GTA AGT - A - --------
CC
GAM33649 10974 TCCCTATCACGTGCAGCTTT --- -- G GTCA-- GAGATAAA
4 GCTGACGTCATTGAGAGATA TCCCTA TCACGTGCAG CTTTGCT AC TTGA
AATTAGGTACAAGTGGGCAG AGGGAT AGTGTATGTT GAGACGG TG GATT
AGAATTGTATGTGAGGTTAG TGG AA G AACATG --------
GGA
GAM33649 10539 GGACTACAGGCACATGCAAC A CACA CA C C TTTCT T AGAG
5 CACGTCTGGCTAATTTTCTT GGACT CAGG TG ACCA GTCTGG TAAT TGAG TTTAGT
GAGTTTTAGTAGAGACTGGG CTTGA GTCC GC TGGT CGGACC GTTG GCTC GGGTCA

TCTCGTTATGTTGTCCAGGC - TCGA CC - T TATT- T ----
TGGTCCCGAGCTCCTGAGTT
C
GAM33649 9790 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33649 11289 TTTGATAGATTTTTCCCTCC - A TCCCTC --- CT--- C T CAGCA
7 AGAATGTTTGCATCTATTCA TTTG ATAG TTTT CAGAATGTT TGCAT ATT ACA GTGCAT
CATGTGCATCAGCAGTGCAT AAAC TATC AAAA GTCTTGCAA ATGTG TGA TGT TACGTG

TTGTAGTTAAATGTGTAGTT A - TTTTT- TTG TAAAT - T -----
AACGTTCTGTTTTTAAAACT
ATACAAA
GAM33649 9955 CAGAATGTTTGCATCTATTC --- CT--- C T CAGCA
8 ACATGTGCATCAGCAGTGCA CAGAATGTT TGCAT ATT ACA GTGCAT
TTTGTAGTTAAATGTGTAGT GTCTTGCAA ATGTG TGA TGT TACGTG
TAACGTTCTG TTG TAAAT - T -----
GAM33649 10861 GTGGGTATTCAGAGAGAGAA GGTA AAGATAATGAAT TC A CC T---- CCT
9 GATAATGAATAGGGAGTGTC GTG TTCAGAGAGAG AGGGAGTG AG ATG AGCA CATTTG

AGAATGCCAGCATCATTTGC TAC GAGTCTCTCTT TTTCTCAC TC TGC TTGT GTAAAC
CTCAAATGCCACTTGTTACG AG-- AT---------- CT G A- TCACC ---
TGCTTCCACTCTTTTATTCT
CTCTGAGGACAT
GAM33650 9995 CCAGAGAGTCTCTCCAGGTA G T- C CACA T GCTGTG
2 CGCCACACAGTCTTTGAGCT CCAGA AGTC CTCCAGGTA GC CAG CTTTGA
GTGTCAGAGCTGGATTGTTT GGTTT TCGG GGGGTCCAT TG GTC GAGACT
ACCTGGGGCTGGCTGTTTGG G TC T TTAG - ------
GAM33650 9994 CCACGTGGATTACTGGGCTC -- T -- ---------- AG - CTGA
3 CTCTCAGTGTGGAAGCTGAT CCAC GTGGAT ACTGGG CTCCT CTC TGT GGAAG
TTCCAACAAGGAGCATTCAA GGTG TACTTG TGACCC GAGGA GAG ACA CCTTT
AGATTAGGAGTTCCCAGTGT AA - TT TTAGAAACTTAC GA A ----
TCATAAGTGG
GAM33650 10445 GCATCTTGACACATGTTCTG TT CACAT TCT TC TA-- C
ATCCATTGTTACCACA

4 TGCTCCAGGTCCCAGTAACT GCATC GA GT GTGCTCCAGG CCAG ACTGTG CC
GTGCCCATCCATTGTTACCA TGTGG CT CA TACGGGGTCC GGTC TGACAC GG
CAGGTCACAGTGGCCCTGGC TT CTCT- TAT C- CCGG T ----------
CCTGGGGCATTATACTCTCT
CTTGGTGT
GAM33650 10526 GGAAGTGAAAGAGGGAAGTC ------ TCTCT C CTCCTC GTTACCA
5 TCTCTCCCCATCCCTCCTCT GGAAGTGAA AGAGGGAAG CT CCCATCC TCA
CAGTTACCATGAGGATGGGC CTTTCACTT TTTCCCTTC GA GGGTAGG AGT
AGTTTCTTCCCTTTCCGTTC CTTGCC TTT-- C ------ -------
TTCACTTTC
GAM33650 10540 GGACTACAGGCACATGCAAC A CACA CA C C TTTCT T AGAG
6 CACGTCTGGCTAATTTTCTT GGACT CAGG TG ACCA GTCTGG TAAT TGAG TTTAGT
GAGTTTTAGTAGAGACTGGG CTTGA GTCC GC TGGT CGGACC GTTG GCTC GGGTCA

TCTCGTTATGTTGTCCAGGC - TCGA CC - T TATT- T ----
TGGTCCCGAGCTCCTGAGTT
C
GAM33650 10891 GTTTGGTGCCTATTGGATTT G ---------- T A A GACCTTTATATAAAACAA
7 TAAGCATTGGGAGTTGACCT GTTTG TG CCTATTGGATT TAAGC TTGGG GTT
TTATATAAAACAAAACCCCT CAAAT AC GGATGACTTAA ATTCG AATCC CAA
AAGCTTATAATTCAGTAGGG G AGACAAAGAG T - C ----------
AGAAACAGACAGTAAAC
GAM33650 10890 GTTTGGTGCCTATTGGATTT GTG--- T A A GACCTTTATATAAAACAA
8 TAAGCATTGGGAGTTGACCT GTTTG CCTATTGGATT TAAGC TTGGG GTT
TTATATAAAACAAAACCCCT CAGAC GGATGACTTAA ATTCG AATCC CAA
AAGCTTATAATTCAGTAGGG AAAGAG T - C ----------
AGAAACAGAC
GAM33650 11266 TTGCTTGAACCCGGGAGGTG C AA AGG GT A - AGAT
9 GAGGTTGTAGTGAGCCGAGA TTG TTG CCCGGG TGGAG TGTAGTG GC CG
TCGCGCCACTGCACTCCAGC GAC AAC GGGTCC ACCTC ACGTCAC CG GC
CTGGGCAACAG - -- G-- -- - C ----
GAM33651 10541 GGACTACAGGCACATGCAAC A CACA CA C C TTTCT T AGAG
0 CACGTCTGGCTAATTTTCTT GGACT CAGG TG ACCA GTCTGG TAAT TGAG TTTAGT
GAGTTTTAGTAGAGACTGGG CTTGA GTCC GC TGGT CGGACC GTTG GCTC GGGTCA

TCTCGTTATGTTGTCCAGGC - TCGA CC - T TATT- T ----
TGGTCCCGAGCTCCTGAGTT
C
GAM33651 9791 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33651 10932 TATTGGTTTCATTCTTGGTA G ATTCTT TCA- A T A GAAAGTGA TATA
2 AAGAAATCATAAAAGTCCAG TATTG TTTC GGTAAAGAAA TAA AG CCAGG CA CC
GACAGAAAGTGACCTATAGG ATGAC AAAG TCGTTTCTTT GTT TC GGTCC GT GG
GATGACCTGGCCTCTTGCCC G GTCT-- TCCC C C A AG------ ----
TTTTCTTTGCTTCTGGAAAG
CAGTA
GAM33651 9921 ATGTTATGATTGTTTCATTT TG G- TTG TG AA--- GAAAA

3 GTTGGAAATAAGGAAAACTT A TTAT ATTGTTTCAT T GA TAAG
GCATGGTTTGAATTGTGGAA T GGTG TAACAAGGTG A TT GTTC
CAATAGGTGGTGT GT GA TTA GT GGTAC -----
GAM33651 10277 GAGAATTGCTTGAACCCTGG AA GAAC-- A GT A- CGAGATT
4 AGGTGGAGGTTGCAGTGAGC GAG TTGCTT CCTGG GGTGGAG TGCAGTG GC
CGAGATTGCACCATTGCACT CTC AACGAG GGATC CCACCTC ACGTTAC CG
CCACCCTAGGCAACAAGAGC AA AACAAC - -- CA -------
AAAACTC
GAM33651 9700 AGGAAGATTGTGTGAGTCCA AA-- GTGA AA GC GA TATAATTGT
6 GGAATTGGAGGCTGCAGTGA AGG GATTGT GTCCAGG TTGGAG TGCAGT GC
GCTATAATTGTGCCAACTGT TCC TTGACA CGGGTCC GACCTC ATGTCA CG
ACTCCAGCCTGGGCAACAGT CAGA A--- -- -- AC ---------
TAGACCCT
GAM33651 10449 GCCCCTGCCCAAGAGATCCA - G GAGA ATTT- CCCAGAATAT
8 CTTTATTTTCATCTCACCCA GCCC CT CCCAA TCCACTTT TCATCTCA
GAATATTGAGGTGATCAGCA TGGG GA GGGTT AGGTGGAA AGTGGAGT
AGGTGGAGTGGTTGGGAGAG A - GGTG CGACT ----------
GGT
GAM33651 9792 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33652 10500 GCTTCACTTTCAGGGGCAAG TT- TTC- -- TG A-- G - T CATGTAAC
0 GTTTGGGAAATAAGCTGATA GC CACT AGG GGCAAGGTT GGAA TAA CTG ATAG AAAGT

GTAAAGTCATGTAACACTTT CG GTGA TCC TCGTTCCAG CTTT ATT GAC TGTC TTTCA
CTGTGCAGGTTAACATTTCT TAT CTCT TT GT ACA G G - --------
GGACCTTGCTTTCCTTCTCA
GTGTATGC
GAM33652 9735 AGGGTGCTGTTGCTTCTAGG T TGTT CTA GT TTT- T C A ATACACACATTTTTG

2 TCTTTTGAGAGCATAGAGCC AGGG GC GCTT G CT GAGAGCA AGAG CAGGA GC
AGGAAGCATACACACATTTT TCCC CG TGAG T GA TTCTCGT TTTC GTCCT CG
TGGCTCCTGACTTTTTGCTC - TT-- TTA TG CCCT T A - ----------
TTTCCCAGGTTATTGAGTTT
GCCCCT
GAM33652 9793 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33652 10079 CGAACCAGGTAGAAGTAATG CA T AAGTAA T CAA G C-- AGCCT
4 TGTGCCAGGACAAGAGACGC CGAAC GG AG TGTG GCCAGGA GAGAC CA CCAG
ACCCAGAGCCTCTGGCCTTG GTTTG CC TC ACAC CGGTCCT CTCTG GT GGTC
GTCTCCTATCCTGGCTCACA AA - ACACGA T ATC - TCC -----
AGCACACTCCAAGTTTG
GAM33652 10929 TATGTCACCAAATTTGGTGT ------- - GCTT TT - GCTTCTTTCA
6 GCTTTCTCCTTTGCCTGCTG TATGTCAC CAAATTTGG TGT TCTCC TG CCTGCT
CTTCTTTCAAGTAGGACATG GTGTAGTG GTTTAAACC ACA AGAGG AC GGATGA

GAGACAACAGCCAAATTTGT ACTTCGT G AC-- T- A ----------
GCTTCAGTGATGTG
GAM33652 9930 CAAATTTGGTGTGCTTTCTC - GCTT TT - GCTTCTTTCA
7 CTTTGCCTGCTGCTTCTTTC CAAATTTGG TGT TCTCC TG CCTGCT
AAGTAGGACATGGAGACAAC GTTTAAACC ACA AGAGG AC GGATGA
AGCCAAATTTG G AC-- T- A ----------
GAM33652 10114 CTCCTTAGGTTTTATCAATC A- TTA-- AA- T TTC - A TCCT
8 CTGGTGCCCTTCCATTGTAT CTCCTT GGTT TC TCCTGG GCCC CATTGT ATC CA
CACATCCTTGGATCACAGTG GAGGGA CCAG AG AGGACT TGGG GTGACA TAG GT
ATGGGTTCAGGAATAGACAC AC TACAC ATA - TA- C - ----
ATGACCCAAGGGAG
GAM33652 10070 CCTTAGGTTTTATCAATCCT A TTA-- AA- T TTC - A TCCT
9 GGTGCCCTTCCATTGTATCA CCTT GGTT TC TCCTGG GCCC CATTGT ATC CA
CATCCTTGGATCACAGTGAT GGAA CCAG AG AGGACT TGGG GTGACA TAG GT
GGGTTCAGGAATAGACACAT C TACAC ATA - TA- C - ----
GACCCAAGG
GAM33653 10310 GAGCTGTCCGTGACGTAGGT CT C G GG - AC CC TTCT AATCATTAA
2 TTGTACGTCAACTCAGCCTT GAG GTC GTGAC TA TTTGTAC GTCA TCAG TTA GGGA
ATTCTGGGAAATCATTAATC CTC CAG CACTG AT AAACGTG CAGT AGTC AAT TCCT
CTTAACTCTGATGACTGTGC AC T - GA T -- TC ---- ---------
AAAAGTAGTCACTGACCACT
C
GAM33653 10839 GTGACGTAGGTTTGTACGTC G GG - AC CC TTCT AATCATTAA
3 AACTCAGCCTTATTCTGGGA GTGAC TA TTTGTAC GTCA TCAG TTA GGGA
AATCATTAATCCTTAACTCT CACTG AT AAACGTG CAGT AGTC AAT TCCT
GATGACTGTGCAAAAGTAGT - GA T -- TC ---- ---------
CAC
GAM33653 10643 GGAGAATTGCTTGAACTCAG AA TG GAA-- AGGC A T A- TGAGATC
4 GAGGCGGAAGTTGCAGTGAG GGAG T CTT CTCAGG GGA GT GCAGTG GC
CTGAGATCGCACCACTGCAC CCTC A GAG GGGTCC CCT CA CGTCAC CG
TCCAGCCTGGGCAACAGAGT AG GT ACAAC GA-- - - CA -------
GAGACTCC
GAM33653 10535 GGACCATTGAGGAGGTGGGG CCAT A CA CCC AACCGAAGC
5 CAGCAGCAGGACCCCCAGAA GGA TGAGG GGTGGGGCAGCAG GGAC CAG
CCGAAGCCTGTGTCTCTGCT CCT ACTTC CTACTCTGTCGTC TCTG GTC
GTCTCATCCCTTCATTCTTC TCTT C -- T-- ---------
C
GAM33653 9794 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33653 9772 AGTTTAAGAATGGCTCATGT AAGAAT T A A C- GACTGA
7 AGTACCCAGCTACTCTGGGC AGTTT GGCTCA GT GT CCCAG TACTCTGGGC
GACTGAGCCCAGGGTACTCT TCGAG CCGAGT CA TA GGGTC ATGGGACCCG
GGGATCACTTGAGCCCAGGA GAC--- T C - TC ------
GCT
GAM33653 10887 GTTTAAGAATGGCTCATGTA AAGAAT T A A C- GACTGA
8 GTACCCAGCTACTCTGGGCG GTTT GGCTCA GT GT CCCAG TACTCTGGGC
ACTGAGCCCAGGGTACTCTG CGAG CCGAGT CA TA GGGTC ATGGGACCCG

GGATCACTTGAGCCCAGGAG GAC--- T C - TC ------
C
GAM33653 10850 GTGCCTAGCCAAGCAGATGA TG - AAG GAATGAGGTAGA TCT- A - C TATC

9 ATGAGGTAGAACAGTCTTGT G CCTA GCC CAGAT ACAG TGTTCAT CA TTGC ATTA
TCATACATTGCCATTATATC C GGAT CGG GTCTG TGTC ACAAGTA GT GACG TGAT
TAGTGCAGTTGAATGAACAT GT T --- ---------- TTTT A T - ----
TTTCTGTGTCTGGGCTTAGG
TGC
GAM33654 9705 AGGATCACTTGAGCCCAGGA A-- GA-- AG GC A- TATGATT
0 GTTGGAGGCTGCAGTGAGCT AGGATC CTT GCCCAGG TTGGAG TGCAGTG GC
ATGATTGCACTACTGCACTC TCCTAG GAG CGGGTCC GACCTC ACGTCAT CG
CAGCCTGGGCAACAGAGCAA AAC ACAA -- -- CA -------
GATCCT
GAM33654 10127 CTCTTGAACCCAGGAAGTGG AA- AAG GT A- AGA
1 AGGTTGCAGTGAGCTGAGAT CTCTTG CCCAGG TGGAG TGCAGTG GCTG
AGCAACACTGCACTCCAGCC GAGAAC GGGTCC ACCTC ACGTCAC CGAT
TGGGCAACAAGAG AAC G-- -- AA ---
GAM33654 10597 GGAGAATCGCTTGAACCCGG AA-- G AA- GGG - A CGAGCTT
5 GGGGTGGAGGTAGTGGTGAG GGAG TC CTTG CCCGGG TGGAG GTAGTGGTG GC

CCGAGCTTGCACACCATTGC CCTC AG GAAC GGGTCC ACCTC CGTTACCAC CG
ACTCCAGCCTGGGCAACAAG AAAG A AAC G-- A A -------
AGAGAAACTCC
GAM33654 9795 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33654 10925 TATCTCATCTGGTTTTAATC ATCT- AA T - TATGA
8 CTGAAGGCATATATGTATGA TATCTC GGTTTT TCCTGAAGGCA ATA TG
CATTATCTGTCTTTAGGGAG ATGGAG CCAGAG GGGATTTCTGT TAT AC
GAGACCCAACAGAGGTA ACAAC GA C T -----
GAM33654 9796 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33655 9633 ACAGCTCACCTGCAAGGCTT CA-- CAA CA- - G - TCAG
0 TCAACTCTGCTGACCTTCAG ACAGCT CCTG GGCTTT ACT CT CTGAC CT
AGTGTCAGAGCAGTGCCGAA TGTCGG GGAC CCGAAG TGA GA GACTG GA
GCCCAGGACATGGCTGT TACA --- CCG C - T ----
GAM33655 10696 GGCCTTCTCTCTGAGTTAAG C T - GC GA-- AT-- AAATA
1 CAAAGAGAGGAAGAATGGCA GGCCTT TCTC GA GTTAA AAAGA GGAAGA GGC
AATAGTTTGAGTCTTCCCAA TCGGAA AGAG TT CGATT TTTCT CCTTCT TTG
ATCTTTTTAGCATTTGAGAA A T A -- AAAC GAGT -----
AAGGCT
GAM33655 9653 ACTGAAGCCTCCTGCCAATA - TCC CCA CA G A - TGAAT
2 GTCACATGAGTGAGTCTGGA ACTG AAGCC TG ATAGTCA TGA TG GT CTGGAAG
AGTGAATCTTTCAGCACCAT TGAC TTCGG AC TGTCAGT ACT AC CA GACTTTC

CAGATGACTGTATCACTGGC A TC- TA- AG - - C -----
TTACAGT
GAM33655 10931 TATTCCAGATTTCTTAGTTT ATTTC - TCAGCA G GG GCTGGTTTA
3 TGCTCAGCAGGATGGTTGGA TATTCCAG TTAGT TTTGC GGATG TT ACTGAAGGGG

CTGAAGGGGGCTGGTTTACT ATAAGGTC GATCA AAACG CTTGT AA TGACTTCTTC
TCTTCAGTGGAAGTGTTCAT ATT-- T TTTTTA G GG ---------
TTTTGCAAATACTAGTTACT
GGAATA
GAM33655 9997 CCAGCTGCCACCCTTCTACC CCA--------- ACCCAA --- ATAGAA-- A ACCT
6 CAACCCCATCTCATAGAACT CCAGCTG CCCTTCT CCCC ATCTC CTC CAACA
CACAACAACCTTGTTGGGAG GGTCGAT GGGGAGA GGGG TAGGG GAG GTTGT
AAAAGGAGGGGATACAGGGG ATACCAATAAAG AATTC- ACA GAGGAAAA G ----
CTTAAAGAGGGGGAAATAAC
CATATAGCTGG
GAM33655 9797 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
7 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33655 10580 GGAGAATCGCTTGAACCCAG AA GAA-- AGG GT AGC AGGT
8 GAGGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG TG
CTGAGGTCACACCACTGCAC CCTC AGCGAG GGGTCC ACCTC ACGTCAC AC
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- CAC ----
GAGACTCC
GAM33655 9640 ACCCACATTCTTAGCTTGGC ATTCTT GTT C GTCTTA
9 TTCAGTTTCTTTCCGGGTCT ACCCAC AGCTTGGCTTCA TCTTTC GG
TACTGAGAGGTGAAGCCAGG TGGGTG TCGGACCGAAGT GGAGAG TC
CTTCTGGGTGGGT GGTCT- --- - ------
GAM33656 11234 TTCACCCTCTCAGCCAGGCT CTCTCA - CTTGAACTC G - CC T - - CCAC
0 GGTCTTGAACTCCTGACTTT TTCACC GCCAGGC TGGT CT AC TTTGTGAT ACC GC CTT GG

GTGATCCACCTGCCTTGGCC AAGTGG CGGTCCG GCCA GA TG GAACATTA TGG CG GAA
CC
ACCCAAAGTGCTGGTATTAC C----- C CC------- G T -- T T A ----
AAGTGTGAGCCACCGCGCCT
GGCCGGTGAA
GAM33656 10482 GCTCTGTCTTGAGAATCGAG T CTT -- C ATG TT-- CTT TT GCTAT
1 AAATATGGGGCTCTTTTCTG GCTC GT GAGA AT GAGAAAT GGGCTC TTCTGT TGCGA TTG

TCTTTGCGATTTTGGCTATC CGAG CA CTCT TA TTCTTTG CCTGGG AAGACG ATGTT AAC

AATTTGTAGCAGAACACTGG T TTT AT C A-- TCAC --- T- -----
GTCCAGTTTCTTCATTATCT
CTTTACTGAGC
GAM33656 9704 AGGATCACTTAAGGCCCAGG A-- AAG- AGTTC C - TATGACT
3 AGTTCGAGGCTGTAGTGAGC AGGATC CTT GCCCAGG GAGG TGTAGTGA GC
TATGACTGTGTCACTGCACT TCCTAG GAG CGGGTCC CTTC ACGTCACT TG
TCAGCCTGGGCAATGGAGCA AAC GTAA GA--- - G -------
AGATCCT

GAM33656 10546 GGAGAATAGCTTGAACCTGG ATA GAA--- TG AGG CTTA GC CGAGATT
4 GAGGTGGAGCTTACAGTGAG GGAGA GCTT CC GG TGGAG CAGTGA CAC
CCACCGAGATTGTGTCATTG CCTCT CGAG GG CC ACCTC GTTACT GTG
CACTCCAGCCTGGGCAACAA AAA AACAAC GT G-- AC-- -- -------
GAGCAAATCTCC
GAM33656 9942 CACCTGTCATGCCAGTTACT - G TTAC G TAA G GTGAGCTG
5 TGGGGGGCTAAGGTGGGAGG CAC CTGTCAT CCAG TTGGGG GC GGTGG AGGATTA

ATTAGTGAGCTGTGATTCTG GTG GACAGTG GGTC GACCTT CG TCACC TCTTAGT
CCACTGCATTCCAGCCTGGG A - C--- A --- G --------
TGACAGAGTG
GAM33656 10911 TAGAAGCATCTTTAGTTTTA G A TTAGTT A-- C -- - TAGATAGCTTTAGGAT
7 AGGAAGTGTCTCTTGGCTGG TA AAGC TCT TTAAGGA GTGT TCT TGGCTGGC CCC
CCCCTAGATAGCTTTAGGAT AT TTCG AGA AGTTCCT CACA AGA ACTGATCG GGG
GGGAGCTAGTCACCAGAAAC G A TT---- AAC A CC A ----------
ACCAATCCTTGATTAGAAGC
TTGTA
GAM33656 10215 CTTTAGTTTTAAGGAAGTGT AGTT A-- C -- - TAGATAGCTTTAGGAT
8 CTCTTGGCTGGCCCCTAGAT CTTT TTAAGGA GTGT TCT TGGCTGGC CCC
AGCTTTAGGATGGGAGCTAG GAAG AGTTCCT CACA AGA ACTGATCG GGG
TCACCAGAAACACCAATCCT ATT- AAC A CC A ----------
TGATTAGAAG
GAM33656 11287 TTTAGTTTTAAGGAAGTGTC TT A-- C -- - TAGATAGCTTTAGGAT
9 TCTTGGCTGGCCCCTAGATA TTTAGTT AAGGA GTGT TCT TGGCTGGC CCC
GCTTTAGGATGGGAGCTAGT AGATTAG TTCCT CACA AGA ACTGATCG GGG
CACCAGAAACACCAATCCTT -- AAC A CC A ----------
GATTAGA
GAM33657 10522 GGAACAGTACACTCACGGCA C AC CACG CCCT C- --- CTGAGTGAAT
0 CCCTGGAGAGGAGCGGTCAC GGAA AGT ACT GCA GGAGAGGAGCGGT AC TGGTTG

TGGTTGCTGAGTGAATTAAC CCTT TTA TGA CGT CCTCTTTTCGTCG TG GCCAAT
CGAATGTTTGCTGCTTTTCT A CT CAA- ---- TT TAA ----------
CCTGCAACAGTTCATTATTC
C
GAM33657 10501 GCTTCATCATCCTGGTTCAA A- A - CAA A - TC CAGG T- G G-
1 GCAGTGTTTCTTCTCTATCA GCTTC TC TC CTGGTT GC GTGTTT CT TCTAT CC GGT GCT
TTGTTTTGGG
GGCCTGGTGGCTGTTGTTTT CGAAG AG AG GACCAG TG CACAGA GG GGGTG GG CCG CGG
AGCGGAACCC
GGGCTCCCCAAGGCGAGAGG GG A A --- G A TT AACA TC G AG
CGGCCCTGGACAAGTGGGTT CTC
GGAAGACACGGTGACCAGAG
AAGAGGGAAGC

GAM33657 10410 GAGTGACCCCATCTCTACAA CATC ACAAAA TAAAT - AT-- GTATA
2 AAAGTTTTTTTAAATTAGCT GAGTGACCC TCT AGTTTTTT TAGCTAGG C GGTG
AGGCATGGTGGTATACACTT TTCACTGGG AGG TCGAAGGA ATCGATCC G TCAC
GTAGTCCTAGCTACTTAGGA ---- ACGGAG TTC-- T ATGT -----
AGCTGAGGCAGGAGGGTCAC
TT

GAM33657 10623 GGAGAATTGCTTGAACCCAA AA TG GA-- AGA - GT A - CGAT
3 GAGGTGGAGGTTGCAGTGAG GGAG T CTT ACCCA GG TGGAG TGCAGTG GC CA
CCACGATTGTGCCATTGCAC CCTC A GAG TGGGT CC ACCTC ACGTTAC CG GT
TCCAGCCTGGGTGACAGAGT AG GT ACAG --- G -- - T ----
GAGACTCC
GAM33657 11253 TTCTGTGATGGGTGTACGAC ---------- - - A -- C- TCAAATC
4 AGATTATTTTGTGACTGCAG TTCTGTGATG GGTGTAC GACAGATTATTTT GTG CTGC AGT
TGT
TCTGTTCAAATCACATCACT AAGGTACTAC TTACGTG TTGTTTAGTAGAG CGC GACG TCA
ACA
AAGCAGCGCTGAGATGATTT GTTTTGGAAAA G T - AA CT -------
GTTGGTGCATTAAAAGGTTT
TGCATCATGGAA

GAM33657 10624 GGAGAATTGCTTGAACCCAA AA TG GA-- AGA - GT A - CGAT
5 GAGGTGGAGGTTGCAGTGAG GGAG T CTT ACCCA GG TGGAG TGCAGTG GC CA
CCACGATTGTGCCATTGCAC CCTC A GAG TGGGT CC ACCTC ACGTTAC CG GT
TCCAGCCTGGGTGACAGAGT AG GT ACAG --- G -- - T ----
GAGACTCC
GAM33657 11111 TGAGGCAGGAGAATTGCTTG CA AA GAAC AA A- GT A- CGAAATT
8 AACTTGAAAGGCAGAGGTTG TGAGG GGAG TTGCTT TTG AGGC GAG TGCAGTG GC

CAGTGAGCCGAAATTGCACC ACTCT CCTC AACGAG AGC TCCG CTC ACGTCAC CG
ACTGCACTCCAGCCTGGCGA A- AG AC-- GG AC -- CA -------
CAGAGCAAGACTCCATCTCA
GAM33657 10372 GAGGCAGGAGAATTGCTTGA CA AA GAAC AA A- GT A- CGAAATT
9 ACTTGAAAGGCAGAGGTTGC GAGG GGAG TTGCTT TTG AGGC GAG TGCAGTG GC

AGTGAGCCGAAATTGCACCA CTCT CCTC AACGAG AGC TCCG CTC ACGTCAC CG
CTGCACTCCAGCCTGGCGAC A- AG AC-- GG AC -- CA -------
AGAGCAAGACTCCATCTC
GAM33658 10566 GGAGAATCACTTGAGCCCTG AA GA--- TGG AGA A A C GGT
0 GAGGCAGAAGATGCAGTGAG GGAG TCACTT GCCC AGGC AG TGCAGTG GC TG
CCTGGGTCATGCCACTGCAC CCTC AGTGAG CGGG TCCG TC ACGTCAC CG AC
TCCAGCCTGGGCAACAAGAG AG AACAA --- ACC - - T ---
TGAGACTCC
GAM33658 10496 GCTGTCCTGGAGCTGTTGGA T A T---------- GG G ATCTA
1 GAAATGGGGAAGATCATCTA GCTGTCC GG GCTGT GGAGAAAT GGAA ATC
GATATTCCAGTTTCTCCTTC CGATAGG CC TGATA CCTCTTTG CCTT TAG
CACTCACCCTATAGTACCGG - A TCCCACTCACCTT A- A -----
ATAGC
GAM33658 10625 GGAGAATTGCTTGAACCCAA AA TG GA-- AGA - GT A - CGAT
2 GAGGTGGAGGTTGCAGTGAG GGAG T CTT ACCCA GG TGGAG TGCAGTG GC CA
CCACGATTGTGCCATTGCAC CCTC A GAG TGGGT CC ACCTC ACGTTAC CG GT
TCCAGCCTGGGTGACAGAGT AG GT ACAG --- G -- - T ----
GAGACTCC
GAM33658 10770 GGGTGTGGTGGAGCACGCCT GA ---- TG CC A---- AGGA G GAGAA
3 GTTATCCCAGCTACTCAGGA GGGTGTGGTG GCACG CC TTAT CAGCT CTC GGCT AGGTGG

GGCTGAGGTGGGAGAATCAC CTCACACCAC TGTGC GG AGTG GTTGG GAG CCGA TCCACT

CTGAGCCCGGGAGGTAGAGG -- TAGA TG AC AGATG GGC- G -----
TTGCAGTGAGTGGAGATCGT
GTCACCACACTC

GAM33658 10873 GTGTGGTGGAGCACGCCTGT GA ---- TG CC A---- AGGA G GAGAA
4 TATCCCAGCTACTCAGGAGG GTGTGGTG GCACG CC TTAT CAGCT CTC GGCT AGGTGG

CTGAGGTGGGAGAATCACCT CACACCAC TGTGC GG AGTG GTTGG GAG CCGA TCCACT

GAGCCCGGGAGGTAGAGGTT -- TAGA TG AC AGATG GGC- G -----
GCAGTGAGTGGAGATCGTGT
CACCACAC

GAM33658 11284 TTGTGGTCTTGCTGATTTTG T - - GA A- G C ACCTTC
5 AGAATGGAGCCCCAGACCTT TTG GGTC TTG CT TTTTGAGA TG AGC CCAG
CCTGGTGTTACAGCTCTCAA AAC CCAG AAC GA GAAACTCT AC TTG GGTC
AGAAGACAAGGACCCAA - G A A- CG A T ------

GAM33658 10637 GGAGAATTGCTTGAACCTGG AA GAAC- AG - GT A - AGAT
6 AGGCGGAGGTTGCAGTGAGC GGAG TTGCTT CTGG GC GGAG TGCAGTG GC CG
CGAGATTGTGCCACTGCACT CCTC AACGAG GGCC CG CCTC ACGTCAC CG GT
CCAGCCCGGCAACAGAGCAA AG ACAAC -- A -- - T ----
GACTCC

GAM33658 10662 GGATACATAGTGGTCACTTC A TCA TC TT T G TTT-- TT AATTCAA
7 CATTTAAGATGTTTGCATTT GGATACAT GTGG CT CA TAAGA GTTT CA CAGCACT TAT
CAGCACTTTTATAATTCAAA TCTATGTA CACC GA GT GTTCT CAGA GT GTCGTGG ATA
TATGGTGCTGTCCCTTGAGA - --- GA T- - - TCCCT T- -------
CTCTTGTTGAGAGCCACATG
TATCT

GAM33658 10412 GATACATAGTGGTCACTTCC A TCA TC TT T G TTT-- TT AATTCAA
8 ATTTAAGATGTTTGCATTTC GATACAT GTGG CT CA TAAGA GTTT CA CAGCACT TAT
AGCACTTTTATAATTCAAAT CTATGTA CACC GA GT GTTCT CAGA GT GTCGTGG ATA
ATGGTGCTGTCCCTTGAGAC - --- GA T- - - TCCCT T- -------
TCTTGTTGAGAGCCACATGT
ATC

GAM33658 10762 GGGGGCCACATTCTCTGGGC G A CT- TTCAGAA CA AGGCC
9 ATTCAGAAGCCAGGATTTCA GGGG CCAC TTCT GGGCA GC GGATTTCAT
TAGGCCATGAAATCTGCTGT CCTC GGTG AAGA TCTGT CG TCTAAAGTA
CTTTTAGAAGTGGGCTCC G - TTT ------- -- -----

GAM33659 10028 CCCTAAAAGTGACTGAATTG -- T---------- GCCC T ATG G TTACTC
0 CCCAAGTGCTTGAACATGGC CCCTA AAAGTGAC GAATT AAGTGC TGAAC GCAGAG TAG

AGAGGTAGTTACTCCTATTT GGGGT TTTCATTG CTTAA TTCACG GTTTG CGTTTT ATC
TGCAGTTTGTGCACTTAAAA CA TTAGTGACATC AAA- T A-- - ------
ATTCCTACAGTGATTGTTAC
TTTACTGGGG

GAM33659 9798 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT

GAM33659 10722 GGGACAAGGCAAATGAGAGA ----- CAAAT G G C A --- CTTCTC
2 GGAAGGCCGTAGGGAAGGGC GGGA CAAGG GA AGA GAAGGC GT GGGA AGGG
TTCTCTCCTACCTCCCACGT CCCT GTTCC CT TCT TTTCTG CA CCCT TCCT
CTTTATCTGTCCAAATCCTT TTATC TAAAC G A - - CCA ------
GCTATTTCCC
GAM33659 10898 TAAATCTGGGCTGAGGGAAA ATC TGAG- ---- T C ---- -- - TCT TG
3 GCATGTCCACACCAGGTGCC TAA TGGGC GGAAA GCA GTCCA AC CAGGTGCC CAG ACA
GGT GC
CAGACATCTGGTTGGCTTTG ATT ACCCG CCTTT CGT TAGGT TG GTCCACGG GTC TGT
TTA CG
GCTGATTTGTCCTGCAGGCA --- TTGAA CACA T C TTCC AC C --- GT
CCTGCCTTGTCTGGATTTGC TTTG
ACACTTTCCAAGTTGCCCAT
TA

GAM33659 11183 TGGGCTGAGGGAAAGCATGT TGAG- ---- T C ---- -- - TCT TG TTTG
4 CCACACCAGGTGCCCAGACA TGGGC GGAAA GCA GTCCA AC CAGGTGCC CAG ACA GGT
GC
TCTGGTTGGCTTTGGCTGAT ACCCG CCTTT CGT TAGGT TG GTCCACGG GTC TGT TTA CG

TTGTCCTGCAGGCACCTGCC TTGAA CACA T C TTCC AC C --- GT ----
TTGTCTGGATTTGCACACTT
TCCAAGTTGCCCA
GAM33659 10732 GGGAGCTCTTTTGCAAAACA ---------- TG AACAAAA CT - TA C G TTGTT
5 AAAGATGTCTTCTTTTCCCT GGGAG CTCTTT CAA GATGT TCTTTTC CCT GCC TT GTT
TAGCCCTTGGTTTTGTTTGG CCCTC GAGAAG GTT TTACA AGAGAAG GGA TGG AG CGG

CAGATGGTGTAGGTGAAGAG AGTATGTATG GT GA----- -- T TG T A -----
AACATTAGTTGTGGAAGAGG T
TATGTATGACTCCC

-
GAM33659 10135 CTCTTTTGCAAAACAAAAGA TG AACAAAA CT - TA C G TTGTTT
6 TGTCTTCTTTTCCCTTAGCC CTCTTT CAA GATGT TCTTTTC CCT GCC TT GTT
CTTGGTTTTGTTTGGCAGAT GAGAAG GTT TTACA AGAGAAG GGA TGG AG CGG
GGTGTAGGTGAAGAGAACAT GT GA----- -- T TG T A ------
TAGTTGTGGAAGAG
GAM33659 10092 CGGTGAGATGGCTGAAAGGT GA --- AA GACAT G- TTTTA AA TTCTTCTC
7 AGACATCGAGAAGTTTTAAT CGGTGA TGGC TGA GGTA CGA AAG ATATTCAG TCTT
ATTCAGAATCTTTTCTTCTC GCCACT ACCG ACT CCAT GTT TTC TGTAAGTC AGAA
AAGACGCTGAATGTAATCTT G- TCC AC AAAT- GA TAA-- GC --------
AGTTGTAAATACCCATCACC
TGCCAGTCACCG
GAM33659 9799 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33659 11095 TGAGGCAGGAGAATCGCTTT GAA AA--- AGGCA GT TG A - AGAT
9 AACCCGGGAGGCAGAGGTTG TGAGGCAGGA TCGCTTT CCCGGG GAG TG GTG GC CG

TGGTGAGCCGAGATCGCGCC ACTCTGTCTT GGCGAGA GGGTCC CTC AC TAC CG GC

ATTGCACTCCAGCCTGGGCA AA- ACAAC GAC-- -- GT - C ----
ACAAGAGCGGAATTCTGTCT
CA

GAM33660 10349 GAGGCAGGAGAATCGCTTTA GAA AA--- AGGCA GT TG A - AGAT
0 ACCCGGGAGGCAGAGGTTGT GAGGCAGGA TCGCTTT CCCGGG GAG TG GTG GC CG

GGTGAGCCGAGATCGCGCCA CTCTGTCTT GGCGAGA GGGTCC CTC AC TAC CG GC

TTGCACTCCAGCCTGGGCAA AA- ACAAC GAC-- -- GT - C ----
CAAGAGCGGAATTCTGTCTC

GAM33660 9969 CAGGCAGCAGGATGATCTCT ---------- -- CTC GTAAAA TTTTTTTTT
1 TGTGGAGTAAAATGTCAGGT CAGGC AGCAGGA TGAT TTGTGGA TGTCAGGTG
TTAA

GTTTTTTTTTTTAAGAAATC GTCTG TCGTCTT ACTA GGCACCT ACGGTTTAC GATT
GATTTTTAGTTGTGACGTCA GAAAATTTTTAT TC T-- GTCGG- TGCAGTGTT
TTTGGCAGGCTGTCCACGGT ATCGA
ATCACTTTCTGCTTATTTTT GAA
AAAAGGTCTG TTT

GAM33660 11116 TGAGGCCTGAGAATTGCTTG CT AATT GAA-- AGGTA GT A- TGAGATC
2 AACCCAGGAGGTAGAGGTTG TGAGGC GAG GCTT CCCAGG GAG TGCAGTG GC
CAGTGAGCTGAGATCGCACC ACTCCG CTC CGAG GGGTCC CTC ACGTCAC CG
ACTGCACTCCAGCCTGGGCA T- AGAT ACAAC GAC-- -- CA -------
ACAGAGCTAGACTCTGCCTC
A

GAM33660 11147 TGCTAAAGAAAGAGGGGCTG AG TGTC A TCTATAACTAG GCCATATA

5 ATTTGTCAGACTATTTTGTC TGCTAAAGAA AGGGGCTGATT AGACT TTTTG GGTA
TATAACTAGGGTAGCCATAT ACGGTTTTTT TCTTCGATTAG TCTGA GGAAC CCGT
ATGCCAATTTCCCCAAGGCA A- T--- C CCCTTTAA--- --------
GTCTTGATTAGCTTCTATTT
TTTGGCA

GAM33660 10677 GGCAGGAGAATCACTTGAAC G AA -- AA- AGGCA GT A CAAGATCAT
6 CCAGGAGGCAGAGGTTGCAG GGCAG AG TCA CTTG CCCAGG GAG TGCAGTG GC

TGAGCCAAGATCATGCCACT CTGTC TC AGT GAAC GGGTCC CTC ACGTCAC CG
GCACTCCAGCCTGGGCAACA - AA AA AAC GAC-- -- - ---------
AGAATGAAACTCTGTC

GAM33660 11100 TGAGGCAGGAGAATGGCGTG A AATG G- AA- AGGCA CT A C AGATT
7 AACCCGGGAGGCAGAGCTTG TGAGGC GGAG GC TG CCCGGG GAG TGCAGTG GC C

CAGTGAGCCCAGATTGCGCC ACTCTG CCTC CG AC GGGTCC CTC ACGTCAC CG G
ACTGCACTCCAGCCTGGGCA - AGAG AG AAC GAC-- -- - C -----
ACAGAGCGAGACTCCGTCTC
A

GAM33660 10356 GAGGCAGGAGAATGGCGTGA A AATG G- AA- AGGCA CT A C AGATT
8 ACCCGGGAGGCAGAGCTTGC GAGGC GGAG GC TG CCCGGG GAG TGCAGTG GC C

AGTGAGCCCAGATTGCGCCA CTCTG CCTC CG AC GGGTCC CTC ACGTCAC CG G
CTGCACTCCAGCCTGGGCAA - AGAG AG AAC GAC-- -- - C -----
CAGAGCGAGACTCCGTCTC
GAM33660 10414 GATCATAAGCTCCCTGAAAA ATAA T AAA C C G - ACTTCCACAAA
9 CACGTTGCATCTGTGTCTCT GATC GC CCCTG ACACGTTG AT TGT TCTCTAG CA
AGCAACTTCCACAAATGTTT CTGG CG GGGAC TGTGTAAT TA ATA AGAGGTT GT
GGAGAATAAATTAATGTGTG ---- C GG- - A - T ----------
GCAGGGCGCGGTC
GAM33661 10150 CTGAGGCAGGAGAATGGCAT A AATG A- AA- AGG CT A CGAGATCAC
0 GAACCCAGGAGGTGGAGCTT CTGAGGC GGAG GC TG CCCAGG TGGAG TGCAGTG GC

GCAGTGAGCCGAGATCACGC GACTCTG CCTC CG AC GGGTCC ACCTC ACGTCAC CG

CACTGCACTCCAGCCTGGGC - AGAG AC AAC G-- -- - ---------
AACACAGCGAGACTCCGTCT
CAG
GAM33661 10783 GGTCGTTTGCTTTTCAGTGA CG TTTTCA - TC T T AT------- TCACA
1 CCAGGTTCTTCATACACATG GGT TTTGC GTGACCA GGT TTCA ACACA GG GTC
GATGTCTCACAGATCAGCTA CCG GAACG CACTGGT CCA AAGT TGTGT CC TAG
AGGCCTGTGTTTGAACACCT AG TCCC-- T C- T - GGAATCGAC -----
TGGTCACCCCTGCAAGGAGC
C
GAM33661 9800 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33661 9968 CAGGCAAAGGTGGCTTAATG CAA G TA C-- TTA GGTGGTA
5 AAGAGCAAGGGGTTTTTAGA CAGG AG TGGCT ATGAAGAG AAGGGGTTT GATGACAT

TGACATGGTGGTAGTGTTAT GTCC TT GTCGA TATTTCTC TTTCTCAAA TTATTGTG
TAATAAACTCTTTTTCCTCT --- G CG CTT TAA -------
TTATGCAGCTGGTTCCTG
GAM33661 10292 GAGACAGGGGAATCGCTTGA C GAA C GAATC A - GT A TGAGATTGT
7 ATCTGCAAGGTGGAGGTTGC GAGA AGGG TCG TT TGC AGG TGGAG TGCAGTG GC

AGTGAGCTGAGATTGTGCCA CTCT TCTC AGT AG ACG TCC ACCTC ACGTCAC CG
CTGCACTCCAGCCTGGCAAC A AG- A ACA-- G G -- - ---------
AGAATGAGACTCTATCTC
GAM33661 10180 CTGGTCTGGCAGCACTAAGA G GG GCAC G GCA ATCA TCC- TCCCA
8 GGCAGGCATTCTGGGTATCA CTG TCT CA TAAGAG CAG TTCTGGGT GACATAAA CC

GACATAAATCCCCTCCCAGG GAC AGA GT GTTCTC GTC GAGACCCA CTGTGTTT GG
AACTTTTGTGTCCTGACCCA A -- AAGA G AG- GTC- TCAA -----
GAGGACTGGCTCTTGAGAAT
GAGAACAG
GAM33661 10901 TAAGAGGCAGGCATTCTGGG G GCA ATCA TCC- TCCCA
9 TATCAGACATAAATCCCCTC TAAGAG CAG TTCTGGGT GACATAAA CC
CCAGGAACTTTTGTGTCCTG GTTCTC GTC GAGACCCA CTGTGTTT GG
ACCCAGAGGACTGGCTCTTG G AG- GTC- TCAA -----

GAM33662 9607 AAGAGGCAGGCATTCTGGGT G GCA ATCA TCC- TCCCA
0 ATCAGACATAAATCCCCTCC AAGAG CAG TTCTGGGT GACATAAA CC
CAGGAACTTTTGTGTCCTGA TTCTC GTC GAGACCCA CTGTGTTT GG
CCCAGAGGACTGGCTCTT G AG- GTC- TCAA -----
GAM33662 10667 GGATTAGATGATGGTGACAG A ATG C G- C AGCA A - TTTAGAGT
1 CAGTAGCAGCAGGAGCAGGT GGATT GATG GTGA AGCA TAG AGCAGG GGTA CAT TCA

AACATTCATTTAGAGTTGAG CCTGA CTAT TATT TCGT ATC TCGTCC CCGT GTA AGT
ATGTGCCACACCCTGCTCTA A AGG - AA - CACA - G --------
AATGCTTTATGGATATCAAG
TCC
GAM33662 10489 GCTGCTTTCCTATCTTACCC TG TT- - CC - T - GTAG- ATGAGGAA
2 TTCCTGCTCTCCTTTTTGTA GC CT CCTA TCTTAC TTCCT GC CT CCTTTTT TG
GTGATGAGGAACAATGAAAA CG GG GGGT GGAGTG AAGGA TG GA GGAGAAA AC
AGAGGTAGTGTAAGGAATTG GT TAC C TT A T T AAGTA --------
TGAGGCTGGGCATGGTGGC
GAM33662 9801 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33662 9679 AGAGTCACCTATGAAGCATT C ATGAA A T TAA - A TC- TTCAATAAATCT
8 AAAATAATTAAAGTGTCTGA AGAGT ACCT GC TTAAAA AAT AGT GTCTG GGCCT CCC
GGCCTTCCCCTTCAATAAAT TCTTA TGGA CG AATTTT TTG TCA CGGAC CCGGG GGG

CTGGGATTGGGCCCAGGCAA T CCCA- - - TG- A - TTA ----------
CTGTGTTTTTTAAGCACCCA
GGTTATTCT
GAM33662 10446 GCATTAAAATAATTAAAGTG A T TAA - A TC- TTCAATAAATCT
9 TCTGAGGCCTTCCCCTTCAA GC TTAAAA AAT AGT GTCTG GGCCT CCC
TAAATCTGGGATTGGGCCCA CG AATTTT TTG TCA CGGAC CCGGG GGG
GGCAACTGTGTTTTTTAAGC - - TG- A - TTA ----------
GAM33663 11110 TGAGGCAGGAGAATTGCTTG A AA GAA-- AGGC T T A- CAATATC
0 AACTCGGGAGGCGGATGTTG TGAGGC GGAG TTGCTT CTCGGG GGA GT GCAGTG GC

CAGTGAGCCAATATCGCACC GCTCTG CCTC AACGAG GGGTCC CCT CA CGTCAC CG

ACTGCACTCCAGCCTGGGCA - AG ACAAC GA-- - - CA -------
ACAGAGCAAGACTCCGTCTC
G
GAM33663 10644 GGAGAATTGCTTGAACTCGG AA GAA-- AGGC T T A- CAATATC
1 GAGGCGGATGTTGCAGTGAG GGAG TTGCTT CTCGGG GGA GT GCAGTG GC
CCAATATCGCACCACTGCAC CCTC AACGAG GGGTCC CCT CA CGTCAC CG
TCCAGCCTGGGCAACAGAGC AG ACAAC GA-- - - CA -------
AAGACTCC
GAM33663 10008 CCATGTTAATTTCCTGGTAG T TG G T G GTGATTATATAGG
2 TGATGACAGCACTGTGATTA CCATGT AATTTCC GTA TGA GACA CACT
TATAGGAGTGTGTCCTTGGT GGTACA TTAAGGG TGT GTT CTGT GTGA
GTTTGGGAATTACATGG - TT G C - ----------
GAM33663 11263 TTGCTTGAACCCGGGAGGTG GAA-- AGG AT A - AGAT

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3          GAGATTGCAGTGAGCTGAGA TTGCTT    CCCGGG   TGGAG  TGCAGTG GC TG
           TCATGCCACTGCACTCCAGC AACGAG    GGGTCC   ACCTC  ACGTCAC CG AC
           CTGGGCGACAGAGCAA         ACAGC     G--    --      - T ----
GAM33663 10263  GAGAAGATAAATGCGTTTTC        A----  C  TT    GAT--    CT-----      GCTTTTCTCTG    TG
4          AGGGATGTCATCTTGGGCCT GAGAAGATA    ATG GT  TCAGG    GTCAT     TGGGCCT        ATCG

           GCTTTTCTCTGATCGTGTAG CTCTTCTAT    TGC CG  AGTCC    TAGTG     ACTCGGG        TAGC
           CGATGGGCTCATTTTGCAGT       CCAAG  - GT    ATATT    ACGTTTT    ----------   --
           GATTTATACCTGATGGCCGT TAG
           GAACCTATCTTCTC

                      ---
GAM33663 10814  GTATGGGGCAACTTGGGGCG  --    CAACT   --     GT  GCC   T   CCACC
7          TGATGTCAGCCAGAGTCCTT GT  ATGGGG    TGGG  GCGTGAT  CA   AGAG CCTT
           CCACCAAGGCTTTTATGGTG CA  TACCCC    ACCT  TGCATTG  GT   TTTC GGAA
           TTACGTGATCCACCACCCCA  AT    ACC--   AG     TG  AT-   -   -----
           TTAAC
GAM33663 9802   AGTTTTAGGGTACATGTGCA    TTA    A  T TG  -    - G  T   T  ATAT
8          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA    TTA   C - GT   G    C  G  C   - ----
           CT
GAM33663 10453  GCCCTTAGAAATTGTTATGA        --  TG-    A  G     AA   AGG-   A    A   TCAGGT
9          TTGTCCCAGAAATCCAGGCT GCCCTTAGA  AAT   TTATG TT TCCCAGA  TCC    CTT AATG TAC

           TAAATGATACTCAGGTGTAA TGGGAGTTT  TTA   AATAT AA AGGGTCT  GGG    GAA TTAT ATG

           TATTCAAGATAAGGGTCTGG        AA   TAA    - G     --  AATA  C    A  ------
           GAGAATATAAAATATTAATT
           TGAGGGT
GAM33664 10802  GGTTGGAATGAGGAAGGGTG        GA---  A   GTG  CTTCG  TAAAATTT
0          TGGTCTTCGGCTAAAATTTG GGTTGGAAT    GGA GGGT   GT    GC
           CATAAAACGGAACCCATCCG TCAACCTTA    CCT CCCA   CA    CG
           GGCGATTCCAACT              GCGGG   A   AGG  AAATA --------
GAM33664 10794  GGTGGTAAAGCCCTGGAGTG  T  AAA  C     -     AACCCCAAA   C-   ACACCC
2          AGGCAGGAACCCCAAAGCCC GG GGT   GCC TGGAGTG AGGCAGG        GCC  TATG
           TATGACACCCCATATAGGTA CC CCG   CGG ACTTCAT TCCGTCC        TGG  ATAC
           CCCCCAAACCTGCCTATACT  -  GAC  -     A     AAACCCCCA   AT   ------
           TCAGGCCAGGCCCC
GAM33664 10795  GGTGGTAAAGCCCTGGAGTG  T  AAA  C     -     AACCCCAAA   C-   ACACCC
3          AGGCAGGAACCCCAAAGCCC GG GGT   GCC TGGAGTG AGGCAGG        GCC  TATG
           TATGACACCCCATATAGGTA CC CCG   CGG ACTTCAT TCCGTCC        TGG  ATAC
           CCCCCAAACCTGCCTATACT  C  GAC  -     A     AAACCCCCA   AT   ------
           TCAGGCCAGGCCCCC
GAM33664 10516  GGAAAAGAACCATGGGTTAG   AA   AC     TTAG      G    AG     CA---  TTTTGAT
6          GCCTTTTTGGGAAGAGACAG GG  AAGA  CATGGG   GCCTTTTT GGAAG  ACAGTT    GC
           TTCAGCTTTTGATGTAAAAC CT  TTCT  GTACCC   TGGAGAGA TCTTC  TGTCGA    TG
           AGCTGTACCTTCTGAGAGAG  AC   --    CGA-     G    CA     CAAAA -------
           GTAGCCCCATGTCTTCATC
GAM33665 10102  CTCAGACTCACCAAACAGTC        C-  AA  G     C  ACCC    TAAG
```

1 TGCTTCTTACCCCAGTGTAA CTCAGACTCA CA CA TCTGCTT TT CAGTG
GCACTGAACAGGCAGGTGGG GAGTCTGGGT GT GT GGACGGA AA GTCAC
TGTATGGGTCTGAG AT GG - C ---- ----
GAM33665 9732 AGGGAGAGTCTTGGGGTGAA TCTT GAAGA G CTTCTCC----- GTCCGT
2 GAGGTTTGAGCCTTCTCCTG AGGGAGAG GGGGT GGTTT AGC TGCTCT
CTCTGTCCGTGGAGCAAGTC TTCCTCTT CCTCG CCAGA TCG ACGAGG
AAATAAATGCTGAGACCGTC TACT ACTG- G TAAATAAACTGA ------
AGCTCCTCATTTCTCCTT
GAM33665 10400 GAGGTGGGAGGATCGCTTGA AGGATC GA-- A- TCAA C A - TGAT
3 GCCCAGGAGGTCAAGGCTGC GAGGTGGG GCTT GCCCAGG GG GG TGCAGTG GT TG

AGTGAGTTGTGATCATGCCA CTCTACCC CGAA CGGGTCC CC TC ACGTCAC CG AC
CTGCACTCCAGCCTGGGCAA CAGAA- ACAA GA ---- - - T ----
CAAAGCAAGACCCCATCTC
GAM33665 9803 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33665 11203 TGGTTGTTATGAGTCTGGTT GT GTC --------- TG GT TT AAAGTAGAGAA
7 GTTAAGTGCTGGTTGTTAGT TGGTT TATGA TGGT TGTTAAG CTG TGTTAG GTT
TGTTAAAGTAGAGAAAACCC ACCAA ATACT ACCG ACGGTTC GAC ACGATC CAA
CTAGCACAGTGCTTGGCACA -- --- AAATCACAC GT -- CC ----------
CACTAAAGCCATCATAAACC
A
GAM33665 10720 GGGAAGAACTACCAATCTAG AA- - TC ---------- - - T TGATTAT
8 GGCACACGTCTCTCTGAATT GGG GAACTAC CAA TAGGGCACACG TCTCT C TGAA TGT

GTTGATTATGCGCTTTATGA CCC TTTGGTG GTT ATTTCGTGTGC AGAGA G ATTT GCG

AGAGATTTTTCAATCTCGTG AGA T TC TCTAACTTTTT A T C -------
TGCTTTACTTTGTGTGGTTT
AGACCC
GAM33665 10280 GAGAATTGCTTTAACCCGGG AA TG AA-- AGG GT A- AGAT
9 AGGTGGAGGTTGCAGTGACT GAG T CTTT CCCGGG TGGAG TGCAGTG CTG
GAGATCGGGCCACTGCACTC CTC A GAGA GGGTCC ACCTC ACGTCAC GGC
CAGCCTGGGCAACAGAGAGA AG GA CAAC G-- -- CG ----
GACTC
GAM33666 9804 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33666 10382 GAGGCGGGAGAATTGCTTGA G AA GAA-- AGG GT A - AGAT
1 ACCCGGGAGGTGGAGGTTGC GAGGCGG AG TTGCTT CCCGGG TGGAG TGCAGTG GC CG

AGTGAGCCGAGATCGCGCCA CTCTGTC TC AACGAG GGGTCC ACCTC ACGTTAC CG GC

TTGCACTCCAGCCTGGGCAA - AG ACAAC G-- -- - C ----
CAGAGCAAGACTCTGTCTC

GAM33666 10698 GGCGGGAGAATTGCTTGAAC G AA GAA-- AGG GT A - AGAT
2 CCGGGAGGTGGAGGTTGCAG GGCGG AG TTGCTT CCCGGG TGGAG TGCAGTG GC CG

TGAGCCGAGATCGCGCCATT CTGTC TC AACGAG GGGTCC ACCTC ACGTTAC CG GC

GCACTCCAGCCTGGGCAACA - AG ACAAC G-- -- - C ----
GAGCAAGACTCTGTC
GAM33666 10634 GGAGAATTGCTTGAACCCGG AA GAA-- AGG GT A - AGAT
3 GAGGTGGAGGTTGCAGTGAG GGAG TTGCTT CCCGGG TGGAG TGCAGTG GC CG

CCGAGATCGCGCCATTGCAC TCTC AACGAG GGGTCC ACCTC ACGTTAC CG GC
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- - C ----
AAGACTCT
GAM33666 11265 TTGCTTGAACCCGGGAGGTG GAA-- AGG GT A - AGAT
4 GAGGTTGCAGTGAGCCGAGA TTGCTT CCCGGG TGGAG TGCAGTG GC CG
TCGCGCCATTGCACTCCAGC AACGAG GGGTCC ACCTC ACGTTAC CG GC
CTGGGCAACAGAGCAA ACAAC G-- -- - C ----
GAM33666 10456 GCCTCTGGACAATACTGTTA TG CAAT AAACTAAATACTTGC TGGC
5 AAACTAAATACTTGCCAGGT GCCTC GA ACTGTTA CAGGTGTGG
GTGGTGGCTCACACCTGTGA CGGAG TT TGATAGT GTCCACACT
TAGTTCTTTTGGAGGC GT TCT- ---------- ----
GAM33666 9805 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33667 9598 AAATAGCCATTCCCTCGTGC T ATTCC G CGACA TC T - A AAAACTAGG
0 TGCGACAGTTCCATTCCTAA AAA AGCC CTCGT CTG GT CAT CCTAATGC AG CTTACA

TGCAGACTTACAAAAACTAG TTT TCGG GAGTA GAC CG GTG GGATTACG TC GAATGT

GTGTAAGGCTGGCATTAGGG T GACGA G ----- GA - G G ---------
TGAGGCCAGGATGAGAGCAG
GGCTTTTT
GAM33667 9693 AGCCATTCCCTCGTGCTGCG ATTCC G CGACA TC T - A AAAACTAGG
1 ACAGTTCCATTCCTAATGCA AGCC CTCGT CTG GT CAT CCTAATGC AG CTTACA
GACTTACAAAAACTAGGTGT TCGG GAGTA GAC CG GTG GGATTACG TC GAATGT
AAGGCTGGCATTAGGGTGAG GACGA G ----- GA - G G ---------
GCCAGGATGAGAGCAGGGCT
GAM33667 10115 CTCGTGCTGCGACAGTTCCA G CGACA TC T - A AAAACTAGG
2 TTCCTAATGCAGACTTACAA CTCGT CTG GT CAT CCTAATGC AG CTTACA
AAACTAGGTGTAAGGCTGGC GAGTA GAC CG GTG GGATTACG TC GAATGT
ATTAGGGTGAGGCCAGGATG G ----- GA - G G ---------
AG
GAM33667 11036 TGACCCTCCAGACCTCACAT C -- CACATTTG T- - A - TC TTTA
3 TTGTTCTGGAGCCCATACTC TGACCCT CA GACCT TTC GGAGCC CAT CTC ACCAA AGC

ACCAATCAGCTTTAGCTTTT ACTGGGA GT CTGGG AAG CTTTGG GTA GAG TGGTT TCG

GGTCGAGATGAGGTTTCTCG C CT -------- CT A - C T- ----

AAGGGTCTCTGCAGGGTCA
GAM33667 10073 CCTTGGCATTCATTATTTTC TG T T TT GT GCAC GGCACAT AGGA
4 ATTCCAGTTCTCAGCACAGC CCT GCAT CATTA T CATTCCA TCTCA AGCGCTT AGT
GCTTGGCACATAGTAGGAAC GGA TGTA GTAGT G GTAAGGT AGGGT TTGTGAA TCA
TCAGGAAGTGTTTATGGGAT GT - - GG -- AT-- GGAC--- ----
GGAATGGGGTGATGATGTTG
AGG
GAM33667 10284 GAGACAGGAGAATCACTTGA CA AA GA-- GAG - A T A - AGAT
5 ATCTGAGAGGTGGAAGTTGC GAGA GGAG TCACTT ATCT AGG TGGA GT GCAGTG GC CG

AGTGAGCCGAGATTGTGCCA CTCT CCTC AGTGAG TGGG TCC ACCT CA CGTCAC CG GT

CTGCACTCCAGCCTGGGTGA A- AA ACAG --- G - - - T ----
CAGAGTGAAACTCCATCTC
GAM33667 11174 TGGCTTCCCAAAGTGCTGGC C ---------- C TA- AGCCAC
6 GTTACAGGTGTGAGCCACCG TGGCTTC CA AAGTGCTGG GT CAGGTGTG
CACCTGGCCATCCCGGCATT ATCGGAG GT TTTACGGCC TA GTCCACGC
TTTCTATTCTGCTGTGAGGC T CGTCTTATCTT C CCG ------
TA
GAM33667 10934 TCAATACTTTAAAGGCACAC A TTA- - AC- G TT- A GT- - GGAGAAG
7 TTGTCTGCTTTCTACACTGT TCA TACT AA GGC ACTT TCTGCT CT CACT TG CC
TGCCGGAGAAGGGTCATAAA AGT ATGA TT CCG TGAA AGACGG GA GTGA AC GG
GTGAAGTTTGGCAGAAAAGT C TCTG A GTT A TTT A AAT T -------
TTGGCCATTGTCTAGTACTG
A
GAM33668 9661 AGAATCGCTTGAACCCAGGA AA GA-- A- CACA T A - AGAT
1 GGCACAGGTTGCAGTAGGCC AG TCGCTT ACCCAGG GG GGT GCAGT GGC CG
GAGATTGTGCCACTGCACTC TC AGTGAG TGGGTCC CC TCA CGTCA CCG GT
CAGCCTGGGTGGCAGAGTGA AG ACGG GA ---- - - T ----
GACT
GAM33668 11101 TGAGGCAGGAGAATGGCGTG A AATG G- AA- AGGC CT A - AGAT
3 AACCCGGGAGGCGGAGCTTG TGAGGC GGAG GC TG CCCGGG GGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC TG AC GGGTCC CCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AGAG AG AAC GA-- -- - C ----
ACAGAGTGAGACTCCGTCTC
A
GAM33668 11026 TCTTTCTCTAATTTGTCCAC AA TG A AG--- A A TCTCCA GC G ATGG
5 CAGTAGTATGCATCTTTTTC TCTTTCTCT TT TCC CC TAGT TGC TCTTTT CTA CAGGG CT

TCCACTAGCCAGGGGCTATG AGAGAGAGA AG AGG GG ATCG ACG AGAAGA GAT GTCCC
GA
GAGGCCCTGAATAGAACAGA -- GA C GAACG - - CAA--- AA G ----
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AAGGAAGAGAGAGA
GAM33668 11087 TGAGGCAGGAGAATCGCTTG G AATC GAA--- GGA A- - T AGCTGAGATTG

6 AACCCGGAAGGCAGAGGTTG TGAGGCAG AG GCTT CCC AGGC GAG GT GTGGTG

TGGTGAGCTGAGATTGCACC ACTCTGTC TC CGAG GGG TCCG CTC CG TACCAC
ATTGCACTCCAGCCTGGGCA - AAAA AATAAC --- AC A T ----------
ATAAGAGCAAAACTCTGTCT
CA
GAM33668 10191 CTGTTGCCCAGGCTGGAGTG TG- -- - AG AGT CC--- TCAGCTCA - GTCT
9 CAGTGGCACCATCTCAGCTC CTGT CCCAG GC TGG TGC GGCA ATC CTGGAG C
ACTGGAGCGTCTGCCTCCAG GACA GGGTC TG ACC ACG CCGT TAG GACCTC G
GTTCAAGTGATTCTCCTGCC TCA GA A CT ACT CCTCT TGAACTTG C ----
TCAGCATCCCAAGTAGCTGG
GACTACAG
GAM33669 11037 TGAGAAGGAGTCTCATTCTG A- TC C TT -- CC -- -- TGATCT
0 TTGCCTAGGCCGGAGTGCAG TGAG AGGAG TCATT TG GCCT AGG GGAG TGCAGTGA CA

TGACATGATCTTGGCTCACT ACTC TCCTC AGTGA AC TGGA TCC CCTC ACGTCACT GT

GCAATCTCCACCTCCAGGTT CG TT - T- CC A- TA CG ------
CAAGTGATTCTCCTGCCTCA
GAM33669 10871 GTGTGACTTTAGTGCTACTC - ---------- A A GTTCAGGAA
1 TGATTTTACTGTTCAGGAAA GTGTGACTTT AGT GCT CTCTG TTTTACT
GTGAAGCAGAGAGGTTCAAT CACACTGGAA TCA TGG GAGAC GAAGTGA
GTCTTACTCAAGGTCACAC C TTCTGTAACT A - ---------
GAM33669 10950 TCACTTGAGCCCAGGAGTTG GA-- AG GC A- TATGATT
7 GAGGCTGCAGTGAGCTATGA TCACTT GCCCAGG TTGGAG TGCAGTG GC
TTGCACCACTGTACTCCAGC AGTGAG TGGGTCC GACCTC ATGTCAC CG
CTGGGTGACAGAGTGA ACAG -- -- CA -------
GAM33669 10052 CCTATCACAGACCTGCCAGA CAGA C- T T A-- C TCCCTCT
9 TTCCTCTGGTAAACTGCAGG CCTATCA CCTG CAGA TCC CTGGT AACTG AGGT
TTCCCTCTGCCTCAGTTGTG GGGTAGT GGAC GTCT AGG GACCG TTGAC TCCG
GCCAGGGATTCTGACCAGGA AGA- CA T - GTG - -------
GATGATGGG
GAM33670 10881 GTTACTTCAGCAAGTAGAAG AGCA GAA AT- --- GCC TTGTCTT CGTCCA
1 ATGGATATTTTTGATGCCCA GTTACTTC AGTA GATGG ATTT TTGAT CAGAGTG CCC
GAGTGTTGTCTTCCCCGTCC CGGTGAAG TCAT CTACC TAAG AACTA GTCTTAC GGG

AGGGTATCTCATTCTGATCA AG-- AC- GGT CCA --- TCTAT-- ------
AACCGAATTGGCCATCCATA
CTGAGAAGTGGC
GAM33670 9806 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33670 10303 GAGATTGCTTGAGCCCAGGT TG--- ----- AGT AC AAC GATT
3 AGTTGAGACTGCAGTGAACC GAGAT CTTGA GCCCAGGT TGAG TGCAGTG CAT
ATGATTGTGCCACTGCACTC CTCTG GAATT TGGGTCCG ACTC ACGTCAC GTG
AGCCTGGGTGACAGTTAAGA TCCCA GACAG --- -- C-- ----
CCCTGTCTC
GAM33670 10642 GGAGAATTGCTTGAACGCCG AA GAAC G C GT A- CATGATC
4 GGGTCGGAGGTTGCAGTGAG GGAG TTGCTT GCC GGGT GGAG TGCAGTG GC
CCATGATCGCGCCACTGCAC TCTC AGCGAG CGG TCCG CCTC ACGTCAC CG

TCCAGCCTGGGCAACAGAGC AG ACAA G A -- CG -------
GAGACTCT
GAM33670 10279 GAGAATTGCTTGAACGCCGG AA GAAC G C GT A- CATGATC
5 GGTCGGAGGTTGCAGTGAGC GAG TTGCTT GCC GGGT GGAG TGCAGTG GC
CATGATCGCGCCACTGCACT CTC AGCGAG CGG TCCG CCTC ACGTCAC CG
CCAGCCTGGGCAACAGAGCG AG ACAA G A -- CG -------
AGACTC
GAM33670 10317 GAGGCAGAACTTCCAGTGAT AACT-- TGAT A TT TGGG
6 TCATTTGGTTGTTCATTTTG GAGGCAG TCCAG TCATTTGGTTGTTC TT GT
TTGGGACTGAGAACAGCCAG CTCCGTC AGGTC AGTAGACCGACAAG AG CA
ATGACTGGATCCACACTGCC ACACCT ---- - T- ----
TC
GAM33670 10455 GCCGTAGAAGAGAGCCAGCA GTAGAAGA- CAGCA G GC T TCCTGGGTT

7 TGGTGTGGCAGAAGGCTCTG GCC GAGC TGGT TG AGAAGGCTC GGATTAG
GATTAGTCCTGGGTTCTAGT CGG CTCG ACCA AC TCTTCTGGG CTTGATC
TCTGGGTCTTCTACAAACCA ATTAAGTAC ----- A A- T ---------
GCTCCATGAATTAGGC
GAM33670 10298 GAGATGAGAGGATTGCTTGA G A - G A--- AGG G- AGTGA GATT
9 ATCCAGGAGGTGGAGGCTGT GAGAT AG GG ATT CTTG ATCCAGG TGGA GCTGT GCTAT

AGTGAGCTATGATTGTGGCA TTCTG TC CC TAG GAAC TGGGTCC ACCT CGACA CGGTG

CAGCAGTCCAGCCTGGGTGA - - A - ACAG G-- GA ----- ----
CACAAGGATACCCTGTCTT
GAM33671 10169 CTGGAGGCAGCAAAGATTAT A TA TA AT TT G TATT
0 CTTATTTATTTTATTTTGTT CTGGAGGCAGCA AGAT TCT TTTATTTT TTTGTT CT CTA
TTCTGCTATATTTAGAGTGG GACCTCTGTCGT TTTG AGA AGATAAAA AAACGG GA GAT

CAAAAAAATAGAGCAGAGGG C GG CG -- T- - ----
TTTCTGCTGTCTCCAG
GAM33671 10029 CCCTACTATTTTCTTGGGAA A T G C A AC GTGGGAGGGCAGTAAG
3 ACATCCAGCACATACTCAAG CCCTACT TT TCTT GGAAACATC AGC CAT TCAAG
GTGGGAGGGCAGTAAGCTTG GGGATGA AA AGAA TCTTTGTAG TCG GTG AGTTC
ATGGTGGCTAGATGTTTCTG G C G A - GT ----------
AAGACAAGAGTAGGG
GAM33671 10271 GAGAATCTCTTGAACCCAGG AAT-- AA- AGGCA - TG AGTCGAGATAG
5 AGGCAGAGGTGGTGGTGAGT GAG CTCTTG CCCAGG GAG G GTGGTG
CGAGATAGCACCATTGCACT CTC GAGAAC GGGTCC CTC C TACCAC
CCAGCCTGGGCAACAAGAGC AAAGC AAC GAC-- A GT ----------
GAAACTC
GAM33671 10551 GGAGAATCACTTGAACCCAG AA -- AA- AGAC TT- AGCCGAGATCA
6 GAGACGGAGTTTGTGGTGAG GGAG TCACT TG CCCAGG GGAGT GTGGTG
CCGAGATCACACCATTGCAC CCTC AGTGA AC GGGTCC CCTCA TACCAC
TCCAGCCTGGGCAACAACAG AA CA AAC GA-- CGT ----------
TGAAACTCC
GAM33671 10945 TCACTTGAACCCAGGAGACG -- AA- AGAC TT- AGCCGAGATCA
7 GAGTTTGTGGTGAGCCGAGA TCACT TG CCCAGG GGAGT GTGGTG
TCACACCATTGCACTCCAGC AGTGA AC GGGTCC CCTCA TACCAC
CTGGGCAACAACAGTGA CA AAC GA-- CGT ----------

GAM33671 9698 AGCTGCAGCTCTTTCTTCCC A --- ATGAG GG ATCAA AAC
8 TATGAGCTTGGACACATCAA AGCTGC GCTCT TTCTTCCCT CTT ACAC TCCTA
TCCTAAACTAGGAGTGTGAA TTGACG CGAGG GAGGAGGGA GGA TGTG AGGAT
GGAGGAAGGGAGGAGCAGGG A GAC AGGA- AG ----- ---
AGCAGCAGTT
GAM33671 10600 GGAGAATCGCTTGAACCTGG AA C-- AA- TG AGGC GT A - AGAT
9 GAGGCGGAGGTTGCGGTGAG GGAG TCG TTG CC GG GGAG TGCGGTG GC CG
CCGAGATCGCGCCATTGCAC CCTC AGC AAC GG CC CCTC ACGTTAC CG GC
TCCAGCCTGGGCAACAAAAC AA CAA AAC GT GA-- -- - C ----
CGAAACTCC
GAM33672 9745 AGTATCACTTGAACCAGGGA C GAA--- --- - A CTGCA GAGCCAAG
0 GGCAGAGGCTGCATGCAGTG AGTATCA TT CCAGG GAG GCAG GG TGCAGT
AGCCAAGATTGCACCACTGC TCATAGT AG GGTCC CTC CGTC CC ACGTTA
ACTCTAACCTGGGCAACAGA A ACAACG AAT A A ----- --------
ATGATACT
GAM33672 9807 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33672 10264 GAGAATCACTTGAACCCAGG AA GA-- AGGCA GT A TGAGATTAT
3 AGGCAGAGGTTGCAGTGAGC GAG TCACTT ACCCAGG GAG TGCAGTG GC
TGAGATTATGCCATTGCACT CTC AGTGAG TGGGTCC CTC ACGTTAC CG
CCAGCCTGGGTGACAGAGTG AA ACAG GAC-- -- - ---------
AAACTC
GAM33672 10863 GTGGTCATAAGGTCCTTTCT GG ---------- TTCT TAAC G TGTTAT
7 GGCTCTAATAACCTGAGCTT GT TCATAAG GTCCT GGCTCTAA CT AGCTTC
CTGTTATGAAGCTGGGACCC CG AGTGTTT TAGGA CCGAGATT GG TCGAAG
TTAGAGCCTCAGGATGATCC A- GTTTGTCTCCTAG CT-- CCCA G ------
TCTGTTTGTTTGTGAAGC
GAM33672 9753 AGTCTCACTCTGTTGCCCAG T CT - CCC AGTCAAC TCTCA CAC C
CCACCTCCT
8 GCTGAAGTCAACGGCATGAT AGTC CA CTG TTG AGGCTGA GGCATGA GCT TG AACCT

CTCAGCTCACTGCAACCTCC TTAG GT GAT AAC TCCGACT CCGTGCT CGA AC TTGGG

ACCTCCTGGGTTCAAGCAAT - TC G CC- ------- CTTAA --- - ---------
TCTCGTGCCTCAGCCTCCCA
AGTAGCTTGGATT

GAM33672 10650 GGAGACCCAGGACCCGGGAG CCA C G GTAGAGG - C--- CACCA
9 AGAGGTAGAGGGGAGCAGAG GGAGAC GGAC CG GAGAGAG GGAGCAGA GA AGC

ACAGCCACCAGCTTCTATCT CCTTTG TTTG GC CTTTCTT TCTCGTCT CT TCG
TCTGCTCTAAGCACATTCTT AA- A A ACACGAA T ATCT -----
TCACGAGTTTAAGTTTCC
GAM33673 10417 GATCCCAAAAACTCATCTCA T CT- T TCTA TCC CTAT- CAAAA AATGTAAA

0 GTCTATGTCCTTGCTATGTA GA CCCAAAAA CA CTCAG TG TTG GTATGTA ATGAGA
TTG

TGTACAAAAATGAGAAATGT CT GGGTTTTT GT GAGTT AC AAC CATACAT TACTCT AAT
AAATTGTGTTTAAAAACCTT - ACT - TCTC CA- TCTTT ----- ATTCCAAA
ATCTCATTACATACTTTCTC TGTT
AAACCACTCTTTGAGTGTCA
TTTTTGGGTC

GAM33673 11278 TTGGGCCCAGGAGGCTTTGA GG G TTGA - G - CTGG
1 GAAAGCCTTCTCTGTGTACT TTG CCCAGGAG CT GAAAGC CTTCTCTGT TA CT
CTGGAGATAGATGGAGAAGT GAC GGGTCCTT GA CTTTTG GAAGAGGTA AT GA
GTTTTCAGATTCCTGGGAAC AA A ---- T G A ----
AG
GAM33673 11180 TGGGCCCAGGAGGCTTTGAG GG G TTGA - G - CTGG
2 AAAGCCTTCTCTGTGTACTC TG CCCAGGAG CT GAAAGC CTTCTCTGT TA CT
TGGAGATAGATGGAGAAGTG AC GGGTCCTT GA CTTTTG GAAGAGGTA AT GA
TTTTCAGATTCCTGGGAACA AA A ---- T G A ----
GAM33673 10432 GCAGAGGCAGATGGGACTCT C AC G TT GA- TGGG
4 GTGCCCATTGAAGAACTTGG GCAGAGG AGATGGG TCTGT CCCA GAA ACT
GAGTGTATTCTGGGAACAGG CGTCTCT TCTACCC GGACA GGGT CTT TGA
CACCCATCTTCTCTGC - AC A -- ATG ----
GAM33673 9808 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33673 11076 TGAGGCAGGAGAATCACTTG G AA A-- AA- AGGCA GT A- CAAGATC
8 AACCCGGGAGGCAGAGGTTG TGAGGCAG AG TC CTTG CCCGGG GAG TGCAGTG GC

CAGTGAGCCAAGATCGCACC ACTCTGTC TC AG GAAC GGGTCC CTC ACGTCAC CG
ACTGCACTCCAGCCTGGGCA - AG CGG AAC GAC-- -- CA -------
ACAAGGGCGAGACTCTGTCT
CA
GAM33673 10170 CTGGAGGCTCAGGAGTCTTT GA TC TTTT AA CAATGATTC
9 TATCTGCAATAGGACAATGA CTG GGC AGGAGTC ATCTGC TAGGA
TTCTCCTAGCAGATCTGTGA GAC TCG TCCTCAG TAGACG ATCCT
CTCCTATGCTCAG -- TA TGTC -- ---------
GAM33674 9904 ATCTGCATGTTTTGTTGTCT -- - TGT CA GGAGGAGAA
0 CTGTGTTGTACAGTGGAGGA ATCTGCAT GTTTT GTTGTCTCTG TGTA GT
GAAACAATGCATTTTGGGGA TAGACGTA CAGGA CGACAGGGGT ACGT CA
CAGCTAGGACCCATGCAGAT CC T TTT AA ---------
GAM33674 10083 CGCACATCTGTTACTCCACA A TTA-- -- - AGAG - TTT GATA
3 TCAGAGACTTCATTTTGTTG CGCAC TCTG CT CCACAT C AC TTCAT GTT
ATAAACCCTATGAATGTAAG GCGTG AGAC GA GGTGTA G TG AAGTA CAA
GAATGTGGGAAGGCGTTCAG - TTGCG AG A GAA- T TCC ----
AGTGCG
GAM33674 10903 TAAGGAATGTGGAAAAACCT A- - T GGAAA T TGT ------ GA TCGA CACAGAA
4 TTATTTGTGGCTCAGACCTT T AG GAA GT AACC TTATT GGCT CA CCTTAC CAT TTCA
ACTCGACATCACAGAATTCA A TC CTT CA TTGG GATGA CCGA GT GGAATG GTA
GAGT
CACTGGTGAGAAACCCTATG GC A - AAC-- T TTT AAGGGT AA TAA- TCCCAAA
AATGTAAGGAATGTGGGAAA ACTG

GCCTTTAGTAGTGGTTCAAA C
CTTCACTCGA G

GAM33674 9701 AGGAATGTGGAAAAACCTTT - T GGAAA T TGT ------ GA TCGA CACAGAA AC
5 ATTTGTGGCTCAGACCTTAC AG GAA GT AACC TTATT GGCT CA CCTTAC CAT TTCAC
TCGACATCACAGAATTCACA TC CTT CA TTGG GATGA CCGA GT GGAATG GTA GAGTG

CTGGTGAGAAACCCTATGAA A - AAC-- T TTT AAGGGT AA TAA- TCCCAAA --
TGTAAGGAATGTGGGAAAGC TG
CTTTAGTAGTGGTTCAAACT
TCACT
--
GAM33674 10269 GAGAATCGCTTGAACCCAGG ATC---- GAA--- AGG GC AA - AGAT
6 AGGTGGAGGCTGCAGTAAGC GAGA GCTT CCCAGG TGGAG TGCAGT GC CG
CGAGATTGTGCCACTGCACT CTCT CGAG GGGTCC ACCTC ACGTCA CG GT
CCAGCCTGGGCAACAAGAGC ATCAAAA AACAAC G-- -- C- T ----
AAAACTATCTC
GAM33674 10506 GCTTGAACCCAGGAGGTGGA GAA--- AGG GC AA - AGAT
7 GGCTGCAGTAAGCCGAGATT GCTT CCCAGG TGGAG TGCAGT GC CG
GTGCCACTGCACTCCAGCCT CGAG GGGTCC ACCTC ACGTCA CG GT
GGGCAACAAGAGC AACAAC G-- -- C- T ----
GAM33674 10810 GTAGTCCACCTCATAAAATC AG - ATAA - - TA-- TGGT C TT TATTAAC
9 AGAAAGTATTACTGGTCTCC GT TCCA CCTC AATCA GA AAG TTAC CTC CACT TAGGC
CACTTTTAGGCTATTAACGC CG GGGT GGGG TTGGT CT TTC GATG GAG GTGA GTTCG

TTGTAGTGAGAGTTTGTAGG G- C ACCG G G TTTG TTT- A T- -------
TTTCTTGTCGTGGTTGCCAG
GGGCTGGGGGC
GAM33675 11102 TGAGGCAGGAGAATGGCGTG A AATG G- AA- AGGC CT A - AGAT
0 AACCCGGGAGGCGGAGCTTG TGAGGC GGAG GC TG CCCGGG GGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC TG AC GGGTCC CCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AGAG AG AAC GA-- -- - C ----
ACAGAGTGAGACTCCGTCTC
A
GAM33675 9706 AGGATCACTTGAGCCTGGTA A A-- --- A TC GC A TATGATCGT
1 TGTCGAGGCTGCAGTGAGCT AGG TC CTTG AGCCTGGT TG GAG TGCAGTG GC
ATGATCGTGCCACTGCACTC TCC AG GAGC TCGGACCA AC CTC ACGTCAC CG
CAACCAGGCTGACCGAGCCA C ACC CAG - -- -- - ---------
GACCCT
GAM33675 9915 ATGCCTAATTTAGCACATAG CTAA - A- CTGTCCCCA AT- TAATAAAT
2 TTCCTGTCCCCAAAATCTAA ATGC TTTAGC AC TAGTTC AAATCTA AAACTCAGAAG
TAAACTCAGAAGTAATAAAT TACG AAATTG TG ATCGAG TTTGGGT TTTGGGTCTTT
TTTCTGGGTTTTTGTGGGTT TTGA A GG TCTCCCG-- GTT --------
TGCCCTCTGAGCTAGGGTAG
TTAAAAGTTGCAT
GAM33675 11083 TGAGGCAGGAGAATCGCTTG CA AA GAA--- AGG - T GA TGAGATT
5 AACCCAGGAGGTGGAGGCTG TGAGG GGAG TCGCTT CCCAGG TGGAG GC GTGGT GC

TGGTGAGCTGAGATTGCGCC ACTCT CCTC AGCGAG GGGTCC ACCTC CG TACCG CG

ATTGCACTCCAGCCTGGGCA A- AA AACAAC G-- A T -- -------
ACAAGAGCGAAACTCCATCT
CA

GAM33675 10577 GGAGAATCGCTTGAACCCAG AA GAA--- AGG - T GA TGAGATT
6 GAGGTGGAGGCTGTGGTGAG GGAG TCGCTT CCCAGG TGGAG GC GTGGT GC
CTGAGATTGCGCCATTGCAC CCTC AGCGAG GGGTCC ACCTC CG TACCG CG
TCCAGCCTGGGCAACAAGAG AA AACAAC G-- A T -- -------
CGAAACTCC

GAM33675 10134 CTCTTTGAGGTCTGTTGTTC ------ - A TC- GGAA
7 AGAAAAATTTCTTGGAAAAT CTCTT TGAGGTCTGTTGTTCA GAA AATT TT
ATGATTGTTCATGGACAACG GAGAA ACTCCAGGCAACAGGT CTT TTAG AA
GACCTCATCACCCAAGAG CCCACT A G TAT ----

GAM33676 11258 TTGCTTGAACCCAAGAGGTG GAA--- AGA - GT A- TGAGATT
0 GAGGTTGCAGTGAGCTGAGA TTGCTT CCCA GG TGGAG TGCAGTG GC
TTGCGCCACTGCACTCCAGC AACGAG GGGT CC ACCTC ACGTCAC CG
CTGGGCAACAAGAGCAA AACAAC --- G -- CG -------

GAM33676 9638 ACCAGAGGCTCAGAGAATGG T AC - T TCCACATTT
1 CACAGCTGTCCTGTTCTCCA ACCAGAGGCTCAGAGAA GGC AG CTG CCTGTTC
CATTTGAATAGGCCGGACTC TGGTTTTTGAGTCTCTT TTG TC GGC GGATAAG
AGTTTTCTCTGAGTTTTTGG - AC A C ---------
T

GAM33676 11227 TGTTGGCCAGGATTGTCTTG T - GGAT - CTG C T TC CACCTC
2 ATCTCCTGACCTTGTGATCG TG TGGC CA TGTCT TGATCTC AC TTG GA GGCC
GCCCACCTCGGCCTCCCAAA AC ACCG GT GCAGA ATTAGAG TG AAC CT CCGG
GTACTGAGATTACAGACGTG C A ---- C TCA A C -- ------
AGCCACCA

GAM33676 10653 GGAGATGGTTTCCAGTTCAC A TT TT C - AA CTTCA A GCAAA
3 CGTCAACCCAAAAGCTCTCT GGAG TGGT CCAG CAC GTCA ACCCA AGCTCT GGTC TG

TCAGGTCATGGCAAACAGAC CCTC GTCA GGTT GTG CGGT TGGGT TCGGGA CCAG AC

CAGGGCTGTGGGTGTGGCTG A C- C- T G G- ----- - -----
TGCTTGGCACTGACTCC

GAM33676 10314 GAGGATGGTTTGAGCCCAGG A- GA-- A- C AAGT A - AAAT
4 AGGCAGAAGTTGCAGTGAGC GAGG TGGTTT GCCCAGG GG AG TGCAGTG GC TG
TGAAATCATGCCACTGCACT TTCC ACCGAG TGGGTCC CC TC ACGTCAC CG AC
CCAGCCTGGGTGATAGAGCC AA ATAG GA - ---- - T ----
AAACCTT

GAM33676 11206 TGGTTTGAGCCCAGGAGGCA GA-- A- C AAGT A - AAAT
5 GAAGTTGCAGTGAGCTGAAA TGGTTT GCCCAGG GG AG TGCAGTG GC TG
TCATGCCACTGCACTCCAGC ACCGAG TGGGTCC CC TC ACGTCAC CG AC
CTGGGTGATAGAGCCA ATAG GA - ---- - T ----

GAM33676 10725 GGGACCGTTAGCTGAAATGC -- GCT-- -- TGA - - TGTGA
7 TGTTGATTTTAGTGGCTGTG GGGACC GTTA GAAATG CTGT TTTTA GTG GC
AGCACACATAAGGATACAGG CCCTGG TAAT CTTTAC GACA GGAAT CAC CG
TCATTTCCCTTATAATTAGG AT ATTCC TG TA- A A -----
TCCC

GAM33676 10379 GAGGCATAAGAATCGCTTGA TAA A -- TGA AGG GT AGCCAAGATCACAC

8 ATTCGGGAGGTGGAGGTTGC GAGGCA GA TC GCT ATTCGGG TGGAG TGCAGTG
AGTGAGCCAAGATCACACCA CTCTGT CT AG CGA TGGGTCC ACCTC ACGTCAC
CTGCACTCCAGCCTGGGTGA --- C AA CAG G-- -- ----------
CAGCAAGACTCTGTCTC
GAM33677 10933 TCAAGTCCTGTACTGCTCAA - -- ---- T A GACC GTG---- ACTG
0 TTCAGTGACCACTAGCCATA TCAAG TCC TGTACT GC CA TTCAGT ACTAGCCATAT GCT

TGTGGCTACTGAGCACTTGA AGTTT AGG ACATGA CG GT GAGTCA TGATCGGTGTA CGA

AATGTGGCTAGTTTGAACTG T TC ATCT T A AGTT AAGTTCA ----
AGATGTGCTCTAAGTACACT
GGATTTTGA
GAM33677 10827 GTCCTGTACTGCTCAATTCA -- ---- T A GACC GTG---- ACTG
1 GTGACCACTAGCCATATGTG GTCC TGTACT GC CA TTCAGT ACTAGCCATAT GCT
GCTACTGAGCACTTGAAATG TAGG ACATGA CG GT GAGTCA TGATCGGTGTA CGA
TGGCTAGTTTGAACTGAGAT TC ATCT T A AGTT AAGTTCA ----
GTGCTCTAAGTACACTGGAT
GAM33677 10569 GGAGAATCATTTGAGCCCAG AA GA-- AAGCA GT A CAAGATCAC
2 GAAGCAGAGGTTGCAGTGAG GGAG TCATTT GCCCAGG GAG TGCAGTG GC
CCAAGATCACGCCACTGCAC CCTC AGTGAG CGGGTCC CTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGT AG ACAA GAC-- -- - ---------
GAGACTCC
GAM33677 10807 GTAGAGGGTATGCCTGGGAA GG T ---- CAGG AGCT
3 AACAGGAGTCACAGAAGCTT GTAGA GTA GCCT GGGAAAA AGTCACAGA
CTGTGACTGTATTTTCCCAA TATTT TAT TGGA CCCTTTT TCAGTGTCT
AGAGGTTTATTATTTAT AT T GAAA ATG- ----
GAM33677 10857 GTGGCATAGGGTGGGCCTTT G AGGGTG AA A A G CA AGAGGTGGAGAAA

5 AATCCAATGTGACTGGTGTC GTG CAT GGCCTTT TCC ATGTG CTG TGTC TATA
CATATAAGAGGTGGAGAAAT CAC GTA CCGGAAG AGG TACAC GAC ACAG ATGT
GTAGAGACACAGACACATGG G GTGTA- -- G A - AG ----------
GAGAAGGCCATGTGATGGCA
C
GAM33677 10923 TAGTGTTCAAGACCTACACT --- CTACAC CCTCCTTTA AGTG TGACACTT

6 CCATCCTCCTTTAATTTGCC TAGTGTTCA AGAC TCCAT ATTTGCCC GCC
CAGTGGCCTGACACTTGGCA ATTACAAGT TTTG AGGTA TGAACGGG CGG
GGGCAAGTGCTGTCATATGG GCA TCTAGA TACTGTCG- A--- --------
AAGATCTGTTTACGTGAACA
TTA
GAM33677 9809 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
7 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33677 10958 TCATACTGTAATGTTAGTTT A TA TT GAAA GG AGTG
8 GCATGAAAAGCTCTGTGGTG TC TACTG ATGTTAGT GCAT AGCTCTGT TGC
CAGTGGCAAACAGGGCTAAG AG GTGAC TGTAGTCG TGTA TCGGGACA ACG
GATGTTTGCTGATGTCGCAG - GC TT GGAA A- ----
TGGA

GAM33678 9613 AAGGAGGGAAGTTTAAATTT A G AATT T GCCTT - GT- GATACTA
0 TGTAATATGGCCTTGGTTGC AAGG GGGAA TTTA TTGTAA ATG GGTTGC AGAA CCT
AGAAGTCCTGATACTAAGGT TTCC CCCTT AGAT GACATT TAT CCAACG TCTT GGA
AATTCTAGCAACCTTAATAT - - ---- T AATT- A AAT -------
TTTACAGTAGATTCCCCCTT
GAM33678 9695 AGCCTGGGTCACTGTATGGT CCT T GG---- G G TC CACGAGA
1 ACCAGTGTCAGCTTCCTGTG AG GGGTCAC GTAT TACCAGT TCA CT CTGTGTTA
TTACACGAGATGGCACAGTT TC CCCAGTG TATG GTGGTCG AGT GG GACACGGT
GGGTGAAGCTGGTGATGAAG TC- - GAAGTA A G TT -------
GTATGTGACCCCTCT
GAM33678 10766 GGGTCACTGTATGGTACCAG T GG---- G G TC CACGAGA
2 TGTCAGCTTCCTGTGTTACA GGGTCAC GTAT TACCAGT TCA CT CTGTGTTA
CGAGATGGCACAGTTGGGTG CCCAGTG TATG GTGGTCG AGT GG GACACGGT
AAGCTGGTGATGAAGGTATG - GAAGTA A G TT -------
TGACCC
GAM33678 10232 GAACATCCAGGTCTGGGGCA ---- CTGG A - TG T ATTT - CGTTA
3 TGAACCTGGCATACAATGTA GAACA TCCAGGT GGC TGAA CC GCA ACAATGTAG CTGT GTT

GATTTCTGTGTTCGTTAGGC CTTGT AGGTCCA TCG ACTT GG CGT TGTTACATC GACA CGG

AACAGCTACATTGTCTGCTG ACAA ---- G T GT C ---- A -----
GGTTTCAGGCTACCTGGAAA
CATGTTC
GAM33678 10966 TCCAGGTCTGGGGCATGAAC CTGG A - TG T ATTT - CGTTA
4 CTGGCATACAATGTAGATTT TCCAGGT GGC TGAA CC GCA ACAATGTAG CTGT GTT
CTGTGTTCGTTAGGCAACAG AGGTCCA TCG ACTT GG CGT TGTTACATC GACA CGG
CTACATTGTCTGCTGGGTTT ---- G T GT C ---- A -----
CAGGCTACCTGGA
GAM33678 11210 TGTCTATAGAGTATGTGGGC AGAGTA T TT- TG C- A TT T CTCTCTCT
5 CATTTTCTGCCCGTAAAATG TGTCTAT TG GGGCCA TTC CC GTA AATG CAAA GTTTT
TTCAAATGTTTTCTCTCTCT ACAGATG AC CTTGGT AAG GG TAT TTAC GTTT CGAAA
AAAGCTTTGTTCATTGTATC AGGG-- T TTT GT TC G TT - --------
TGGTGGAATTTTGGTTCTCA
GGGAGTAGACA
GAM33678 9810 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33678 9708 AGGCAAGGTCTCACTCGGTC C C A C TCA --- AA- -- GATC
7 ATCCAGGTTGGAATGCAGTG AGG AAGGT TC CT GG TCCAGG TTGG TGCAGTGG TGT

GTGTGATCACAGTTCACTGT TCC TTCTA AG GA CT GGGTCC AACT ATGTCACT ACA
AAACTCAAACTCCTGGGCTC - - - A C-- TCA CAA TG ----
AAGGAATCTTCCT
GAM33678 10779 GGTATTGGGAGAAAAGTGTG ATT GAA G CTA -- CA TCTT
8 TTATCTAGGTAGTCCAGGAA GGT GGGA AAGTGT TTAT GGTA GTC GGAAGG
GGTCTTCCTTTCATGACAAT TCA CCCT TTCACA GATA CCAT CAG CTTTCC
ACCCATAGACACTTAGTCCC GTT GA- - C-- AA TA ----
TTGACT

GAM33678 10380 GAGGCCAGGAGTCTGAGATC -- T GA- GCTTG ACT TTTAT T TTGT
9 AGCTTGGGCAACTGATTTAT GAGGCC AGGAG CT GATCA GGCA GA GGT TGGAT
GGTTTGGATTTGTGTCCATG CTCCGG TCCTT GA TTAGT CCGT CT CCG ACCTG
CCCTTCCTCTTCTGCCATGA AG T ATA A---- CTT CCTTC T ----
TTATAAGTTTCCTGAGGCCT
C
GAM33679 10075 CCTTGGGGGCTTAATGATTC TT TTAATG CGT G --- TG T GGACAGAAAA
0 AGCGTGGAATGAGTTTTGTT CC GGGGGC ATTCAG GGAAT AGT TTTGT T AGGGT
GTTAGGGTGGACAGAAAAAC GG TTCCCG TGAGTC CTTTA TCA AAACG A TCCCA
CCTATGGCAAAGTCACTGAT T- TG---- C-- G CTG GT - ----------
TTCCCTGAGTGTGCCCTTTG
G
GAM33679 9720 AGGCCCTGGGTGGCGTGAGG C - - TG GG A TGTGTGTGT - G G AGGAA
2 GGGAAGGTGTGTGTGTGGGG AGGCC TGGGT GGC G AGGG A GG GGGGTG GCA GGAG
AGA
TGGCAGGGAGGAGAAGGAAT TTCGG ACCCG CCG C TTTC T CC TCTTAT CGT TCTC TCT

CTGCTCTGTGCTTATTCTTG C T A GT TT G CCTGT---- T G G -----
TCCCCGTTTCTTTTGCAGCC
TGCCCACGGCTT
GAM33679 11193 TGGGTGGCGTGAGGGGGAAG - - TG GG A TGTGTGTGT - G G AGGAA
3 GTGTGTGTGTGGGGTGGCAG TGGGT GGC G AGGG A GG GGGGTG GCA GGAG AGA

GGAGGAGAAGGAATCTGCTC ACCCG CCG C TTTC T CC TCTTAT CGT TCTC TCT
TGTGCTTATTCTTGTCCCCG T A GT TT G CCTGT---- T G G -----
TTTCTTTTGCAGCCTGCCCA
GAM33679 11196 TGGTGGAAGGAAAACCTGTC T AA A- CC GA- -- ATGACA
4 ATTCCAAGGACAGTCCCATG TGG GG GGA AACCTGTCATT AAG CAGT CCC
ACAGGGAAGCTGACACTTCA ACC CC CCT TTGGACGGTGA TTC GTCG GGG
GTGGCAGGTTAATCCCCCCA - -- AA C- ACA AA ------
GAM33679 11018 TCTGCCAGTTTTTATGCCAC CCAGT A AC- TGCTTC T -- TTA
5 ACTGGCTCTGTGCTTCTAGT TCTG TTTT TGCC ACTGGCTCTG TAG ATCT GCAT
ATCTGCATTTAATGCTTAGA AGAC GAAA ACGG TGATCGAGAC ATC TAGA CGTA
TTCTACCAGAGCTAGTTTGG CTTT- C GTT C----- T TT ---
GCACAAAGTTTCCAGA
GAM33679 9922 ATGTTCTGAAGTACTGAGGG - A ------ - TC TAC GGT
6 TTAGGGCTTCAACTTACGAA ATGTTCTG AAGT CTGAGG GTTA GGGCT AACT GAATTT

TTTGGTGAGTTCACAGTTCA TGCGAGAC TTTA GACTTC CAAT TCCGA TTGA CTTGAG
GCCTGTAACACATTTCTTCA C G TTTACA G C- CA- ---
GGATTTCCAGAGCGT
GAM33679 11242 TTCATTAGGAAAGGGTTTTG AGGAA G GAGG ATGGGTA TGGT GGAG TG T
A
7 AGGTCAGGACATGGGTATCT TTCATT AGG TTTT TCAGGAC TC GTACATG TT G
GGCCTCT
GGTGTACATGGGAGTTTGGT AAGTAG TTT AAGG AGTCCTG GG TATGTGT AG T
TCGGAGG
GGCCTCTATTGTAGGAGGCT GG--- G AGGG GAG---- TTGT AA-- GT - -
TTGGAAATGTGTATTGTTGG TTGTA
GAGGTCCTGAGGGAGGAAGT

```
          TTGGGATGAA
                    -----
GAM33679 11092  TGAGGCAGGAGAATCGCTTG      A    AAT--     AA-  TG  AGGCA   GT  TG    G  GAGATGA

8          AACCTGGGAGGCAGAGGTTG TGAGGC GGAG     CGCTTG   CC  GG     GAG  TG  GTGA CC
           TGGTGAGCCGAGATGAGGTC ACTCTG CCTC     GTGAAC   GG  CC     CTC  AC  TACT GG
           ATTGCACTCCAGCCTGGGCA      -    AAAGT     AAC  GT  GAC--   --  GT    - -------
           ACAAGTGTGAAACTCCGTCT
           CA
GAM33679 10345  GAGGCAGGAGAATCGCTTGA     A    AAT--     AA-  TG  AGGCA   GT  TG    G  GAGATGA

9          ACCTGGGAGGCAGAGGTTGT GAGGC GGAG     CGCTTG   CC  GG     GAG  TG  GTGA CC
           GGTGAGCCGAGATGAGGTCA CTCTG CCTC     GTGAAC   GG  CC     CTC  AC  TACT GG
           TTGCACTCCAGCCTGGGCAA      -    AAAGT     AAC  GT  GAC--   --  GT    - -------
           CAAGTGTGAAACTCCGTCTC
GAM33680 9947   CACTCCCTGAGTGAAGGTGT       - G  AA    G    TT   AAATGTGCTTAC   T     AACAGAG
0          GTGTGTTAGGAAATGTGCTT CACTCCCT GA TG  GGTGT TGTG  AGG          TGGG GAACAC
           ACTGGGTGAACACAACAGAG GTGAGGGA CT AC  CCATA GTAC  TCC          ACCC CTTGTG
           GTGTTCCCCACCTCATGATA       T  G  AC    -    --  ------------   -     -------
           CCCACAGTCTAGGGAGTG
GAM33680 9811   AGTTTTAGGGTACATGTGCA     TTA    A  T TG   -     - G  T   T  ATAT
1          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA     TTA    C  - GT   G     C  G  C   - ----
           CT
GAM33680 10711  GGCTGGGGAAGTTACTTACC       AA-  T   -   -      -  TCTCA   -     -    TAAAA
4          TACTCCGTGTCTCAGTTTTA GGCTGGGG   GT ACT TAC CTACTCC GTG     GTT TTACTT ATCTC

           CTTATCTCTAAAAGGGGTAG CCGACCCT   TA TGG GTG GGTGAGG CAC     CGA AATGAG TGGGG

           AGTAACAGCACTCACTGGAG       CCG  T   T   A      T   TCA--   C     A    -----
           TGGAGTGTGGTTATGCCTCC
           CAGCC
GAM33680 9812   AGTTTTAGGGTACATGTGCA     TTA    A  T TG   -     - G  T   T  ATAT
6          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA     TTA    C  - GT   G     C  G  C   - ----
           CT
GAM33680 10162  CTGCCTAGCTTAGTGAGGGA       C     A   AATCCATTCT  C       AGTCTG
7          ATCCATTCTGGCTTCAGACC CTGCCTAG TTAGTG GGG        GG TTCAGACC
           AGTCTGGGTTTGAAACCTAC GACGGATT AATCAC CCT        CC AAGTTTGG
           ACATCCCACTAACTTAGGCA       C     -   ACACAT----  A       ------
           G
GAM33680 9614   AAGGATGTGTTCACTGAAGC       TGTTCACT    C       CAT   TGAC     TAGTTACAC
9          CTACCATACATATGTGACCC AAGGATG       GAAG CTACCATA   ATG    CCTTAT
           TTATTAGTTACACATAAGGC TTTCTAT       TTTC GGTGGTAT   TAC    GGAATA
           ATTTTTATGGTGGTCTTTGC       TCCCCCG-   T       TTT   ----     ---------
           CCCCTTATCTTT
GAM33681 9742   AGGTTCACACATTGGTGCCT     -    CAT    CCTTT      CAAAAAA--     TT   TGA
0          TTGCTGGGACAAAAAAGAGA AGGT TCACA   TGGTG    GCTGGGA       GAGAC  TCC
```

CTTTCCTGAGGGTTGTCTTG TCCA AGTGT ACCAC CGACTCT TTCTG GGG
TTCCAGTTTCTCAGCCACTC T --- TCAC- TTGACCTTG TT ---
ACCATGTGATACCT
GAM33681 10800 GGTTCACACATTGGTGCCTT - CAT CCTTT CAAAAAA-- TT TGA
1 TGCTGGGACAAAAAAGAGAC GGT TCACA TGGTG GCTGGGA GAGAC TCC
TTTCCTGAGGGTTGTCTTGT CCA AGTGT ACCAC CGACTCT TTCTG GGG
TCCAGTTTCTCAGCCACTCA T --- TCAC- TTGACCTTG TT ---
CCATGTGATACC
GAM33681 10461 GCGCTGTCTTCCTGGGCTCA G C - A TC C GACATTGTAG AGCATC
2 GCATCCTGGGACACAGGACA GC CTGTCTT CTGGG CTC GCA CTGGGACA AG TGG

TTGTAGTGGAGCATCCCAAC TG GGTAGAA GACCC GAG TGT GACTCTGT TC ACC
CTGAAACTTTGTCTCAGTGT G A A A -- T AAAGTCCA-- ------
AGAGACCCAGAAAGATGGGG
T
GAM33681 10436 GCAGCTGCAGAAAACACAGC C AGAAAA CGA GCTAG AAGG
4 CGAGTTGCTAGCTAAGGGGA GCAG TGC CACAGC GTT CT
AACAGACGCCGCTGTGGGAA TGTT ACG GTGTCG CAG GG
AGCACTTGT C AAAGG- CCG ACAAA ----
GAM33681 11063 TGAGGCAGGAAGATCACTTG C AAGA GA-- AGG GC ACC ATTC
5 AGCCCAGGAGGTGGAGGCTG TGAGG AGG TCACTT GCCCAGG TGGAG TGCAGTG CAT

CAGTGACCCATATTCATGCC ACTCT TCC AGTGAG CGGGTCC ACCTC ACGTCAC GTA

ACTGCACTCCAGCCTGGGCA C CAG- ACAA G-- -- C-- ----
ACAGAGTGAGACCCTCTCTC
A
GAM33681 10153 CTGCAATGCTGTTTACTTAT AT- TA- A- - T A TTGTAGT
6 AGGATGAAACTGTATCAGAC CTGCA GCTGTTTACT TAGGATG AAC TGTA CAG CT
TTTGTAGTGGCTGTGCATGT GACGT TGACGGATGA GTCCTAT TTG ACGT GTC GG
TGATATCCTGGCCAGTAGGC GCG CCG AG T - - -------
AGTGCGTGCAG
GAM33681 10428 GCAATGCTGTTTACTTATAG AT- TA- A- - T A TTGTAGT
7 GATGAAACTGTATCAGACTT GCA GCTGTTTACT TAGGATG AAC TGTA CAG CT
TGTAGTGGCTGTGCATGTTG CGT TGACGGATGA GTCCTAT TTG ACGT GTC GG
ATATCCTGGCCAGTAGGCAG GCG CCG AG T - - -------
TGCGTGC
GAM33681 10035 CCCTGGCTGAGGTGGGATCC C ATCCCGAG - C TCCC
8 CGAGGCCTCTCCAGTCCCCT CCCTGG TGAGGTGGG GC CTCTC AG
GAGGGTGCACCACTGGCCCA GGGACC ACTCTACCC CG GGGAG TC
TCTCACCCAGGG C GGTCACCA T - ----
GAM33681 9590 AAAAGCCATGTTACAGATGG GC G ATG TCT CTATT- TCCGG
9 CTCTCCTTGGATGGCTATTC AAAA CAT TTACAG GC CCTTGGATGG CCAGTCGGTT
CAGTCGGTTTCCGGGGCTGA TTTT GTG AGTGTC TG GGGATTTACC GGTCAGTCGG

CTGGCCCACTCCATTTAGGG AT - GA- TGT TCACCC -----
TGTGTAGCTGTGAGTGTATT
TT
GAM33682 11054 TGAGGCAAGGTCAGAAAAGG A- CAGAAAA AA C -- TT AA CTCCCTT
0 TCAGGCAATTTTTGCCTTGT TG GGCAAGGT GGTCAGGC TTTTTG CTTG TTCA GC CA

TCATTGCAACACTCCCTTTG AC TCGTTCCA TCAGTCTG AAGAAT GAAT GAGT CG GT
GAGCTCTGAGTTTAAGCTAA CG ------- -- C TT CT AG -------
GAAGTCTGACTACCTTGCTG
CCA
GAM33682 11064 TGAGGCAGGAAGATCACTTG C AAGA GA-- AGG GC ACC ATTC
1 AGCCCAGGAGGTGGAGGCTG TGAGG AGG TCACTT GCCCAGG TGGAG TGCAGTG CAT

CAGTGACCCATATTCATGCC ACTCT TCC AGTGAG CGGGTCC ACCTC ACGTCAC GTA

ACTGCACTCCAGCCTGGGCA C CAG- ACAA G-- -- C-- ----
ACAGAGTGAGACCCTCTCTC
A
GAM33682 10045 CCGTCACAGCACTTGCCCTC G A A TCAATGTTCAT - ACA- C TTTCTC
2 AATGTTCATCACTGAAGACA CC TCAC GC CTTGCCC CACT GAAG AG ATGTGAT
AGCATGTGATTTTCTCATCA GG AGTG CG GGACGGG GTGA CTTC TC TACACTA
CATCCTCCCACTTCAAGTGG - A - ---------- A ACCC C ------
GGCAGGGCAGTGAGG
GAM33682 9736 AGGGTGTGCACTGGGCAAGG T CTGG G CGG GG - CCGG
3 GCAGGGCGGCAGGTGTCAGG AGGG GTGCA GCAAGG CAGGG CA TGTC AGG
CCGGCTTGGACAATGAAACC TTCC TACGT CGTTCC GTCCC GT ACAG TTC
CTGACCTTGCTGCATTCCTT T ---- A AAA A- G ----
GAM33682 10592 GGAGAATCGCTTGAACCCGG AA GAA-- AGGCA GT AGC AGAT
4 GAGGCAGAGGTTGCAGTGAG GGAG TCGCTT CCCGGG GAG TGCAGTG CG
CCGAGATCGCACTACTGCAC CCTC AGTGAG GGGTCC CTC ACGTCAT GC
TCCAGCCTGGGCAACAGAGT AG ACAAC GAC-- -- CAC ----
GAGACTCC
GAM33682 10268 GAGAATCGCTTGAACCCAGG ATCG-- AA------ AGA AG T GA - AGAT
5 AGACTGAGGTTGCAGTGAGC GAGA CTTG CCCAGG CTG GT GCAGT GC TG
TGAGATCATGCAACTGCACT CTCT GAAC GGGTCC GAC CA CGTCA CG AC
CCAGCCTGGGCAACACAGCA ACTTCA GACACAAC --- CT - A- T ----
AGACTTCATCTC
GAM33682 10504 GCTTGAACCCAGGAGACTGA - AA- AGA AG T GA - AGAT
6 GGTTGCAGTGAGCTGAGATC GCT TG CCCAGG CTG GT GCAGT GC TG
ATGCAACTGCACTCCAGCCT CGA AC GGGTCC GAC CA CGTCA CG AC
GGGCAACACAGC C AAC --- CT - A- T ----
GAM33682 11249 TTCTCTGTCTTCCATTCCCC ------ CC CC - GACTG
7 TCCTACGCCCCCAGACTGTG TTCTCT GTCTTCCATT CCT TACGCCCC CA
AGGGGTGTAAGGAAGATGGA GGGAGG TAGAAGGTAG GGA ATGTGGGG GT
AGATGTTGCGGGAGGG GCGTTG AA -- A -----
GAM33682 11014 TCTCTGTCTTCCATTCCCCT ------ CC CC - GACTG
8 CCTACGCCCCCAGACTGTGA TCTCT GTCTTCCATT CCT TACGCCCC CA
GGGGTGTAAGGAAGATGGAA GGAGG TAGAAGGTAG GGA ATGTGGGG GT
GATGTTGCGGGAGG GCGTTG AA -- A -----
GAM33682 11008 TCTCAACTTCTTTATGTCTC - C TAT G TGT A - ACAGG
9 TGTACAGTGGGTGTAGGGAC TCT CAA TTCTT GTCTCTGTACA TGGG AGGGACC GCC AC

CAGCCACACAGGGTCGGTGG AGA GTT GAGAG TAGAGACGTGT GCCC TTTTTGG TGG TG

GTTTTTCTCCCCGTGTGCAG T A --- - CTC G C -----
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GAM33683 10030 CCCTCAGCACAGGTTTTGGC A -- CTCTT T AAAA
0 TCTTAGAATGGGTTTTTTAA CCCTCAGC CAGG TTTTGG AGAA GGGTTTTTT
AAAAAGGATCTTTCTTAATT GGGGGTTG GTCC AGGACC TCTT TCTAGGAAA
CCAGGACTCCTGAGTTGGGG A TC TTAAT - ----
G
GAM33683 9927 ATTTCCTGCTGCCAGCTTAA - G T TA - CA GCAGATTCACA
2 TACTCACCAGGGCAGATTCA ATTTCCTG CTGCCA CT AA CTCA C GG
CACCAAGTTGGGGTTTCAGT TGAAGGAC GACGGT GA TT GGGT G CC
GGCAGTCAGGAAGT T - C TG T AA ----------
GAM33683 10300 GAGATGGCAATTTAAACTGC GA -- AAA - T C - ---- - AAGAA- -- A
3 TTTGATGACCAGGTTTCATT GA TGGCA ATTT CTG CTTTGA GA CAG GTT TCATT AGGT
GGCC CG
AGGTAAGAAGGCCCGATTAA TT ACCGT TGAA GAC GAAACT TT GTC CAG GGTGA TCCA
CCGG GC
GCAACGGTGGCCCAAATAAC AA TC GAC C T T A ACTT C ATAAAC TG -
CTCAGTGGTTCAGACACTGT TTAAGCAA
TTTTCAAAGCCAGCAGAAGT
CTTGCCAAATT

GAM33683 10514 GCTTTGATGACCAGGTTTCA T C - ---- - AAGAA- -- ATTAAGCAA
4 TTAGGTAAGAAGGCCCGATT GCTTTGA GA CAG GTT TCATT AGGT GGCC CG
AAGCAACGGTGGCCCAAATA CGAAACT TT GTC CAG GGTGA TCCA CCGG GC
ACCTCAGTGGTTCAGACACT T T A ACTT C ATAAAC TG ---------
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GAM33683 11065 TGAGGCAGGAAGATCACTTG C AAGA GA-- AGG GC ACC ATTC
5 AGCCCAGGAGGTGGAGGCTG TGAGG AGG TCACTT GCCCAGG TGGAG TGCAGTG CAT

CAGTGACCCATATTCATGCC ACTCT TCC AGTGAG CGGGTCC ACCTC ACGTCAC GTA

ACTGCACTCCAGCCTGGGCA C CAG- ACAA G-- -- C-- ----
ACAGAGTGAGACCCTCTCTC
A
GAM33683 11028 TCTTTTTCTCAGTGTCTCTG T TC T TG CA A AT AGACT
6 TTGTGGCAGTCATGAATGAG TCT TT TCAG GTCTCTGT TGG GTC TGA G
ACTCTGTCAGATCTCCATGG AGA AG AGTC CAGGGACG ACC TAG ACT C
CAGGGACCTGATTGACAGA C TT - GT TC - GT -----
GAM33683 10259 GACCATGAAGCCAGAGTCTC CCAT - - T CCA ---- - GCCATGGA
7 CAGGACTCCTCACTCAACCT GA GAAG CC AGAG CT GGACTCCT CACTCAACCT CG
CGGCCATGGACGCAGGTTGG CT CTTC GG TTTC GA CCTGGGGG GTGGGTTGGA GC

GTGTGAGGGGGGTCCCAGCC TTAT T C C C-- GAGT C --------
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GAM33683 10442 GCAGGTATGATGGCCTTTTC TGAT C A T TCCT AGCTGA
8 TCTTATCCTGGTTCCTGCAG GCAGGTA GG CTTTTCTCTT TCC GGT GCAG
AGCTGACTGCCATGCTTGGG TGTCCGT TC GAAAAGGGAG GGG TCG CGTC
AGAGGGAAAAGACTTATTTG TTAT A A T TAC- ------
CCTGT
GAM33684 10640 GGAGAATTGCTTGAACCTGG AA GAACCTGG CA T- A - AGAT
0 GAGGCAGTGGTTGCAGTGAG GGAG TTGCTT GAGG GTGG TGCAGTG GC CG
CCGAGATTGTGCCACTGCAC CCTC AACGAG CTCC CACC ACGTCAC CG GT

TCCACCCTCAGCAACAGAGC AA ACAACGA- -- TC - T ----
AAAACTCC
GAM33684 11086 TGAGGCAGGAGAATCGCTTG GAGAA GAAC-- AGG GT A - AGAT
1 AACCCCGGGAGGTGGAGGTT TGAGGCAG TCGCTT CCCGGG TGGAG TGCAGTG GC CG

GCAGTGAGCCGAGATCGCGC ACTCTGTC AGTGAG GGGTCC ACCTC ACGTTAC CG GC

CATTGCACTCCAGCCTGGGC ACAA- AACAAC G-- -- - C ----
AACAAGAGTGAAACACTGTC
TCA
GAM33684 10864 GTGGTGCATACCTGTAATCT G C---- AT A GGA G TG AGG
2 CAGATACTTGGGAGGTTGAG GTGGT CATA CTGTA CTCAGAT CTTG GGTT AGG GT
GTGGTAGGATTGCTTGAGCT CACTA GTAT GACGT GAGTTTG GGAC TCGA TTC TA
CAGGAGTTTGAGGCTGCAGT - CGAAT CG A --- G GT ---
AAGCTATGATCAC
GAM33684 9970 CAGGCTGGTTCGTCGTTTCT G C CTG C- T TT- TCTTTGT
4 GCCTCTCCATTCTTGTCTTT CAGGCT GTTCGT GTTT CCTCTC ATTCT GTCTT TAAT
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AGATGGAGTTTGAGAGGGAA A - --- TT - TTT -------
TATGAACAAGCCTG
GAM33684 9728 AGGCTGGTTCGTCGTTTCTG G C CTG C- T TT- TCTTTGT
5 CCTCTCCATTCTTGTCTTTT AGGCT GTTCGT GTTT CCTCTC ATTCT GTCTT TAAT
TAATTCTTTGTGTTATTTGA TCCGA CAAGTA TAAG GGAGAG TGAGG TAGAG ATTG
GATGGAGTTTGAGAGGGAAT A - --- TT - TTT -------
ATGAACAAGCCT
GAM33684 10746 GGGCATTTTGCCTCTGGTAG CAT- T -- - - G TG CCA TCCT
6 GGATGGCCATGGTGCCAGCC GGG TT GCC TCTG GTAGG GATG CCA GTG GCCC
CTCCTGGGCCTCATTGGGTA CCC AA CGG AGAC TATCC CTAT GGT TAC CGGG
TCACCTATACAGAAAGGCCA AGAT C AA A A G -- TC- ----
ATAGACCC
GAM33684 9813 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
7 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33684 10918 TAGGGGCAGTGGCAGAGAAT G ---------- CAGAGAATGAA - TT C- G TATAA
8 GAATGTATGTGTGGGTTTCT TAGG GC AGTGG TGTATGT GTGGGT CT AGCCTT AGG

CAGCCTTGAGGTATAAGGTC ATCC CG TCACC ACATACG CACTTA GG TCGGAA TCT
TAAAGGCTCTGGGGATTCAC G AACTTGACCT ---------- T GG TC A -----
TGCATACACCACTTCCAGTT GG
CAAGCGCCTA

--
GAM33684 10745 GGGCAGTGGCAGAGAATGAA C CAGAGAATGAA - TT C- G TATAAGG
9 TGTATGTGTGGGTTTCTCAG GGG AGTGG TGTATGT GTGGGT CT AGCCTT AGG
CCTTGAGGTATAAGGTCTAA CCT TCACC ACATACG CACTTA GG TCGGAA TCT
AGGCTCTGGGGATTCACTGC - ---------- T GG TC A -------
ATACACCACTTCC
GAM33685 11066 TGAGGCAGGAAGATCACTTG C AAGA GA-- AGG GC ACC ATTC

2 AGCCCAGGAGGTGGAGGCTG TGAGG AGG TCACTT GCCCAGG TGGAG TGCAGTG CAT

CAGTGACCCATATTCATGCC ACTCT TCC AGTGAG CGGGTCC ACCTC ACGTCAC GTA

ACTGCACTCCAGCCTGGGCA C CAG- ACAA G-- -- C-- ----
ACAGAGTGAGACCCTCTCTC
A

GAM33685 9943 CACGAGCAGTTTGTGTCACA C C T ------- - - C ACTCTTT GTTA
3 GATGGCCGGAAGAGACTCTT CA GAG AGTT GTG TCA CAG ATGGC GGAAGAG TGCCTG

TTGCCTGGTTACAGGCATGT GT TTC TCAA TAC AGT GTC TACCG TCTTTTT ACGGAC
TTTTCTGCCATCCTGTTGAA - C C CCTTTTA T C - GT----- ----
TTTTCCCATCAACTCCTTTG

GAM33685 10272 GAGAATTGCTTAAACCCGGG AA TG AAA-- AGG GT A CAAGATCAC
4 AGGTGGAGGTTGCAGTGAGC GAG T CTT CCCGGG TGGAG TGCAGTG GC
CAAGATCACGCCACTGCACT CTC A GAG GGGTCC ACCTC ACGTCAC CG
CCAGCCTGGGCAACAGAGTG AG GT ACAAC G-- -- - ---------
AGACTC

GAM33685 10430 GCACCAGAAAGTCCAGGAAG - AAGTCC A A ------ TTA- GG A ATGGT
5 AGCTGATTAAAGTGTTAGCT GCAC CAGA AGG AG GCTG ATTAAAGTG GCT CTG CACATT

GGCTGACACATTATGGTGGT CGTG GTCT TCC TC TGAC TAATTTTAC TGA GAT GTGTGG

GTGGTAGAAAGTGTCTCATT T AA---- G G ACTGAA TCTG AA G -----
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CTAATCTGTGTGC

GAM33685 11020 TCTGTCTCTCTCTCATCTTC T CTCTCATC TT- CAC-- GAA T G TGAT
7 CTTTTGCCACCCAGGCTGGA TCTG CTCT TTCCT TGC CCAGGCTG TG AGT GTG
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CTCACTACAGCCTGGATTCA T CT------ CAC ACTTA ATC - A ----
GCACACAGGAATCAGAGTCA
GA

GAM33686 9814 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT

GAM33686 10091 CGGGTGAGGAAGTGTTATTG G A- T T G GG CAGAA TTGG
1 TCAGGGTCTCCCTTTCAGAA CG GTG GGAAG GT ATT TCAG TCTCCCTTT GGCC
GGCCTTGGGGCCAAGGGGAG GT CGC CCTTC CG TAA GGTC GGAGGGGAA CCGG

GAGCTGGAATTGCCTTCCAC G CA - T - GA ----- ----
CGCGTG

GAM33686 10788 GGTGAGGAAGTGTTATTGTC GA T T G GG CAGAA TTGG
2 AGGGTCTCCCTTTCAGAAGG GGT GGAAG GT ATT TCAG TCTCCCTTT GGCC
CCTTGGGGCCAAGGGGAGGA CCA CCTTC CG TAA GGTC GGAGGGGAA CCGG
GCTGGAATTGCCTTCCACC -- - T - GA ----- ----

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3 GGTGGAGGTTGCAGTGAGCC AG TC CTT ACCTGGG TGGAG TGCAGTG GC CG
GAAATTGTGCCACTGCACTC TC AG GAG TGGATCT ACCTC ACGTCAC CG GT

CAGTCTAGGTGACAGAGCGA AG C ACAG G-- -- - T ----
GACT
GAM33686 10702 GGCGTGAGGGAAAGCATGAA --- ---- GAAAAA GATAAAAT C AAAC
4 AAATCCAGGATAAAATCATC GGCGTGA GGGA AAGCAT TCCAG CATCAT AGGG
ATCAGGGAAACTCCTATGAT CCGTACT CCCT TTTGTG AGGTC GTAGTA TCCT
GCTGGAACTGGACAACAGTG GAT AGAT ACAAC- AAGGTC-- - ----
TTTTAGATCCCTAGTCATGC
C
GAM33686 10815 GTCAGCACCGAGGTAGCAGA A--- TA ---- AC CAG GAGAA
6 GAATTAACATTCTTGTCAGC GTCAGC CCGAGG GCAGAG AATTA ATTCTTGT CA
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AATAGCTGAT
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7 CCGTGCCAACAGGAAACCCC GGGGAC AAC TAGG TGG GTGCCA CAGG GGAA TGGCT

AGGAAGTCTGGCTTCAGAGC CTTCTG TTG GTTC GTC CACGGT GTCT CCTT ACCGA
CATTCCCTTTAGCTCTGATG AC AT T A- A CGATTTC- --- ----
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GTCTTC
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8 GAGGTGGAGGTTGTGGTGAG GGAG TCGCTT CCCAGG TGGAG TG GTG GC
CCAAGATCGTGACATTGCAC CCTT AGCGAG GGGTCC ACCTC AC TAC TG
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- GT AG -------
GAGATTCC
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9 GAGGTTGCAGTGAGCTGAGG TCACTT CCCGGG GGAG TGCAGTG GC TG
TCGTGCCACTGCACTCCAGC AGTGAG GGGTCC CCTC ACGTCAC CG GC
CTGGGCAACAAGAGTGA AACAAC GA-- -- - T ----
GAM33687 10575 GGAGAATCGCTTGAACCCAG AA GA-- AGGC GT A- TGAGATT
0 GAGGCGGAGGTTGCAGTGAG GGAG TCGCTT ACCCAGG GGAG TGCAGTG GC
CTGAGATTGCACTATTGCAC CCTC AGTGAG TGGGTCT CCTC ACGTTAT CG
TCCAGTCTGGGTGACAGAGT AG ACAG GA-- -- CA -------
GAGACTCC
GAM33687 11173 TGGCTCACACCTGTAATCCC AC CCC A AGGA CAGGAGAATCA
1 CGCTACTCAGGAGGTTTAGG TGGCTCAC CTGTAATC GCT CTC GGTTTAGG
CAGGAGAATCACTTGAACCC ACTGAGTG GACATTGG CGG GAG CCAAGTTC
GAGAGGCAGAGGTTACAGTA AT AGA A C--- ----------
GTGAGTCA
GAM33687 10798 GGTGGTTATGGTGATGTGCA T G - G C T GCTTTGG
2 CCTGTAGTCTCATCTGCTTT GGTGGT ATGGT AT GT CAC TGTAGTCTCA CT
GGAGTTGAGGCTGCAGTGAA TCACCG TGCTA TA CA GTG ACGTCGGAGT GA
CTATGATCGTGCCACT - G T A - T -------
GAM33687 11279 TTGGGCTACTTATAGGAGTG ACTTATA- T -- AC- AT- CCAG
3 AAAATAAACTCTGTGATGTG TTGGGCT GGAG GAAA ATAA TCTGTG GTG
CCAGCACCAGCACAGGCTCT GACTCGG CCTC CTTT TGTT GGACAC CAC
TGTAGTTTCCTCCCAACTTT GTTTCAAC - GA CTC GAC ----
GGGCTCAG
GAM33687 10713 GGCTTCCCCAGTCATATATT CC - T A- AAA CAAAG CCCA
4 CTCAGATTCAAAGGAACAAA GGCTTCC AGTCAT ATATTC CAG TTC GGAA TGGC

GTGGCCCCAGTCAGCCTTTC CCGAAGG TCGGTG TGTGAG GTC AAG CCTT ACTG
CCAGAAACCTGTGAGTGTGG -- G T CA AC- TCCG- ----
TGGCTGGAAGCC
GAM33687 10483 GCTCTTCCCATACCATGCAT TCCCATACCA TCCT CAC AAA - CTGG T T
GATTG
5 TCCTAGCCCCACAGAAATCC GCTCT TGCAT AGCCC AG TC CACTAGT GCT TCTC GC

ACTAGTCTGGGCTTTCTCTG CGAGG ACGTG TCGGG TC GG GTGGTCA CGA GGAG CG

CGATTGGCTGAGGCAGCAAC ---------- ---- --- CAC A A--- C T -----
TGGTGAGGCACCTGGGCTGT
GCAGGAGC
GAM33687 9929 CAAATCAGTGGCATATTAGA A GT C - AT - GTGTTGTGA ATGCGA
6 TTCTCATAGGAATGTGAACC CA ATCA GG ATATTAGATTCTCAT AGGA GTG AACC CC
GTGTTGTGACCATGCGAGGG GT TAGT TC TATAATCTAAGAGTA TTCT TAC TTGG GG
ATCTAGGTTGCATGCTCTTC C AG - C CG G ATCTAG--- ------
ATGAGAATCTAATATCTGAT
GATCTG
GAM33687 9900 ATCAGTGGCATATTAGATTC TGGC - AT - GTGTTGTGA ATGCGA
7 TCATAGGAATGTGAACCGTG ATCAG ATATTAGATTCTCAT AGGA GTG AACC CC
TTGTGACCATGCGAGGGATC TAGTC TATAATCTAAGAGTA TTCT TAC TTGG GG
TAGGTTGCATGCTCTTCATG ---- C CG G ATCTAG--- ------
AGAATCTAATATCTGAT
GAM33687 10916 TAGGAGGGAGGATTGCTTGA - A- GA-- TC AGTT AG TAC GCTTTGATCACA

8 GTCCAGGAGTTGAAGGCTAC TAGGAGG GAGG TTGCTT G CAGG GA GC AGTGA
AGTGAGCTTTGATCACATCA ATTCTCT CTCC AACGAA C GTCC CT CG TCACT
CTGCACTCTAGCCTGAGCAA A AG ACAA GA GAT- CA --- ----------
CAAAGCAAGACCTCATCTCT
TA
GAM33687 10993 TCGCTCTTTGTTGCCCAGGC CTT TT C-- -- - A ATCT
9 TAGAGTGCAGTGGCATGATC TCGCT TG GCCCAGG TAGAG TGCAGTG GC TG
TCGGCTCACTGCAACCTCTG AGCGA AC TGGGTCC GTCTC ACGTCAC CG GC
CCTCCTGGGTTCAAGCGA --- T- TCC CA T - ----
GAM33688 10327 GAGGCAGGAGAATAACTTGA A AATAA AA- AGAC GT T A - AGAT
0 ACCCAGGAGACGGAGGTTGT GAGGC GGAG CTTG CCCAGG GGAG TGT GTG GC CG

TGTGAGCCGAGATCGCGCCA CTCTG CCTC GAGC GGGTCC CCTC ACG TAC CG GC
TTGCACTCCAGCCTGGGCAA - AAAGC AAC GA-- -- T - C ----
CGAGCGAAACTCCGTCTC
GAM33688 10832 GTCTCTCAGAGGTAGAGTGT AGA - AT TGTCA TAA- TTCT
2 GTCTATGGAAGGGGTTGTCA GTCTCTC GGTA GAGTGTGTCT GGAAGGGGT TGG CAGC

TGGTAACAGCTTCTGTTGGC TAGGGAG TCGT CTTACACAGG TCTTTTCCA ATC GTTG

TTCTAGCCCTACCTTTTCTG A-- A -- TCCCG TTCG ----
GACACATTCATGCTAGAGGG
AT
GAM33688 9958 CAGATAACCAGACACACCCC TAA ACAC - CT A TT TATTT
3 TGGGCTGGGCACACAGTTCC CAGA CCAG ACC CCTGGG GGGC CACAG CCT

TTATTTGGGTTTTGTGGTTT GTCT GGTC TGG GGACCC TTTG GTGTT GGG
TCCCAGGTGGTAGCTGGGAC CAG GA-- T T- - TT -----
TCTG
GAM33688 10316 GAGGCAAGAGAATTGCTTGA AG AA GA-- A- CGAA T A TGAGATGGT
6 GCCCGGGAGGCGAAGGTTGC GAGGCA AG TTGCTT GCCCGGG GG GGT GCAGTG GC

AGTGAGCTGAGATGGTGCCA CTCTGT TC AACGAG CGGGTCC CC TCA CGTCAC CG
CTGCACTCCAGCCTGGGCAA G- AG ACAA GA ---- - - ---------
CAGAGCAAGACTGTGTCTC
GAM33688 10374 GAGGCAGGAGACTCGCTTGA GAGA C GAA-- AGGC GT GA AGATGG
7 ACCCAGGAGGCGGAGGTTGC GAGGCAG CTCG TT CCCAGG GGAG TGCAGT GGTG

AGTGAGGTGAGATGGCGCTA CTCTGTC GAGT AG GGGTCC CCTC ACGTCA TCGC
CTGCACTCCAGCCTGGGCAA A--- T ACAAC GA-- -- -- ------
CAGATTGAGACTGTCTC
GAM33688 10395 GAGGTAAAGCTGGGGCTGGG ---- TG GG TG T GC GCTG
8 GTTCCTTATGCAAAGAGAGC GAGGTAA AGC G C GGGTTCCT AT AAAGAGA
TGTCTCTTTAGTAGGAACTC TTTCGTT TCG T G CTCAAGGA TG TTTCTCT
TGGATTGGCTCATTTTGCTT TTAC GT A- GT - A- ----
T
GAM33688 9916 ATGCTCAAGTATACTGATGT C AA A CAGAA AT GACCAGAG
9 CACCAGGCAGAATTCAGATA ATG TC GTAT CTGATGTCACCAGG TTCAGATA GGT
ATGGTGACCAGAGATCCTGT TAC AG CATA GATTACAGTGGTCC GAGTCTGT CTA
CTGAGCAACCTGGTGACATT - AC - AAC-- C- --------
AGATACCAGACAT
GAM33689 11038 TGAGAAGTCAGTCCTGATGG AGAA - CT- T G G AGT- AG GCCAA
2 CAGCTGTGCAGAGTGGGGGT TG GTCA GTC GA GGCA CTGT CAG GGGGGTG GAG

GAGGAGGCCAACTTACTGCT AC CGGT CAG CT CCGT GACG GTC CCTTCGT TTC
TCCTGAACTGGGCAGTGCCT ---- A TAT T - G AAGT CA -----
TCTATGACATGGCCA
GAM33689 10817 GTCAGTCCTGATGGCAGCTG - CT- T G G AGT- AG GCCAA
3 TGCAGAGTGGGGGTGAGGAG GTCA GTC GA GGCA CTGT CAG GGGGGTG GAG
GCCAACTTACTGCTTCCTGA CGGT CAG CT CCGT GACG GTC CCTTCGT TTC
ACTGGGCAGTGCCTTCTATG A TAT T - G AAGT CA -----
ACATGGC
GAM33689 9635 ACATATGGCAGAATGGAAGT TAT AT GTGATT CT AT- TTTT
4 GATTTCTCCTAATGAAAATG ACA GGCAGA GGAA TCTC AATGAAA GAAGTGCTC
AAGTGCTCTTTTGAGTATTT TGT CCGTCT CCTT AGAG TTATTTT CTTTATGAG
CTTGTTTTATTGAGATTCCT TC- AT ------ -- GTT ----
ATCTGCCCTTGT
GAM33689 10672 GGCAGAATGGAAGTGATTTC AT GTGATT CT AT- TTTT
5 TCCTAATGAAAATGAAGTGC GGCAGA GGAA TCTC AATGAAA GAAGTGCTC
TCTTTTGAGTATTTCTTGTT CCGTCT CCTT AGAG TTATTTT CTTTATGAG
TTATTGAGATTCCTATCTGC AT ------ -- GTT ----
C
GAM33689 9691 AGCAGGATTAGGAAGAGAAG GATT AA-- T - G A TG GTTTTG
6 CATTGTGAGAAACAGGTTTT AGCAG AGGAAGAG GCA TG TGA AA CAGGTTT G
GGGTTTTGCTGAAATTTGCT TTGTC TCCTTTTC CGT AC ACT TT GTTTAAA C
TGTCAGCATTGCATCACTTT AAT- ACTA T G G C GT ------

TCCTTAACTGTT
GAM33689 10462 GCGGGCTAGGCAGTCTCAGT GCTAGGCA TCA- GGT- TTAGT
7 TGTTGGGTTTTCTTAGTGAA GCGG GTC GTTGTTG TTTC
ATAAGCAGCAACAAACGACA CGCC CAG CAACGAC AAAG
ACAAAACCGC AAAACAA- CAAA GAAT -----
GAM33689 10598 GGAGAATCGCTTGAACCCTG AA GAA---- --- - A T GAGCCAAG
8 GAGGCAGAGGTTGCGGTGAG GGAG TCGCTT CC CTGGAG GCAG GGT GCGGT
CCAAGATCGTGCCATTGCAC CCTC AGTGAG GG GACCTC CGTT CCG TGCTA
TCCAGCCTGGGCAACAAGAG AA AACAACG TCC A A - --------
TGAAACTCC
GAM33690 9815 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33690 11047 TGAGACGGAGTTTCGCTCTT A - TT CTC TCC CTTTAGTGCAA C TCTC
CACCGC
3 GTCCCCCAGGCTTTAGTGCA TGAG C GGAG TCG TTG CCCAGG TGGCG GA GGCT
ATGGCGCGATCTCGGCTCAC ACTC G CCTC AGC AAC GGGTCC ACCGC CT CCGA
CGCAGCCTCCGCCACCTGGG C T TT A-- TT- ---------- - ---- ------
TTCAAACGATTCTCCTGCCT
CA
GAM33690 11077 TGAGGCAGGAGAATCACTTG CA AA GAA--- AGG CT A - AGAT
6 AACCCGGGAGGTGGAGCTTG TGAGG GGAG TCACTT CCCGGG TGGAG TGCGGTG GC CG

CGGTGAGCCGAGATCGCGCC ACTCT CCTC AGTGAG GGGTCC ACCTC ACGTTAC CG GC

ATTGCACTCCAGCCTGGGCA A- AA AACAAC G-- -- - C ----
ACAAGAGTGAAACTCCATCT
CA
GAM33690 10558 GGAGAATCACTTGAACCCGG AA GAA--- AGG CT A - AGAT
7 GAGGTGGAGCTTGCGGTGAG GGAG TCACTT CCCGGG TGGAG TGCGGTG GC CG

CCGAGATCGCGCCATTGCAC CCTC AGTGAG GGGTCC ACCTC ACGTTAC CG GC
TCCAGCCTGGGCAACAAGAG AA AACAAC G-- -- - C ----
TGAAACTCC
GAM33690 9816 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33690 10660 GGAGGTGGGATGTGTGTGCT G - GT- - CAT
9 ACTGGCATCTAGTGGCTGCT G AG GTGGGATGT GT GCTACTGG
AAACATCCTACACTGC C TC CATCCTACA CG CGGTGATC
G A AAT T ---
GAM33691 10875 GTGTTAGAGACCAGTTAAAG AGAGA TAAAGTT- AAA GTATAT
1 TTAAGACACTTTCTAAATAG GTGTT CCAGT AAGACACTTTCT TAGAAGTCTT
AAGTCTTGTATATGGGGCTT CACAA GGTCG TTTTGTGAAAGA GTTTTCGGGG
TTGAGAAAGTGTTTTCCCGT AGGGG TAGTGCCC --- ------
GATGCTGGGGGGAAACAC

GAM33691 9642 ACCTCATCTCTACAAAAAAT - A AAATACGAAAAT TGT--- GCATG
3 ACGAAAATTAGCTGGGTGTG ACCTCA TCTCT CAAA TAGCTGGG GGTG
GTGGCATGTACCTGTAGTCC TGGAGT AGAGA GTTT ATCGACCC CCAT
CAGCTATTTGAGAGACTGAG C - ---------- TGATGT -----
GT
GAM33691 10055 CCTCATCTCTACAAAAAATA - A AAATACGAAAAT TGT--- GCATG
4 CGAAAATTAGCTGGGTGTGG CCTCA TCTCT CAAA TAGCTGGG GGTG
TGGCATGTACCTGTAGTCCC GGAGT AGAGA GTTT ATCGACCC CCAT
AGCTATTTGAGAGACTGAGG C - ---------- TGATGT -----
GAM33691 10247 GAATAGCGAGTTGCCCAAGC A G- ----- AAAGTATGT T
TTCAAACCCAGGCC
6 TCACAAAGTATGTGATGGAG GAATAGCG GTT CCCA AGCTCAC GA GGAGCTAGAGA

CTAGAGATTCAAACCCAGGC TTTATCGT TAA GGGT TCGGGTG CT CCTCGGTCTCT
CTCTCTGGCTCCTTCTTTGG A AA CTCGT GGGTTT--- T ----------
GGTGGGCTTGCTCTGGGAAA
ATATGCTATTT
GAM33691 10078 CCTTTGCTTTGGCCTTTAAC - TTG TTAACAA TGTT C-- AG TTGAG
7 AACTCAGTGTTTTGGTCTAA CCTTT GCT GCCT CTCAG TTGGTCTAAT TTCAAG GAAT
TCTTCAAGAGGAATTTGAGG GGAGA CGA TGGG GAGTT GATCAGATTG AAGTTC CTTG

TTCACTTGAATAAGTTAGAC T TG- TG----- T--- AAT A- -----
TAGTTTGAGGTGGGTGTAGC
TAGAGG
GAM33691 10515 GCTTTGGCCTTTAACAACTC TG - ACA-- GTGTT-- C-- AG TTGAG
8 AGTGTTTTGGTCTAATCTTC GCTT G CCTTTA ACTCA TTGGTCTAAT TTCAAG GAAT
AAGAGGAATTTGAGGTTCAC TGAA T GGAGAT TGGGT GATCAGATTG AAGTTC CTTG
TTGAATAAGTTAGACTAGTT GT A CGATG GGAGTTT AAT A- -----
TGAGGTGGGTGTAGCTAGAG
GATTGAAGT
GAM33691 9817 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33692 11192 TGGGTGCCTGTAATCCCAGC GC- - G A AGG TG GCAGGAGAATCA
0 TACTTGGGAGGTTGAGGCAG TGGGT CTGTAATC CCA CT CTTGGG T AG
GAGAATCACTTGAACCCAGG ACCCG GACGTTGG GGT GA GGACCC A TC
AGGTGGAGGTTGCAGTGAGC AGT A G - A-- GT ----------
CCA
GAM33692 11050 TGAGATGGGAGGACTGCTTG GG A - GA-- GGA AG T AC GATC
1 AGCCCAGGAGGTTGAGGTTG TGAGAT GAGG CT GCTT GCCCA GGTTG GT GCAGTGA CAT

CAGTGAACCATGATCATGTC ACTTTG TTCC GA TGAG TGGGT CCGAC CA CGTCACT GTA

ACTGCACTCCAGCCTGGGTA -- A G ACAA --- CT - -- ----
ACAGAGTGAGACCTTGTTTC
A
GAM33692 10544 GGACTGCTTGAGCCCAGGAG A - GA-- GGA AG T AC GATC
2 GTTGAGGTTGCAGTGAACCA GG CT GCTT GCCCA GGTTG GT GCAGTGA CAT

TGATCATGTCACTGCACTCC CC GA TGAG TGGGT CCGAC CA CGTCACT GTA
AGCCTGGGTAACAGAGTGAG A G ACAA --- CT - -- ----
ACC
GAM33692 10403 GAGGTGGGAGGGTCACTTGA G G- GA-- AATTTCAA C A ATGATTA
3 GCCCAGAATTTCAAGGCTGC GAGGT GGAGG TCACTT GCCCAG GG TGCAGTG GCT

AGTGAGCTATGATTAAGCCA TTTCA CCTCC AGTGAG CGGGTC TC ACGTCAC CGA
CTGCACTCCAGCCTGGGCAA A AG ACAA CGACC--- - - -------
CAGAGTGAGACCTCCAACTT
T
GAM33692 9818 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33692 10729 GGGAGACTTGCTTGAACCCA AGA GAA-- AGGC GG A CGACATCAT
5 GGAGGCGGAGGGTGCAGTGA GGG CTTGCTT CCCAGG GGA GTGCAGTG GT
GTCGACATCATGCCACTGCA CCC GAACGAG GGGTCC CCT CACGTCAC CG
CTCCAGCCTGGGCAACAGAG A-- ACAAC GA-- -- - ---------
CAAGACCC
GAM33692 10213 CTTGCTTGAACCCAGGAGGC GAA-- AGGC GG A CGACATCAT
6 GGAGGGTGCAGTGAGTCGAC CTTGCTT CCCAGG GGA GTGCAGTG GT
ATCATGCCACTGCACTCCAG GAACGAG GGGTCC CCT CACGTCAC CG
CCTGGGCAACAGAGCAAG ACAAC GA-- -- - ---------
GAM33692 11245 TTCCATTTTCTCATTGCCTG T A T A CT- ---------- T TG AATGA
7 AAGATCTCTGCTGATGCTCC TTCCATT TCTC TTGCC GA GAT CTG CTGA GCTCC GAG

TGGAGAATGACTTTGGGGGC AGGGTAG AGAG AACGG CT CTG GAC GATT CGGGG TTC

TTTAGAAAGAATATTGCCAG T G - - CCT CGTTATAAGAAA T GT -----
TCCGTCTCGGCAAGGAGATG
ATGGGA
GAM33693 10594 GGAGAATCGCTTGAACCCGG AATC- GAA--- AGGC - TG GAGCCGAGATTGT

1 GAGGCGGAGGTGGTGGTGAG GGAG GCTT CCCGGG GGAG G GTGGT
CCGAGATTGTGCCACTGCAC CCTC CGAG GGGTCC CCTC C CACCG
TCCAGCCTGGGCAACAAGAG AAAAA AACAAC GA-- A GT ----------
CAAAAACTCC
GAM33693 10120 CTCTCTTTGGCTACAGACTT ACAGACTTACC CTG A AA- G AAAA- TCTCC

2 ACCTCAGGCTGGCTGGAGAG CTCTCTTTGGCT TCAGG GCTGG GAGTA TCAG TCT GAG

TAAATCAGGTCTAAAAGAGT GAGAGAGGCCGA AGTCT CGACC CTCAT AGTC GGA CTT

CTCCTTCATAACAGGCTGAG ---------- AA- - AGG - CAATA -----
GATACTCCCAGCAATCTGAA
GCCGGAGAGAG
GAM33693 10235 GAAGAACTGGGTGATCTTGT A TC GAAATCTG- A ACATTG TTAGT
3 GAAATCTGTGGACCCTACAT GAAG ACTGGGTGA TTGT TGG CCCT GCAC
TGGCACTTAGTGTGTACCTA TTTC TGACTTACT AATA ATC GGGA TGTG

AGGGCTAACGTCCCAAATAA G GA AACCCTGCA - ATCCA- -----
AGTCATTCAGTGCTTT
GAM33693 11115 TGAGGCCGGAGAATCGCTTG CC AA G GAA-- TAG A T-
AGCCCAGATTGCATCAC
4 AACCCTAGAGGCAGGTTGCA TGAGG GGAG TC CTT CCC AGGC GG TGCAGTG
GTGAGCCCAGATTGCATCAC ACTCT CCTC AG GAG GGG TCCG CC ACGTCAC
CACTGCACTCCAGCCTGGGC A- AG G ACAAC --- A TC ----------
AACAGAGGGAGACTCCATCT
CA
GAM33693 9901 ATCATCAGGCATTAGATTCT T -- TAG A C AC AG CT AGGCACA
7 CATAAGGAGCACACAACCTA ATCA CA GGCAT ATTCTCATA GGAG AC AACCT ATTG AGC

GATTGCTAGCAGGCACAGTT TAGT GT CCGTA TAAGAGTGT CCTC TG TTGGG TAAC TTG

CACAATAGGGTTCGTTCTCC C CG CGG - T C- A- AC -------
TGTGAGAATGGCATGCCGCT
GCTGAT
GAM33693 10687 GGCATTAGATTCTCATAAGG TAG A C AC AG CT AGGCACA
8 AGCACACAACCTAGATTGCT GGCAT ATTCTCATA GGAG AC AACCT ATTG AGC
AGCAGGCACAGTTCACAATA CCGTA TAAGAGTGT CCTC TG TTGGG TAAC TTG
GGGTTCGTTCTCCTGTGAGA CGG - T C- A- AC -------
ATGGCATGCC
GAM33693 10830 GTCTAGGTCTGATAATTTTC AG GA A TT - TT TCA---------- GA GA-- TCT
9 ATTCATTTCTTTCATGGACA GTCT GTCT TA TT CATT CA TCTT TG CATGGT CTCTTT
TGGTGACTCTTTTCTTGCCA CGGA TAGA AT AA GTGA GT GGAG AC GTACCG GAGGAA

TCCTTAAGGAGAAAAGCCAT CT GG C GG A TT TTTCTAAAACATC AG AAAA ---
GGACACTACAAAATCTTTGA TGCCATCCTT
GGTTTGAAGTGGGAACTAGG
AGATTCAGGC

GAM33694 9819 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33694 11187 TGGGGTACTGAGAGTCAAAG T A CA A - CA -- TC CCT
2 ACTTGGCTGTCAGCCCTGAG TGGGGTAC GAG GT AAG CT TGGCTGT GCCCT GAG TG

TCTGCCTCAACCTCCAAGGG ACTCCGTG CTC CA TTC GG ACCGATA TGGGA CTC AC

TCATAGCCACGGCTTCACCC T C C- - C C- AC CA ---
TCTGTGCCTCA
GAM33694 10181 CTGTAATTCCAGCACTTTGG AAT C TT G A - GA-- A TGA GGGAATTTGA
5 GATGCCGAGTTGAGAGGATC CTGT TCCAG ACT GG ATGCCG GT TGA GG TCACT AGCC

ACTTGAAGCCGGGAATTTGA GACA GGGTC TGA TC TGTGGC CG ACT TC AGTGA TCGG

GGCTGCAGTGAGCTATGATC AC- - CT A - T AGTA G CG- ----------
ATGCCGGTGTACTTCAGTCT

GGGCAACAG
GAM33694 9768 AGTTCCCACGTGCATGGAGC -- - T- ----- T - CC- - TCTTA
6 TGTAGTTTTTCCCACATTCC AGTTCC CACG TGCA GG AGC GTAGT TTTT CACA TTCC
TCTTAGGAGCTGTGCCTAAG TCAAGG GTGT ATGT CC TCG CGTCG AGAA GTGT GAGG

ATGCTGCGCTAGCAACCTCT AA T CT AACGA - T TCC C -----
GTATTGTGAAGGAACT
GAM33694 10990 TCCTTCAGTGGATGATGTTT CA - T G C TCAGGAATTT
7 TCTGTGGTCTTGTTCAGGAA TCCTT GTG GATGA GTTTTCT TGGT TTGT
TTTACAAACTAGAGGAAGCC AGGGA CAC CTATT CGAAGGA ATCA AACA
TTATCTCACCAAGGGA AC T C G - ----------
GAM33695 9820 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33695 10111 CTCCCCCGAGAATGTCAGCC - AA - GCCC A GCG- T AT- ----- TCGTA
1 CCTTGAAGCTGCGGTCTGTC CTCCC CCGAG TGT CA CTTGA GCT GTC GTCT GCT GG

TATGCTGGTCGTACCCTCAG GGGGG GGCTC ACA GT GGACT CGA CAG TAGA CGA CC

AGCCTAAGATGACACAGAGC A CC A AAA- - GACA - ATC GACTC -----
TCAGGAAATGAACACCCTCG
GAGGGGG
GAM33695 11131 TGAGTAAGAGGAGGTGGGGA AAGA- ACTTT -- ATC AA CTGT
6 ACTTTGAGAGACATCGTAAT TGAGT GGAGGTGGGGA GAG AGAC GT TGG
GGCTGTCCACCACAGTCTTC ACTTA CCTCCACCCCT CTC TCTG CA ACC
CTCCGTCCCCACCTCCCAGT GTGAC GC--- CT A-- CC ----
GATTCA
GAM33695 9605 AAGACGGCAAATATTCTGGG C TATT AA-- A T- CACATTTAT
7 GTGAAGGAGGTATAATGGGG AAGA GGCAAA CTGGGGTG GGAGGT TAA GGGGAAA

AAACACATTTATTTTCCCCT TTCT CCGTTT GACCCCGT CCTTCA ATT CCCCTTT
TTTAAACTTCCCTGCTGCCC T CT-- CGTC A TT ---------
CAGTCTTTGCCTTCTT
GAM33695 10228 GAAATCCTGGGGTTGCAAGA TCC TT G G GTG AATCCTGC
8 CTGCCAGCCTGTGTGATCAA GAAA TGGGG GCAAGACT CCA CCT TGATC
TCCTGCGGTTAGGAAGGTGG CTTT ACCCT CGTTTTGA GGT GGA ATTGG
AGTTTTGCTTTCCCATCTTT TCT TT - - AGG --------
TC
GAM33695 9821 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33696 9893 ATAAGCTGCTCTAATTGCCA GCTC T - AGAAT T TG -- TG CTT -- GAGA
1 AGAATTCACATGTGGTTGTA ATAAGCT TAA TG CCA TCACA G G T TATGCAG TACT GG
TGCAGCTTTACTGGGAGACT TGTTTGA GTT AC GGT AGTGT C C A GTACGTC GTGA TC

GAAGTGTATCTGCATGTGAT AT-- C A ----- - GT TT GT TAT AG ----

TCTGCTGTGATGGACACTTG
TAAGTTTGT
GAM33696 10905 TACATGTGTTACACTCAGTG G CA GTA - AAGA AT A AGCAA
2 TGTAAATAACTGTGAAGAGG TACAT TGTTA CTCAGTGT AATA ACTGTG GGCA TGTC GAT

CAATTGTCAGATAGCAAATT GTGTG GCAGT GGGTCACG TTAT TGGCAT TCGT ACGG TTA

GGGCACCTGCTGTGTACGGT G CG --- A GTG- CC G -----
ATATTGCACTGGGGCTGACG
GGTGTG
GAM33696 11231 TTAGCCTCCCAGATGTCCTT C CAGATG- G --- GTTT GTG
3 GTGCTAGTTTTAGCTGTTTT TTAGC TCC TCCTT TGCTAGTTTT AGCT TCAG
CAGGTGTTGATAAAAGCTCC GATCG AGG AGGAG ACGGTCGAGG TCGA AGTT
AGGAGCTGGCAGGAGGAGAG A AGACGAG G ACC AAAT ---
CAGAGGAAGCTAG
GAM33696 9822 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33696 10222 CTTTTTCCTCCAGTGAACGG TT-- CCAGT GA - C-- A - TTGTTCTCTT
5 TGACTTGACAGAGGTACATA CTT TCCT GAACGGTGACTT CAGAG GTA ATAGG GGCTA C

GGAGGCTACTTGTTCTCTTG GAA AGGA TTTGTTATTGGA GTCTT CGT TGTTC TCGGT G

TTGGCTGCTTGTATTTGCTT TTCT ACT-- AG T TTA G T ----------
TCTGGAAGGTTATTGTTTTC
AAGGATCTTAAG
GAM33696 10983 TCCTCCAGTGAACGGTGACT CCAGT GA - C-- A - TTGTTCTCTT
6 TGACAGAGGTACATAGGAGG TCCT GAACGGTGACTT CAGAG GTA ATAGG GGCTA C

CTACTTGTTCTCTTGTTGGC AGGA TTTGTTATTGGA GTCTT CGT TGTTC TCGGT G
TGCTTGTATTTGCTTTCTGG ACT-- AG T TTA G T ----------
AAGGTTATTGTTTTCAAGGA
GAM33696 11228 TGTTTTGACTCTCCGCCTTC GA - - G - T C T GA TTGAGTAC
7 CCTTAGGTCTGGAATGGTAG TGTTTT CT CT CC CCTTC CCT AGGT TGGAA GGTA GCA

AGCATTGAGTACTGTTATCT ACAGAG GA GA GG GGAAG GGA TCTA ACCTT CTAT TGT
TCCACATCTCAGGAGAAGGG A- T C G A C C - -- --------
GGCAGTAGAGAGACA
GAM33696 10113 CTCCTGTAGTCCTAGAGCGT GTA AGAGC TT - - A- - CAAAGAGT
8 TTCTCTTGAACCCTAATTTT CTCCT GTCCT GT CT CTTGAACC CT ATTTTT AGGTCT
TAGGTCTCAAAGAGTGGGCT GAGGA CGGGA CA GA GGATTTGG GA TAGAGA TTCGGG

TCAGAGATAAAGAGGTTTAG G-- ----- GG C A AA C --------
GCAGGGACAGGGCGAGGAG
GAM33696 9823 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----

CT
GAM33697 9727 AGGCTGGGAACTGTGACTCG GAACTGT --- A -- AG GAGAGGCT
0 TACTTGTAATCCTAGTGCTT AGGCTGG GACTC GT CTT GTAATCCT TGCTTT
TGAGAGGCTGAGGCAGGAGG TCCGACC TTGAG CA GAG CGTTAGGA ACGGAG
ATTGCTTGAGACCAGGAGTT AGAGT-- GAC - TT GG --------
TGAGACCAGCCT
GAM33697 10709 GGCTGGGAACTGTGACTCGT GAACTGT --- A -- AG GAGAGGCT
1 ACTTGTAATCCTAGTGCTTT GGCTGG GACTC GT CTT GTAATCCT TGCTTT
GAGAGGCTGAGGCAGGAGGA CCGACC TTGAG CA GAG CGTTAGGA ACGGAG
TTGCTTGAGACCAGGAGTTT AGAGT-- GAC - TT GG --------
GAGACCAGCC
GAM33697 9824 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33697 11135 TGATGCGCCACAGGTATCAG C ACAG ATCA G G- --- GTTTTAGCCACAA
4 CGTCTGGATCGCCACTTCAC TGATG GCC GT GC TCTGGATC CCACT TCAC
GTTTTAGCCACAAGTGACTC ACTGC CGG CA TG AGACCTAG GGTGA AGTG
AGTGGAAGATCCAGAGTCAA T AGA- AC-- - AA CTC ----------
CAGAGGCTCGTCA
GAM33697 11123 TGAGGTAGGAGAATCACTTG GTA AA A GAA--- AGGCA GT A - AGAT
5 AACCCGGGAGGCAGAGGTTG TGAG GGAG TC CTT CCCGGG GAG TGCGGTG GC CG

CGGTGAGCCGAGATTGTGCC ACTC CCTC AG GAG GGGTCC CTC ACGTCAC CG GT
ACTGCACTCCAGCCTGGGCA TG- AA C AACAAC GAC-- -- - T ----
ACAAGAGCGAAACTCCGTCT
CA
GAM33697 10067 CCTGGTCTTTAAGAGTGATT - TA A AG-- T TGGC
6 GGAGGCTGGGCATGGTGGCT CCT GGTCTT AGAGTG TTGG GC GGGCATGG
TATGCCTGTAATCCCAGCAC GGA CCGGAG TTTCAC GACC TG TCCGTATT
TTTGGGAGGCCAAGG A GG - CTAA - ----
GAM33697 10532 GGACATCAAAGAATAAATAA A CAAA AA C C A TG CA- T TG TTGT G AC
8 GCTGCTCTAATTGCCAAGAA GG CAT GAAT ATAAG TG TCTA T C AGAAT CACATG G ATGCA
CTTT
TTCACATGTGGTTGTATGCA CC GTG TTTG TGTTC AC AGGT A G TCTTA GTGTAC C TATGT
GAAG
GCTTTACTGGGAGACTGAAG - ---- AA - - - GT TCG - GT ---- - --
TGTATCTGCATGTGATTCTG T GAGA
CTGTGATGGACACTTGTAAG GG
TTTGTGCC TC
- ----
GAM33697 9894 ATAAGCTGCTCTAATTGCCA GCTC T - AGAAT T TG -- TG CTT -- GAGA
9 AGAATTCACATGTGGTTGTA ATAAGCT TAA TG CCA TCACA G G T TATGCAG TACT GG
TGCAGCTTTACTGGGAGACT TGTTTGA GTT AC GGT AGTGT C C A GTACGTC GTGA TC

GAAGTGTATCTGCATGTGAT AT-- C A ----- - GT TT GT TAT AG ----
TCTGCTGTGATGGACACTTG
TAAGTTTGT
GAM33698 10246 GAATAAATAAGCTGCTCTAA AA C C A TG CA- T TG TTGT G ACT GAGA

```
0          TTGCCAAGAATTCACATGTG GAAT  ATAAG TG TCTA T  C   AGAAT CACATG  G    ATGCA CTTT   GG

           GTTGTATGCAGCTTTACTGG TTTG  TGTTC AC AGGT A  G   TCTTA GTGTAC  C    TATGT GAAG   TC

           GAGACTGAAGTGTATCTGCA    AA    - -   - GT TCG    -     GT ----    -    --- ----
           TGTGATTCTGCTGTGATGGA
           CACTTGTAAGTTT
GAM33698 9892   ATAAGCTGCTCTAATTGCCA     C  C    A TG CA-     T     TG TTGT     G    ACT  GAGA
1          AGAATTCACATGTGGTTGTA ATAAG TG TCTA T  C   AGAAT CACATG  G    ATGCA CTTT   GG
           TGCAGCTTTACTGGGAGACT TGTTC AC AGGT A  G   TCTTA GTGTAC  C    TATGT GAAG   TC
           GAAGTGTATCTGCATGTGAT    - -   - GT TCG    -     GT ----    -    --- ----
           TCTGCTGTGATGGACACTTG
           T
GAM33698 10878  GTGTTTGGAATAGAGCCCAG        A     -    TCTGAAATTATAA    -    TAC
3          TCTGAAATTATAAGCACTGG GTGTTTGG ATAGAG CCCAG          GCAC TGGGG
           GGTACTCCTATGTGTCTGGG TATGAACC TATCTC GGGTC          TGTG ATCCT
           ACTCTATGCCAAGTAT          G     A    ----------    T    ---
GAM33698 9990   CCAAGTAGAAGCAAACTGTA      AGA-  AA--     G    TGC  GA   -      TGA
4          GTTTGATGCTAGAACACTAT CCAAGT    AGC    ACTGTA TTTGA   TA  ACAC TATTCTT
           TCTTTGAGAGGGTATGTGTG GGTTCG    TCG    TGACGT AAGCT   AT  TGTG ATGGGAG
           ATACTCGAAATGCAGTCATG      GCAC   GTAC     A    C-- AG    T      ---
           GCTCACGGCTTGG
GAM33698 9949   CACTGCCAACTGAGGCAGGA     CCAACT--    ---      CT     A  CTTC
9          GGGCTCAGGAGAGTCTTCGC CACTG      GAGGC   AGGAGGG  CAGGAG GT
           CTCTTGTACCCTCCTTGGGC GTGAC      CTCCG   TCCTCCC  GTTCTC CG
           CTCTCCAAAACCAGTG         CAAAACCT     GGT      AT     - ----
GAM33699 10214  CTTGGCTGGGTTTTTCCACG   T   T    TTTTCCACGT    - T     TT-      CCAGC
0          TGAGATGGTGTCATATTGCT CT GGC GGGT        GAGAT GG GTCATA   GCTGGGT
           GGGTCCAGCACCCAGTTATT GA CCG CCCA        CTTTA CC CGGTGT   TGACCCA
           GTGGCCCAATTTCCTATACC   T   T    TATC------     A -     TAT      -----
           CTGCCTAG
GAM33699 9825   AGTTTTAGGGTACATGTGCA     TTA    A  T TG   -      - G  T    T  ATAT
1          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA     TTA    C  - GT   G     C  G  C   - ----
           CT
GAM33699 11211  TGTCTATAGAGTATGTGGGC       AGAGTA  T     TT-   TG  C-   A    TT    T     CTCTCTCT
2          CATTTTCTGCCCGTAAAATG TGTCTAT     TG GGGCCA   TTC   CC  GTA AATG   CAAA GTTTT
           TTCAAATGTTTTCTCTCTCT ACAGATG     AC CTTGGT   AAG   GG  TAT TTAC   GTTT CGAAA
           AAAGCTTTGTTCATTGTATC      AGGG-- T     TTT   GT  TC   G    TT    -    --------
           TGGTGGAATTTTGGTTCTCA
           GGGAGTAGACA
GAM33699 10572  GGAGAATCGCTTGAACCCAG     AA     GAA---      AAG     GT      A  -  ATAT
5          GAAGTGGAGGTTGCAGTGAG GGAG  TCGCTT     CCCAGG   TGGAG  TGCAGTG GC CA
           CCAATATTGTGCCATTGCAC CCTC  AGCGAG     GGGTTC   ACCTC  ACGTTAC CG GT
           TCCAGCTTGGGCAACAAGAG     AA     AACAAC     G--     --      -  T  ----
           CGAAACTCC
GAM33699 10994  TCGCTTGAACCCAGGAAGTG      GAA---      AAG     GT      A  -  ATAT
6          GAGGTTGCAGTGAGCCAATA TCGCTT     CCCAGG   TGGAG  TGCAGTG GC CA
           TTGTGCCATTGCACTCCAGC AGCGAG     GGGTTC   ACCTC  ACGTTAC CG GT
```

TTGGGCAACAAGAGCGA AACAAC G-- -- - T ----
GAM33699 9718 AGGCATTGTCTCCAACATGT AT TCCA C ------- TTTT
7 ACCACTGGTCTGGCTTTTGT AGGC TGTC ACATGTAC ACT GGTCTGGC
TAGGCCCATTAATAGTGTAC TCCG ACAG TGTACATG TGA CCGGATTG
ATGTGACAGCCT -- ---- - TAATTAC ----
GAM33700 9647 ACTACTGGGTGTATAAATGT G TAT GT T TTA- T C TAC
0 GTTTGTGTGTGTATGTATTT ACTACTGG TG AAATGT TTGTGTG GTATGTAT TAGA GTT
TTTAAGG
ATAGATGTTCTTTAAGGTAC TGGTGACT AC TTTACA AATACAC CGTATGTA ATCT CAA AAGTTCC

CCTTGAAAACTCTACATTAT G --- GT - TTAC - - ---
GTATGCCACATAATGACATT
TCAGTCAGTGGT
GAM33700 10060 CCTGAACCCAGGAGGCGGAG AA- AGGC GC GCCAAGATTAAG
1 GCTGCAGTGGGCCAAGATTA CCTG CCCAGG GGAG TGCAGTGG
AGCCACTGCACTCCAGCCTG GGAC GGGTCC CCTC ACGTCACC
GGCAACAGG AAC GA-- -- ----------
GAM33700 10207 CTTGAACCTGAAAGGCAGAG AA- GAA A- GC A- TGAGATT
3 GCTGCGGTGAGCTGAGATTG CTTG CCT AGGC GAG TGCGGTG GC
CGCCATTGCACTCCAGCCTG GAAC GGG TCCG CTC ACGTTAC CG
GGCAACAAG AAC --- AC -- CG -------
GAM33700 10090 CGGGGATTCAGTCTGTGAGG ATTCAGTCT C CCCACT - TCACTTTGCT

4 CGGGAAGCCCACTAGGAGGA CGGGG GTGAGG GGGAAG AGGAG GACTC
CTCTCACTTTGCTGAGTCTC GTCCC CACTTC TCTTTC TTCTC CTGAG
TCTTTCCCTTCTTTCTTCTT AAATAACC- T TTCCCT T ----------
CACCCAATAAACCCTG
GAM33700 11075 TGAGGCAGGAGAATCACTTG C AA GAA-- AGGCA GT A - AGAT
7 AACCCAGGAGGCAGAGGTTG TGAGG AGGAG TCACTT CCCAGG GAG TGCAGTG GC TG

CAGTGAGCTGAGATCATGCC ACTCT TCCTC AGTGAG GGGTCC CTC ACGTCAC CG AC

ACTGCACTCCAGCCTGGGCA - GG ACAAC GAC-- -- - T ----
ACAGAGTGAGGCTCCTTCTC
A
GAM33700 10108 CTCATGGTCTCCAAAGGTCT G AAGGT ACC CA-- AC G GCTA
8 CTACCCAGACATTTCAACTT CTCAT GTCTCCA CTCT CAGA TTTCA TTT TTGTTCTTTG
TGTTGTTCTTTGGCTACAAA GAGTG CAGAGGT GAGG GTCT GAGGT AGA GACAAGAAAC

GAACAGGAGAAATGGAGGAC A GT--- GT- TCAG AA G ----
TTCTGTGGGAGTGTGGAGAC
AGTGAG
GAM33700 9826 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33701 9827 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG

TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33701 10426 GCAAGGTGCTAGGTTTTTTC T ---------- CCT--- C- TCTCT
1 CTTTCCCCACCTGTCTCTTA GCAAGG GCT AGGTTTTTT TTCCCCA CTG
GCCTGGGGAATTAAATGAGA TGTTCC CGG TCCGAAGAG AAGGGGT GAT
AGCCTTAGAATGGGTGGCCC - TGGGTAAGAT TAAATT CC -----
TTGT
GAM33701 9828 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33701 10368 GAGGCAGGAGAATTGCTTGA G AA GAA--- TG AGGC - T A- CAAG
5 ACCTGGGAGGCGGAGGTTGT GAGGCAG AG TTGCTT CC GG GGAG GT GTGGTG GC

GGTGAGCCAAGGTCGCGCCA CTCTGTC TC AACGGG GG CC CCTC CG TACCGC TG
TTGCACTCCAGCCTGGGCAA - AA AACAAC GT GA-- A T GC ----
CAAGGGCAAAACTCTGTCTC
GAM33701 9935 CAAGTTTGGTCAAGGGGTGA - T ---------- T G G CA ATCTCC
6 GTGTGTCCGACTCCAAGGAG CAAGTTTG G CAAGGG GTGAG GT TCC ACTC AGGAGC

CATCTCCGTTTCTGAGTGGG GTTCGGAC C GTTCCC TACTC CA AGG TGAG TCTTTG
AACTCTCATGACACTGTGTC T C TGTGTCACAG T - G -- ------
CCTTGCCTCAGGCTTG
GAM33701 11146 TGCGGGCAGGATCACATATT G ATCACATATTAG AAC A GGAGAG
7 AGGCAGAAAACAATTCCAAG TGCGG CAGG GCAGAA AATTCCA GCAA
CAAGGAGAGTTGCTGGGATT ACGCT GTCT CGTCTT TTAGGGT CGTT
ATTCTGCTCTGGTCGCA G ---------- A-- - ------
GAM33701 9829 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33701 9830 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33702 11296 TTTTGGTAAAGACATTCATC G -- TCA AGT TTC CTCCCAG TA-- TTAATATT
2 TCAGTCGTTTCTCTCTCCCA TTTTG TAAAG ACAT TCTC CGT TCT CTTGACCT GG
GCTTGACCTTAGGTTAATAT AGAAC ATTTC TGTA AGAG GTA AGA GAACTGGG CT
TTCATTTGGGTCAAGAAAAG A GT TCG GAT TA- AAA---- TTTA --------
AATATGTAGGAGAGCTATGT
TGCTTTAACAAGA
GAM33702 10495 GCTGTCCTGAGGCCTGGAGA T ---- G - - A TAA-- GA GAAC
3 TACTAGAGGGTAAAGGAATG GC GTC CT AGGCC TG GAG TACTAGAGGG AG ATG
GAACCATGTCTGGGGTCCCT CG CAG GG TCTGG AC TTC ATGATTTCCC TC TAC
TTAGTAACTTGCAGGGTCTG T TTAA G G G A TGGGG TG ----
GGAATTGACTGC
GAM33702 10987 TCCTGAGGCCTGGAGATACT G - - A TAA-- GA GAAC

4 AGAGGGTAAAGGAATGGAAC TCCT AGGCC TG GAG TACTAGAGGG AG ATG
CATGTCTGGGGTCCCTTTAG AGGG TCTGG AC TTC ATGATTTCCC TC TAC
TAACTTGCAGGGTCTGGGA - G G A TGGGG TG ----
GAM33702 11169 TGGCAGGAGGCCAGCTCTCA A C TCTC- TTCT AA T TCACTGGTTTATTT

5 TCCTTTTCTGCAACCTGTTT TGGCAGG GGC AGC ATCCTT GC CC GTTTGC
GCTCACTGGTTTATTTGTAA ACCGTCC CTG TCG TGGGAG CG GG TAAATG
ATTGGGGCTATGAGGGTCTA - - TCATC TAT- G- T ----------
CTGCTGTCCCTGCCA
GAM33702 11130 TGAGGTGGGAGGATTACTTG AGGAT GA-- AGA A- GC A - ACAT
7 AGCCCAAGAGGAGGAGGCTG TGAGGTGGG TACTT GCCCA GG GGAG TGCAGTG GT CA

CAGTGAGTCAACATTGCACC ACTCTACCC GTGAG CGGGT CC CCTC ACGTCAC CA GT

ACTGCACTCCAGCCTGGGCA CAGT- ACAA --- GA -- - C ----
ACAGAGTGTGACCCCATCTC
A
GAM33702 10401 GAGGTGGGAGGATTACTTGA AGGAT GA-- AGA A- GC A - ACAT
8 GCCCAAGAGGAGGAGGCTGC GAGGTGGG TACTT GCCCA GG GGAG TGCAGTG GT CA

AGTGAGTCAACATTGCACCA CTCTACCC GTGAG CGGGT CC CCTC ACGTCAC CA GT

CTGCACTCCAGCCTGGGCAA CAGT- ACAA --- GA -- - C ----
CAGAGTGTGACCCCATCTC
GAM33702 10928 TATGGGAAAAAAGGCAGTTT GG AA------- A GAAAAA TA G TACA GAGA
9 AGAAAAAAGTACATTTGGTA TATG AA AAGGC GTTTA AG CATTTG TA TGCATA
TACATGCATAGAGATGTGCA ATAC TT TTCCG TAAGT TC GTAAAC AT ACGTGT
TAGCAAATGGTCTGAATGAA TT GACACCAGA G AAG--- TG G ---- ----
TGGCCTTAGACCACAGTTTT
CATA
GAM33703 11176 TGGGAAAAAAGGCAGTTTAG GAAAA A GAAAAA TA G TACA GAGA
0 AAAAAAGTACATTTGGTATA TGG AAGGC GTTTA AG CATTTG TA TGCATA
CATGCATAGAGATGTGCATA ACC TTCCG TAAGT TC GTAAAC AT ACGTGT
GCAAATGGTCTGAATGAATG AGA-- G AAG--- TG G ---- ----
GCCTTAGACCA
GAM33703 9710 AGGCACCTAGAGACTTCACA ACCT A TCACAA AA CAG C G - AACTT
1 AGCTAATGGCAGTCCCTGGA AGGC AGAG CT GCT TGG TC CT GAGCAGGA AGC
GCAGGAAGCAACTTGTTATT TCCG TCTC GA CGA ACC AG GA CTCGTCTT TTG
CTGCTCAAGAGAATCCACCA GT-- - ------ CC TA- A A A -----
GCAGCTCTTGGCCT
GAM33703 11277 TTGGGAAACTGAGGTAGGAG AAC - A AA GA-- CGG A T A TGAGATTG
2 AATCACTTGAGCCCCGGAGG TTGGGA TGA GGT GGAG TCACTT GCCC AGGC GGGGT
GCAGTG GC
CAGGGGTTGCAGTGAGCTGA AACTCT ACT CTA CCTC AGTGAG CGGG TCCG CCTCA CGTCAC
CG
GATTGTGCCACTGCACTCCA --- A - AA ACAA --- A - - --------
GCCTGGGCAACAGAGTGAAA T
CTCCATCATCATCTCAA

-

GAM33703 10565 GGAGAATCACTTGAGCCCCG AA GA-- CGG A T A TGAGATTGT
3 GAGGCAGGGGTTGCAGTGAG GGAG TCACTT GCCC AGGC GGGGT GCAGTG GC
CTGAGATTGTGCCACTGCAC CCTC AGTGAG CGGG TCCG CCTCA CGTCAC CG
TCCAGCCTGGGCAACAGAGT AA ACAA --- A - - ---------
GAAACTCC
GAM33703 10194 CTTAAGTTTGCTTGCAGTGT G TG ----- AG TG CT GCAT
5 ATGTGTGTATGTCTGTGTGT CTTAA TT CT TGC TGTATGTG TATGT GTGTGT
GCATGCACGCACATGTGCAC GAATT AG GA ACG ACGTACAC GTACA CGCACG
ATGCAGCAGGGAGAGTGGAA A GT GAGGG -- GT -- ----
TTAAG
GAM33703 10769 GGGTGTGAAGGAAACATCCT - AG - C C---- TC C AGTAGGCC
6 CCCCCTTGTTTTCAACCTAG GGGTG TGA GA AACATC TCCC CTTGTTT AA CT
TAGGCCAGTTTAGAAACAAG CTCAT ACT CT TTGTGG AGGG GAACAAA TT GA
CCACAGGGAAGGTGTTGTCA T GA G A ACACC GA T --------
GTCATTACTC
GAM33703 10730 GGGAGAGGCATTGTGAGGGA GC- GAG---- TGTC T A T AAATTC
7 GAGAGGTGTCAGGAATGAAA GGGAGAG ATTGT GGAGAGAGG AGGAA GAAAGA TG CTTA

GAATGTCTTAAAATTCTAAG CTCTCTC TAACG TTTCTCTTC TTCTT CTTTCT AC GAAT
CAGTCTTTCTTCTTCTTCTC AAT ACAATTA ---- - G - ------
TTTATTAACAGCAATTAACT
CTCTC
GAM33703 10652 GGAGAGGCATTGTGAGGGAG GC- GAG---- TGTC T A T AAATTC
8 AGAGGTGTCAGGAATGAAAG GGAGAG ATTGT GGAGAGAGG AGGAA GAAAGA TG CTTA

AATGTCTTAAAATTCTAAGC TCTCTC TAACG TTTCTCTTC TTCTT CTTTCT AC GAAT
AGTCTTTCTTCTTCTTCTCT AAT ACAATTA ---- - G - ------
TTATTAACAGCAATTAACTC
TCT
GAM33703 10297 GAGAGGCATTGTGAGGGAGA GC- GAG---- TGTC T A T AAATTC
9 GAGGTGTCAGGAATGAAAGA GAGAG ATTGT GGAGAGAGG AGGAA GAAAGA TG CTTA

ATGTCTTAAAATTCTAAGCA CTCTC TAACG TTTCTCTTC TTCTT CTTTCT AC GAAT
GTCTTTCTTCTTCTTCTCTT AAT ACAATTA ---- - G - ------
TATTAACAGCAATTAACTCT
C
GAM33704 11257 TTGCTTGAACCCAAGAGGCG GA-- AGA - GT A TAAGATCAT
1 GAGGTTGCAGTGAGCTAAGA TTGCTT ACCCA GGC GGAG TGCAGTG GC
TCATGCCACTGCACTCCAGC AACGAG TGGGT CCG CCTC ACGTCAC CG
CTGGGTGACAGAGCAA ACAG --- A -- - ---------
GAM33704 10689 GGCCACCTGCTGCCTATTCC - GC - C GG -- CTTCTGAT
2 CTGGCACTTCATTCTTCTGA GG CCACCT TG CCTATTC CT C ACTTCATT
TAATGGAGTATGAGAGAGAA CC GGTGGA AC GGGTAAG GA G TGAGGTAA
TGGGACATGAGGTGGACC A GT A A GA TA --------
GAM33704 10823 GTCCCAAAGAAAAGGAAAAC CCAA AAAA C - TCCAT
3 CCAGCAAGGGCATGGTCCAT GTC AGAAAAGG CCCAG AAGGGCA TGG
CTGCTGCCTTTTCTGGGCTC CAG TCTTTTCC GGGTC TTTCCGT GTC
CCTTTTCTGCTGAC TCG- CTC- T C -----
GAM33704 9831 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
5 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC

TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33704 10219 CTTTGTGAGTGGCTTTGAAA CT A - G G TTTA
6 CTGTAATGAGCGCAGTTTAC CTTTGTGAGTGG TTGA ACT GTAATGA C CAG
TGAGTCATTACTAGTCTCGA GAGATGCTTACC AGCT TGA CATTACT G GTC
CCCATTCGTAGAG C- C T - A ----
GAM33704 10889 GTTTGGAGGTCTGTTGCTTC T CTGTTGCTTCCTT C T T TTCCA - G TCACG

7 CTTGAGGCACGGTAAGGAGT GTT GGAGGT GAGGCA GG AAGGAG GG ATTTG GGGT C

GGTTCCAATTTGGGGTGCTC TAG CCTCTA CTCCGT TC TTTCTT CC TAGAC CCTA G
ACGGGATCCACAGATCTCTC T CCC---------- C C T TCTC- A G -----
CTTTCTTTCCTCTGCCTCCC
CATCTCCTGAT
GAM33705 10296 GAGAGAGGAAATGAGAGGAG AAA GAGT GC- C G G C C GTTAG
1 TCGGCTGGGGCGAGTGTGGA GAGAGAGG TGAGAG CG TGGGG GAGT TG AC GCAGCC AGA

CCGCAGCCCAGAGTTAGTCT TTCTTTCC ACTCTT GT ATCTT CTCA AC TG CGTCGG TCT

TGGCTGCAGTGCAACTCTTT CGC ATT- AAA T - G A T -----
CTAAAATGTTATTCTCACGC
CCTTTCTT
GAM33705 9670 AGAGAGGAAATGAGAGGAGT AAA GAGT GC- C G G C C GTTAG
2 CGGCTGGGGCGAGTGTGGAC AGAGAGG TGAGAG CG TGGGG GAGT TG AC GCAGCC AGA

CGCAGCCCAGAGTTAGTCTT TCTTTCC ACTCTT GT ATCTT CTCA AC TG CGTCGG TCT
GGCTGCAGTGCAACTCTTTC CGC ATT- AAA T - G A T -----
TAAAATGTTATTCTCACGCC
CTTTCT
GAM33705 10688 GGCATTAGGTTTCAGTCACA TTA T- TC CAA T ACA G T C- AAGATTC
3 GCCAAGCAAGTGTGGACAGT GGCA GG TTCAG ACAGC GCAAG GTGG GTGA TAA GT TG

GAGTAATGTCTGAAGATTCC CTGT CC AAGTC TGTCG TGTTT CATC CACT GTT CG AC
ATAGCTTGATCACAGCTACT TA- TC -- TCC T GA- A - AT -------
TTTGTCCTGCTGTCTGAACT
CCATTGTC
GAM33705 11238 TTCAGGTACTCCATGTGATA T CA- TG ATATGG -- AA CGTG C A- C AG
5 TATGGTTCCACAATCCTCAG TTCAGG ACTC TG AT TTC CAC TCCTCAG TTAA TG AGC
TTGTTG
CGTGTTAACTGAAGCCTTGT GGGTTT TGAG AC TG AAG GTG AGGGGTC AGTT AC TCG
AACAAT
TGAGTTTAACAAAGCTGCCA - ACA GT ------ AA AA TAGA - CG A --
TTGAAGATCTGGGGAAAGTG TT
AAGAAGTTGCAACAGAGTTT
TGGG
--
GAM33705 9972 CAGGTACTCCATGTGATATA T CA- TG ATATGG -- AA CGTG C A- C AGTT
6 TGGTTCCACAATCCTCAGCG CAGG ACTC TG AT TTC CAC TCCTCAG TTAA TG AGC
TTGTTG

TGTTAACTGAAGCCTTGTTG GTTT TGAG AC TG AAG GTG AGGGGTC AGTT AC TCG
AACAAT
AGTTTAACAAAGCTGCCATT - ACA GT ------ AA AA TAGA - CG A ----
GAAGATCTGGGGAAAGTGAA
GAAGTTGCAACAGAGTTTTG

GAM33705 9937 CACAATCCTCAGCGTGTTAA AA CGTG C A- C AGTT
7 CTGAAGCCTTGTTGAGTTTA CAC TCCTCAG TTAA TG AGC TTGTTG
ACAAAGCTGCCATTGAAGAT GTG AGGGGTC AGTT AC TCG AACAAT
CTGGGGAAAGTG AA TAGA - CG A ----
GAM33705 10982 TCCTCAGCGTGTTAACTGAA CGTG C A- C AGTT
8 GCCTTGTTGAGTTTAACAAA TCCTCAG TTAA TG AGC TTGTTG
GCTGCCATTGAAGATCTGGG AGGGGTC AGTT AC TCG AACAAT
GA TAGA - CG A ----
GAM33705 9961 CAGCCTCAAGTGATCCACCA C- AT CCACC CTTCCC T -- TA A ATCCAC
9 CCTCAGCTTCCCAAAGTGCT CAGCCT AAGTG CCA TCAG AAAG GC TGGGAT CAGGC TG

GGGATTACAGGCATGATCCA GTTGGG TTCGT GGT AGTC TTTC TG ACCCTG GTCCG AC

CCACGCCTGGTCCCATTGTT TT CG ----- TACA-- T TT -- C ------
CTTTACATCTGATGGGCTGC
TTTTGGGTTG
GAM33706 11059 TGAGGCAGGAAAATCGCTTG AAAATC GAA-- A A- GT CA- ATA
0 AACCCAAGGCAGAGGTTGCA TGAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG

GTCAGCAGATATTGCACCAC ACTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
TGCACTCCAGCCTGGGCAAC CAGAA- ACAAC - AC -- CCA ---
AAAGCAAGACTCTGCCTCA
GAM33706 10076 CCTTTGAACAGTGGAACTGG C T -- AT--- - G T ------ - TTCA
1 ATGAAAGAAATGGGATCTGT CCTTTGAA AG GGA ACTGG GA AAGAAAT GGA CTGTG
CAGCTA C
GCAGCTACTTCAGTTAGCTG GGAGACTT TC CCT TGATC TT TTCTTTG TCT GACAT GTCGAT
G
GAATCCTACAGTTCTGGTTT T - TT GTAAT C G T CCTAAG T ----
CTTCTTTAATGCTAGTTTTC
CCTTTTCAGAGG
GAM33706 10581 GGAGAATCGCTTGAACCCAG AA GAA-- AGG GT AGC AGGT
2 GAGGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG TG
CTGAGGTCACACCACTGCAC CCTC AGCGAG GGGTCC ACCTC ACGTCAC AC
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- CAC ----
GAGACTCC
GAM33706 10131 CTCTTGACCAGAGGTTCTCA CT - - AG C T TA TGCC
3 AATGAGGGACATTTTACCTG CT TGACCAGA G GTTCTCAAATG GGA AT T CC
CCGGGGACATTTCCAATGTT GA ATTGGTTT C CAGGGGTTTGT CCT TA A GG
TGGGGACACTTTTGGTTATC CT T A AA T C GG ----
AG
GAM33706 10582 GGAGAATCGCTTGAACCCAG AA GAA-- AGG GT AGC AGGT
4 GAGGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG TG
CTGAGGTCACACCACTGCAC CCTC AGCGAG GGGTCC ACCTC ACGTCAC AC

TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- CAC ----
GAGACTCC
GAM33706 11236 TTCACTCCCAAGTGGCTTTT ----- C G --- G A GG-- GATTATG
6 GTCTGGCAGATTCCGGTGGA TTCA CT CCAA TGGCTT TT TCTGGCAG TTCC TG
TTATGCAAAGAGGGACTGCC AAGT GA GGTT GTCGAG AA AGACCGTC AGGG AC
AGAGAATCTGAGCTGTTGGA CTTCA A - TCT G - AGAA -------
AGACTTCTGAA
GAM33706 10224 GAAAAGGGCTGATCAGTATT ----- T A TT TC TCAGT
8 TTCTGATCCTAGTTCAGTGC GAAAAGG GCTGA CAGT TT CTGA CTAGT
TAGTCAGGGAGACTGTCAGT TTTTTCC TGACT GTCA GA GACT GATCG
AAAGACCTTTTT AGAAA - - GG -- -----
GAM33706 11060 TGAGGCAGGAAAATCGCTTG AAAATC GAA-- A A- GT CA- ATA
9 AACCCAAGGCAGAGGTTGCA TGAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG

GTCAGCAGATATTGCACCAC ACTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
TGCACTCCAGCCTGGGCAAC CAGAA- ACAAC - AC -- CCA ---
AAAGCAAGACTCTGCCTCA
GAM33707 10322 GAGGCAGGAAAATCGCTTGA AAAATC GAA-- A A- GT CA- ATA
0 ACCCAAGGCAGAGGTTGCAG GAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG

TCAGCAGATATTGCACCACT CTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
GCACTCCAGCCTGGGCAACA CAGAA- ACAAC - AC -- CCA ---
AAGCAAGACTCTGCCTC
GAM33707 9725 AGGCTGAGTGCAGTGGTGTG T ----- T TC CTCACT AGCTC
1 ATCTCGGCTCACTGCAAGCT AGGCTGAG GCAG TGGTGTGA C GG GCA
CTGCCTCCCAGGTTCACGCC TCCGACTC CGTC ACCGCACT G CC CGT
ATTGTCCTGCCTCAGCCT - CTGTT T GA CTC--- -----
GAM33707 11044 TGAGACAGGAGAATCGCTTG A AA GAA--- AGG GTTA A- AGAT
4 AACCCGGGAGGTGGAGGTTA TGAGAC GGAG TCGCTT CCCGGG TGGAG CGGTG GTG

CGGTGAGTGAGATCGCGCCA ACTCTG CCTC AGCGAG GGGTCC ACCTC GTTAC CGC

TTGCACTCCAGCCTGGGCAA - AA AACAAC G-- AC-- CG ----
CAAGAGCGAAACTCCGTCTC
A
GAM33707 10288 GAGACAGGAGAATCGCTTGA A AA GAA--- AGG GTTA A- AGAT
5 ACCCGGGAGGTGGAGGTTAC GAGAC GGAG TCGCTT CCCGGG TGGAG CGGTG GTG

GGTGAGTGAGATCGCGCCAT CTCTG CCTC AGCGAG GGGTCC ACCTC GTTAC CGC

TGCACTCCAGCCTGGGCAAC - AA AACAAC G-- AC-- CG ----
AAGAGCGAAACTCCGTCTC
GAM33707 10596 GGAGAATCGCTTGAACCCGG AA GAA--- AGG GTTA A- AGAT
6 GAGGTGGAGGTTACGGTGAG GGAG TCGCTT CCCGGG TGGAG CGGTG GTG
TGAGATCGCGCCATTGCACT CCTC AGCGAG GGGTCC ACCTC GTTAC CGC
CCAGCCTGGGCAACAAGAGC AA AACAAC G-- AC-- CG ----
GAAACTCC
GAM33707 10132 CTCTTGACCAGAGGTTCTCA CT - - AG C T TA TGCC
7 AATGAGGGACATTTTACCTG CT TGACCAGA G GTTCTCAAATG GGA AT T CC
CCGGGGACATTTCCAATGTT GA ATTGGTTT C CAGGGGTTTGT CCT TA A GG

TGGGGACACTTTTGGTTATC CT T A AA T C GG ----
AG
GAM33707 10583 GGAGAATCGCTTGAACCCAG AA GAA-- AGG GT AGC AGGT
8 GAGGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG TGGAG TGCAGTG TG
CTGAGGTCACACCACTGCAC CCTC AGCGAG GGGTCC ACCTC ACGTCAC AC
TCCAGCCTGGGCAACAGAGC AG ACAAC G-- -- CAC ----
GAGACTCC
GAM33707 11052 TGAGGCAAGAGAATCACTTG A AA GAA-- AGG GT A- CAAGAT
9 AACTCAGGAGGTGGAGGTTG TGAGGCA GAG TCACTT CTCAGG TGGAG TGCAGTG GC

CAGTGAGCCAAGATGCACCA ACTCTGT CTC AGTGAG GGGTCC ACCTC ACGTCAC CG

CTGCACTCCAGCCTGGGCAA - AG ACAAC G-- -- CA ------
CAGAGTGAGACTCTGTCTCA
GAM33708 10659 GGAGGGGCCAGGAGGAAATG CC- A CT TGA ACA
0 ATGAGTCTTAGTGATCTGGA GGAGGGG AGGAGGA ATGATGAGT TAG TCTGGAA
AACATTCCAGACTAATTTAT CTTCCCT TTCTCTT TATTATTTA ATC AGACCTT
TATCTTCTCTTTTTTCCCTT TTT C -- --- ---
C
GAM33708 11061 TGAGGCAGGAAAATCGCTTG AAAATC GAA-- A A- GT CA- ATA
1 AACCCAAGGCAGAGGTTGCA TGAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG

GTCAGCAGATATTGCACCAC ACTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
TGCACTCCAGCCTGGGCAAC CAGAA- ACAAC - AC -- CCA ---
AAAGCAAGACTCTGCCTCA
GAM33708 10323 GAGGCAGGAAAATCGCTTGA AAAATC GAA-- A A- GT CA- ATA
2 ACCCAAGGCAGAGGTTGCAG GAGGCAGG GCTT CCCA GGC GAG TGCAGT GCAG

TCAGCAGATATTGCACCACT CTCCGTCT CGAA GGGT CCG CTC ACGTCA CGTT
GCACTCCAGCCTGGGCAACA CAGAA- ACAAC - AC -- CCA ---
AAGCAAGACTCTGCCTC
GAM33708 10737 GGGAGGATTGCTTGAGCCTG G GC--- A- AA CC A- TATCATT
3 GAAGCTGGAGCCTGCAGTGA GG AGGATT TTG GCCTGG GCTGGAG TGCAGTG AC

ACTATCATTGTGCCACTGTA CT TCCTAA AAC CGGATC CGACCTC ATGTCAC TG
CTCCAGCCTAGGCAACAAAA G AGTAA AA -- -- CG -------
TGAAATCCTGTC
GAM33708 9707 AGGATTGCTTGAGCCTGGAA GC--- A- AA CC A- TATCATT
4 GCTGGAGCCTGCAGTGAACT AGGATT TTG GCCTGG GCTGGAG TGCAGTG AC
ATCATTGTGCCACTGTACTC TCCTAA AAC CGGATC CGACCTC ATGTCAC TG
CAGCCTAGGCAACAAAATGA AGTAA AA -- -- CG -------
AATCCT
GAM33708 10437 GCAGGAGGATTGCTTGAGCC AGGA GA-- AGT---------- A ACAATG
7 CAGGAGTTCAAGGCTACAAT GCAGG TTGCTT GCCCAGG TCA GGCT
GAGCTATGATCACACTACTA TGTCC AACGAG CGGGTCC AGT TCGA
CACTCCAGCCTGGGCAACAG CAG- ACAA GACCTCACATCATCACACT A ------
AGCAAGACCCTGT
GAM33708 9750 AGTCCTCTTATGCTGTTGAC CTTA CATTT GTGA ATT CTTT
8 ATTTCCCCATGTGATGCTAT AGTCCT TGCTGTTGA CCCCAT TGCT GCTTCT
TGCTTCTCTTTGGAGGCTAA TCGGGA ACGACAATT GGGGTA ACGA CGGAGG

GCAGTAAATGGGGTTAACAG ---- ----- AATG AT- ----
CAAGGGCT
GAM33708 11154 TGCTGTTGACATTTCCCCAT CATTT GTGA ATT CTTT
9 GTGATGCTATTGCTTCTCTT TGCTGTTGA CCCCAT TGCT GCTTCT
TGGAGGCTAAGCAGTAAATG ACGACAATT GGGGTA ACGA CGGAGG
GGGTTAACAGCA ----- AATG AT- ----
GAM33709 11103 TGAGGCAGGAGAATGGCGTG A AATG G- AA- AGGC CT A - AGAT
1 AACCCGGGAGGCGGAGCTTG TGAGGC GGAG GC TG CCCGGG GGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC TG AC GGGTCC CCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AGAG AG AAC GA-- -- - C ----
ACAGAGTGAGACTCCGTCTC
A
GAM33709 9832 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33709 10759 GGGGCTTCTTCCCTGGCAGG TCTTCCC A GAT AACTA CACCAAC
3 ATTCCTGGGATTTCAAACTA GGGGCT TGGCAGG TTCCTGG TTCA CCT
CCTCACCAACAGGACGCTGA CCCCGG ACCGTCC GAGGACC AAGT GGA
ACCAGGAGCCTGCCACCCAA TCAACCC - --- CGCA- -------
CTGGCCCC
GAM33709 9833 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33709 10511 GCTTGGCATCAGTTTCATTT TCAGTTTC AAA ATA GCATCA
5 TGCAAAACATGGCTTTGATA GCTTGGCA ATTTTGC ACATGGCTTTG ATT
ATTGCATCAGATCTGCAAGG TGAACCGT TAAGACG TGTGTCGGAAC TAG
CTGTGTAGGCAGAATTCTTA TATTCT-- GA- GTC ------
TTGCCAAGT
GAM33709 10329 GAGGCAGGAGAATCACTTGA G AA A GA--- CGG G A A CGAGATCAT
6 ACCCGGGAGGCTGAGGGTAC GAGGCAG AG TC CTT ACC GAGGCT AGGGT CAGTG GC

AGTGAGCCGAGATCATGCCA CTCTGTC TC AG GAA TGG CTCCGA TCTCA GTCAC CG

CTGCACTCTAGCCTCGGTGA - AG - GCCAG --- - C - ---------
CCGAAGGAGACTCTGTCTC
GAM33709 10473 GCTAGTGTGGACACACAGCT G A- ACA -- CA C-- ATAGT
7 CTTGGAAAGCATGTACATTT GCTA TGTGG CAC GCTCTT GGAAAG TGTA ATTTGGAGGAT

GGAGGATATAGTGTCTTCTA CGGT ACATT GTG TGAGAG TCTTTC ATAT TAAATCTTCTG

AATAATTATACACTTTCTAT G CG GGA TA AC TAA -----
GAGAGTAGGGTGGCTTACAG
TGGC
GAM33709 11027 TCTTTTCTTTGGTAGGCTAG TTTCTTT CTA TTCG A TTACCCTCCCCA A CTTTT

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8          CCTTCGAGACTGCATTACCC TCT      GGTAGG  GCC   AG CTGCA        ACTT AAAT    GATAACCC
           TCCCCAACTTAAAATCTTTT AGA      CTATTT  CGG   TC GATGT        TGAA TTTA    CTATTGGG
           GATAACCCAGGCAGCTGGGT  T------     A--  TATG -   TGTTTTTC----   A   ACCC-
           TATCCCCAATTTAAAGTCTT  GCAG
           TTTGTTGTAGCTGTATGGCA AG
           TTTATCTAGA         TC
                      ----
GAM33709 9834   AGTTTTAGGGTACATGTGCA    TTA   A  T TG  -    - G  T   T  ATAT
9          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA    TTA   C - GT   G    C  G  C  - ----
           CT
GAM33710 10512  GCTTGGTATGCTCAGAAGCT       T  T    CTGCT   --       CA   G   AATTTCTTG
0          GCTAAAGTGTGTATGGGCAG GCTTGGTA GC CAGAAG    AAAGT  GTGTATGGG  GGTGT GGGGC

           GTGTGGGGGCAATTTCTTGG TGAATCGT CG GTCTTT    TTTCA  TATATACCT  TCACG TCCTG

           TCCTAGCACTTCCATATATC       - -    TC---    GC       --    A    ---------
           GACTTTCTTTTCTGGCTGCT
           AAGT
GAM33710 10805  GTAGAGAACCTCATCATGAG      AA-     -----       ------ TG   A    TTAG
1          ATTTGAGAATAGCTTTAGAG GTAGAG   CCTCAT    CATGAGAT     T  AGA TAGCT
           TTACTCTTGGGATAGTGTCT CATCTC   GGAGTG    GTACTCTG     G  TCT ATTGA
           CATGGCCCTGTGAGGGAACT      AAG     TCCCG       TGATAG GT   C    ----
           CTAC
GAM33710 10747  GGGCCAAAAATTCAAGATGC   CCAAAAA   GA-  TC   G    GT-    GGG  T    AACC
5          TCATTTGCAAGTTGTCTTCT GGG      TTCAA   TGC  ATTT CAAGTT   CTTCTA   TGT GCCTG
           AGGGTGTTGCCTGAACCTAG CCC      AAGTT   GCG  TGGA GTTCGG   GAAGAT   ACG CGGAT

           GCTGCAGTAGAAGTGGGGCT   TA-----    ATA  GA   G    GGT    G--  T    ----
           TGGAGGTAGGCGATATTGAA
           ATCCC
GAM33710 9966   CAGCTTGCAGCACACACAGC    TT    CAC    A  GT  --  A     CTGCTCT
6          ATTGGTCATGAGGTCAGCTG CAGC  GCAGCA   ACAGC TTG  CA  TG GGTCAG
           CTCTCTGACCCACTTGCTCA GTTG  CGTCGT   TGTTG GAC  GT  AC CCAGTC
           GAGTTGTTTGCTGCCTGTTG    TC    T--    A   TC  TC  -    -------
GAM33710 9967   CAGCTTGCAGCACACACAGC    TT    CAC    A  GT  --  A     CTGCTCT
8          ATTGGTCATGAGGTCAGCTG CAGC  GCAGCA   ACAGC TTG  CA  TG GGTCAG
           CTCTCTGACCCACTTGCTCA GTTG  CGTCGT   TGTTG GAC  GT  AC CCAGTC
           GAGTTGTTTGCTGCCTGTTG    TC    T--    A   TC  TC  -    -------
GAM33710 10751  GGGCTGGGCAAGATGGCTCA      GCA-   -----    T  TT  AG    GTA    GAGG
9          TGTTTGTAGTCTCAGTACTT GGGCTGG   AGAT    GGCTCA GT  GT  TCTCA   CTTTGG
           TGGGAGGCCAAAGATGGGAG TCCGACC   TTTG    CCGAGT CG  TA  AGGGT   GAAACC
           GATTGCTTGAGCCCGTGAGT      AGAG   AGTGC    T  T-  GG    A--     ----
           TTGAGACCAGCCT
GAM33711 9835   AGTTTTAGGGTACATGTGCA    TTA   A  T TG  -    - G  T   T  ATAT
0          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
           TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
           TGGTGTGCTGCACCCATTAA    TTA   C - GT   G    C  G  C  - ----
           CT
```

GAM33711 10301 GAGATGGGAGAATCACTTAA G AA A AA-- AAT C A ATGACTG
1 GCCCAGGAATTTGAGGCTGC GAGATGG AG TC CTT GCCCAGG TTGAGG TGCAGTG GCA

AGTGAGCAATGACTGTGCCA CTTTACT TC GG GAG TGGGTCC GACTTC ATGTCAC CGT

CTGTACTTCAGCCTGGGTAA - AG - ACAA --- - - -------
CAGAGGGGACTTCATTTC
GAM33711 10548 GGAGAATCACTTAAGCCCAG AA A AA-- AAT C A ATGACTG
2 GAATTTGAGGCTGCAGTGAG GGAG TC CTT GCCCAGG TTGAGG TGCAGTG GCA
CAATGACTGTGCCACTGTAC CTTC GG GAG TGGGTCC GACTTC ATGTCAC CGT
TTCAGCCTGGGTAACAGAGG AG - ACAA --- - - -------
GGACTTC
GAM33711 10248 GAATCACTTAAGCCCAGGAA - A- AA-- AAT C A ATGACTG
3 TTTGAGGCTGCAGTGAGCAA GAA TC CTT GCCCAGG TTGAGG TGCAGTG GCA
TGACTGTGCCACTGTACTTC CTT AG GAG TGGGTCC GACTTC ATGTCAC CGT
AGCCTGGGTAACAGAGGGGA C GG ACAA --- - - -------
CTTC
GAM33711 9726 AGGCTGGGAACATTCAGGGC - - C CA CAAGCCC- T- CAACCC
5 TGCTCAAGCCCAGGGTTGGC AGG CTGG GAA ATT GGGCTGCT AGGG TGG
AACCCCCACTCCCTCCAACA TCC GACC CTT TGA CTCGACGA TCCC ACC
CAAGCAGCTCAAGTCTTCTC A T C A- ACACAACC TC ------
CAGACCT
GAM33711 10184 CTGTCCTGTAGATACATGGG --- GGG--- A C A - TATAAGCGC
8 GGATGATCATAAGTGAGCTT CTGTCCTGTA GATACAT GG TGAT ATA GTGA GCTTT
TTATAAGCGCAGAGTATTAC GACAGGACAT CTATGTG CC ACTA TAT CATT TGAGA
CTATATCACCGTGAAAGTGT ACG AAAGTG - - C A ---------
ATCGCATACAGGACAG
GAM33711 10784 GGTCTCCCTCTTGCCCAGGC C- - CCC G T T TGCAATCATAGT GC TTCTG

9 TGGAGTGCAGTGATGCAATC GGTCTC CT CTTG AGGCTG AG GCAG GA TCACT AACC

ATAGTTCACTGCAACCTTCT TCAGAG GA GAAC TCCGAC TC CGTC CT AGTGA TTGG
GGGTTCAAGTGATTTTCCTG TT T CC- - - - TTT--------- AC -----
CCTCAGCCTCCCAAGTAGTT
GAGACT
GAM33712 10305 GAGCCATTAATCTCGGGGTC C GG- CTCT AAC ACCTT
6 TCAGCCTCTCTTAACGGACC GAGCCATTAATCT GG TCTCAGC CTT GG
TTCCAGGCACTGCTGAGAAA TTTGGTAATTGGA CC AGAGTCG GGA CC
ACCAGGTTAATGGTTT - AAA TCAC --- -----
GAM33712 11091 TGAGGCAGGAGAATCGCTTG GAGAATC AA-- T AGG GT AGC AGAT
7 AACCTGGCAGGTGGAGGTTG TGAGGCAG GCTTG CC GGC TGGAG TGCAGTG CG

CAGTGAGCCGAGATCGCACC ACTCTGTC CGAAC GG CCG ACCTC ACGTTAC GC
ATTGCACTCCAGCCTGGGCA AAAACA- AACG T --- -- CAC ----
ACAAGCACAAAACTGTCTCA
GAM33712 10344 GAGGCAGGAGAATCGCTTGA GAGAATC AA-- T AGG GT AGC AGAT
8 ACCTGGCAGGTGGAGGTTGC GAGGCAG GCTTG CC GGC TGGAG TGCAGTG CG
AGTGAGCCGAGATCGCACCA CTCTGTC CGAAC GG CCG ACCTC ACGTTAC GC
TTGCACTCCAGCCTGGGCAA AAAACA- AACG T --- -- CAC ----
CAAGCACAAAACTGTCTC

GAM33712 10357 GAGGCAGGAGAATGGCGTGA A AATG G- AA- AGGC CT A CGAGATCAT

9 ACCCGGGAGGCGGAGCTTGC GAGGC GGAG GC TG CCCGGG GGAG TGCAGTG GC

AGTGAGCCGAGATCATGCCA CTCTG CCTC CG AC GGGTCC CCTC ACGTCAC CG
CTGCACTCCAGCCTGGGCAA - AGAG AG AAC GA-- -- - ---------
CAGAGCGAGACTCCGTCTC
GAM33713 10554 GGAGAATCACTTGAACCCAG AA GAA--- AGG GT A- TGAGATT
0 GAGGTGGAGGTTGTAGTGAG GGAG TCACTT CCCAGG TGGAG TGTAGTG GC
CTGAGATTGCACCACTGCAC CCTC AGTGAG GGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGCGATAAGAG AA AATAGC G-- -- CA -------
TGAAACTCC
GAM33713 11117 TGAGGCGCCCTGAAAACATA A CC AAAA - CT AGAT ---- CAGAAGTATC
1 GGCTGGGCTTGTGTGAGATG TG GGCGC TG CAT AGGCTGGG TGTGTG GGGAGAA AGAC

GGAGAAAGACCAGAAGTATC AC TCGTG AC GTA TTCGACCT ACACAC CCCTCTT TCTG

GTCTAAACTTCTCCCTGCCC A TC G--- C -- CCGT CAAA ----------
ACACATCCAGCTTCATGGCA
CTGTGCTACA
GAM33713 9963 CAGCGCGGCTCCCGCCACCC CG ---- G AC- ---- TTG A - GA ----
3 TCAATAAATGTTGCTTGGAG CAGCG GCTC CC CC CCTCAAT AAATG CTTGG GTGGA CC
GGCT CT
TGGACCGAGGCTCTGCAGGA GTCGT TGAG GG GG GGAGTTG TTTAT GGACC CGCCT GG
CCGG GA
ATGCAGGGAGGGCCGGGCTC CT TGTT A ACA AATC TG- C C G- GAGG
CGCCCCAGGGTTATTTCTAA GGAA
GTTGAGGACAGGAGGTTGTG GCA
AGTTCTGCTG CGT

GAM33713 10469 GCTAGGATTGCACCACTGCA A -------- CCAA CA AGCAAGACC
5 CTCCAACCTGGACAACAGAG GCT GGATTGCA CCACTGCACT CCTGGA ACAG
CAAGACCCTGTCTCTAGGCC CGA CCTAATGT GGTGACGTGG GGATCT TGTC
AGGTGCAGTGGCTCACACCT C CCACACTC ACC- C- ---------
GTAATCCCAGC
GAM33713 10935 TCACATTCTCCATAACTGGA CA TAA G - - -- A ACCA G GGA
6 TATGAGGGAAGCATGGGACC TCA TTCTCCA CTG ATA TGAGG GA AGC TGGG TGATCCCTG AG

ATGATCCCTGGAGGGACTGC AGT AAGAGGT GAC TGT ACTCT CT TCG ACCC GTTAGGGAC TC

AGGGATTGCCCACGCTAGTC CA C-- A C A GA C ---- G ---
ATCTCACTGTACAGCTGGAG
AAACTGA
GAM33713 10293 GAGACCTCTATCTATAAAAA C--- A AAAAAATG ---- A A AGACT AATGA
8 ATGAGGCAGGAGTTGGCAAG GAGAC TCT TCTAT AGGCAGGAGT TGGCA G GGTCA GC

AGGTCAAGACTGCAATGAGC CTCTG AGA GGGTA TCCGTCCTCA ACCGT C CTAGT CG

CATGATCCTGCCACTATACT TCCC - GTGGG--- TATC - - AC--- -----
CCTGCCTGGGTGATGGGAGA

CCCTGTCTC
GAM33714 9964 CAGCGCGGCTCCCGCCACCC CG ---- G AC- ---- TTG A - GA ----
0 TCAATAAATGTTGCTTGGAG CAGCG GCTC CC CC CCTCAAT AAATG CTTGG GTGGA CC
GGCT CT
TGGACCGAGGCTCTGCAGGA GTCGT TGAG GG GG GGAGTTG TTTAT GGACC CGCCT GG
CCGG GA
ATGCAGGGAGGGCCGGGCTC CT TGTT A ACA AATC TG- C C G- GAGG
CGCCCCAGGGTTATTTCTAA GGAA
GTTGAGGACAGGAGGTTGTG GCA
AGTTCTGCTG CGT

GAM33714 10470 GCTAGGATTGCACCACTGCA A -------- CCAA CA AGCAAGACC
3 CTCCAACCTGGACAACAGAG GCT GGATTGCA CCACTGCACT CCTGGA ACAG
CAAGACCCTGTCTCTAGGCC CGA CCTAATGT GGTGACGTGG GGATCT TGTC
AGGTGCAGTGGCTCACACCT C CCACACTC ACC- C- ---------
GTAATCCCAGC
GAM33714 10014 CCCACAGGTGATTCTGTTGT GT- T T C G TG AGGCT
4 GCAGCCATGGTTGGCAGGCT CCCACAG GAT CTGTTG GCAGC AT GT GC
GTTCACGGTGCTGTTCAACA GGGTGTC CTG GACAAC TGTCG TG CA TG
GGTCCTGCTGTGGG GTC - T - G CT -----
GAM33714 11217 TGTGCCTGCCCCAATCTTGT - ----- -- TG TTTAT - CACCTGTA
5 GTTTTATTGCTGGCCACCTG TGTGC CTGC CCCA ATCTTG T TGC TGGC
TAGCCAGGCACTGTGCAGGA ACATG GACG GGGT TAGGAC G ACG ACCG
TGATGGGATCCAGCAGTGTA T ACCTA AG GT TC--- G --------
CA
GAM33714 11041 TGAGACAGAAGAATCGCTTG A AA TGAA GGC A T A- TGAGATT
6 AACTCGGGCGGCGGAAGTTG TGAGACAGA G TCGCT CTCGGGC GGA GT GCAGTG GC

CAGTGAGCTGAGATTGCACC ACTCTGTCT C AGTGA GGGTCCG CCT CA CGTCAC CG

ACTGCACTCCAGCCTGGGCA - AG CAAC A-- - - CA -------
ACAGTGAGACTCTGTCTCA
GAM33714 10281 GAGACAGAAGAATCGCTTGA A AA TGAA GGC A T A- TGAGATT
7 ACTCGGGCGGCGGAAGTTGC GAGACAGA G TCGCT CTCGGGC GGA GT GCAGTG GC

AGTGAGCTGAGATTGCACCA CTCTGTCT C AGTGA GGGTCCG CCT CA CGTCAC CG
CTGCACTCCAGCCTGGGCAA - AG CAAC A-- - - CA -------
CAGTGAGACTCTGTCTC
GAM33714 11004 TCGCTTGAACTCGGGCGGCG TGAA GGC A T A- TGAGATT
8 GAAGTTGCAGTGAGCTGAGA TCGCT CTCGGGC GGA GT GCAGTG GC
TTGCACCACTGCACTCCAGC AGTGA GGGTCCG CCT CA CGTCAC CG
CTGGGCAACAGTGA CAAC A-- - - CA -------
GAM33714 9600 AAATTTTGGGGGAATTTTAC - AT AGA C-- TCTA
9 TGCCCTAGAGGACTGGTTCT AAATTTTG GGGGA TTTACTGCCCT GGA TGGT
AGCCACTTTCCCAGGGCAGT TTTGAAAC TCTCT AGGTGACGGGA CCT ACCG
GGATCTCTGCAAAGTTT G -- C-- TTC ----
GAM33715 10471 GCTAGGATTGCACCACTGCA A -------- CCAA CA AGCAAGACC
0 CTCCAACCTGGACAACAGAG GCT GGATTGCA CCACTGCACT CCTGGA ACAG
CAAGACCCTGTCTCTAGGCC CGA CCTAATGT GGTGACGTGG GGATCT TGTC
AGGTGCAGTGGCTCACACCT C CCACACTC ACC- C- ---------

GTAATCCCAGC
GAM33715 10335 GAGGCAGGAGAATCATTTGA AG AA A- A- AAG GT - CAAGATC
1 ACCTGGGAAGTGGAGGTTGC GAGGC GAG TC TTTG ACCTGGG TGGAG TGCAGTGA GC

AGTGAGCCAAGATCGTGTCA CTCTG CTC AG AAAT TGGATCC ATCTC ACGTCACT TG
CTGCACTCTAGCCTAGGTGA A- AG CG AG G-- -- G -------
TAAAGCGAGACTCAGTCTC
GAM33715 10429 GCACAGTGAGAGAAACAGAC AGAGAA CC CCT T GTGCAAGGA
2 TCCACCACACCTTCTTGGCT GCACAGTG ACAGACTCCA ACA TCT GGCT
GTGCAAGGAAGTCAGATGAT CGTGTCAT TGTCTGAGGT TGT AGA CTGA
GTTGGAGTCTGTGCTACTGT CG---- -- AGT - ---------
GC
GAM33715 10384 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

3 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
GGGGAGCAGAGCTAGACTCT
GTCTC
GAM33715 11078 TGAGGCAGGAGAATCACTTG CA AA A GAA-- AGG GT A- TGAGATT
4 AACCCGGGAGGTGGAGGTTG TGAGG GGAG TC CTT CCCGGG TGGAG TGCAGTG GC

CAGTGAGCTGAGATTGCGCC ACTCT CCTC AG GAG GGGTCC ACCTC ACGTCAC CG

ACTGCACTCCAGCCTGGGCA A- AG C ACAAC G-- -- CG -------
ACAGAGCGAGACTCCATCTC
A
GAM33715 10330 GAGGCAGGAGAATCACTTGA CA AA A GAA-- AGG GT A- TGAGATT
5 ACCCGGGAGGTGGAGGTTGC GAGG GGAG TC CTT CCCGGG TGGAG TGCAGTG GC

AGTGAGCTGAGATTGCGCCA CTCT CCTC AG GAG GGGTCC ACCTC ACGTCAC CG
CTGCACTCCAGCCTGGGCAA A- AG C ACAAC G-- -- CG -------
CAGAGCGAGACTCCATCTC
GAM33715 10559 GGAGAATCACTTGAACCCGG AA A GAA-- AGG GT A- TGAGATT
6 GAGGTGGAGGTTGCAGTGAG GGAG TC CTT CCCGGG TGGAG TGCAGTG GC
CTGAGATTGCGCCACTGCAC CCTC AG GAG GGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGC AG C ACAAC G-- -- CG -------
GAGACTCC
GAM33715 10646 GGAGAATTGCTTGCACCCAG AA - - AGGCA - T T GC AGAT
7 GAGGCAGAGGTTGTGGTGAG GGAG TTGCT TG CACCCAGG GAG GT GTGG GA TG
CTGAGATCGTCCCATTGCAC CCTC AGCGG AC GTGGGTCC CTC CG TACC CT GC
TCCAGCCTGGGTGACAGGGC AA G A GAC-- A T - -- ----
GAAACTCC
GAM33715 10666 GGATGGTTTGGGGAAGAGAA GG GGA G AT T - GA--- CAGA
8 TGTGCATGGATCGCTCAGAA GGAT TTTGG AGAGAAT TGCATGG CGC CAGA ACT CC

CTGACCCAGAGGCAATGAGT CCTG AAACC TCTCTTA GTGTACC GTG GTTT TGA GG
ATTTGTGTGCCATGTGGATT TA --- G -- T A GTAAC ----
CTCTCCAAAATGTCC

GAM33715 9836 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33716 10283 GAGACAGGAGAATCACTTGA CA AA GAA-- A- CAAA T - CAAGATC
0 ATCCGGGAGGCAAAGGTTGC GAGA GGAG TCACTT TCCGGG GG GGT GCAGTG TGT

AGTGTGTCAAGATCACACCA CTCT CTTC AGTGAG GGGTCC CC TCA CGTCAC ACA
CTGCACTCCAGCCTGGGCAA A- AG ACAAC GA ---- - C -------
CAGAGTGAGACTTCATCTC
GAM33716 10882 GTTATGAAGCTTGTAGGGGG - AAG G A CCAC AGACC AGGT
1 TTTAGCTCCACAGGGTCAGA GTT ATG CTT TAGGGGGTTT GCT AGGGTC TGC
CCTGCAGGTGCAAACAGGCC CAG TGC GGA GTCCCCCAAG CGG TCCCGG ACG
CTAGGCGAACCCCCTGGAGG T AAA G - A--- ACAA- ----
AAACGTTGAC
GAM33716 10614 GGAGAATGGCATGAACCCGG AATG A- AA- AGG CT A AGAGATCAC
2 GAGGTGGAGCTTGCAGTGAG GGAG GC TG CCCGGG TGGAG TGCAGTG GC
CAGAGATCACGCCACTGCAC CCTC CG AC GGGTCC ACCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGC AGAG AG AAC G-- -- - ---------
GAGACTCC
GAM33716 10385 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

6 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
GGGGAGCAGAGCTAGACTCT
GTCTC
GAM33716 10527 GGAATAAGAAAGGCAACGTT AAA-- - --- T ATT A AACTAA
7 TTGCAGCTTCCAAATTTCTG GGAATAAG GGCAACGTTTTG C AGCT CCAA TCTGA GA

AAGAAACTAATCTCAGATTG CCTTATTT CCGTTGTAAAAC G TTGA GGTT AGACT CT
GCAGTTAAAGTCAAAATGTT ATAAA T AAA C --- - ------
GCCAAATATTTATTCC
GAM33716 10835 GTCTGGCATTCCCTAGTGAG G - TA- ATGAACC GT CTC AAATGCAGAAATCAC

8 ATGAACCCGGTACCTCAGAT GTCTG CA TTCCC GTGAG CG AC AGATGG
GGAAATGCAGAAATCACCCA CAGAT GT GAGGG TACTC GC TG TCTACC
TCTTCTGTGTCGCTCATGCT - C TCG ------- TG TCT ----------
GGGAGCTGTAGAC
GAM33716 10251 GAATGATTTGAAGGGGGCAG GA TG GG TCAG G - A- GGTCTG
9 TCAGAGAAGTAGGAATATCA GAAT TT AAG GGCAG AGAA TAGGA ATATC GGAGTGGT

GGAGTGGTGGTCTGATTACT CTTA AA TTC TTGTT TCTT GTTCT TGTAG TCTCATTA
CTGAGATGTGTCTTGATTCT -- GT TT TTA- A G AG ------
ATTTTGTTTTCTTTGAAATT
C
GAM33717 10192 CTGTTGTTAAAACCTGCTTC T TTAAA CC A CT CATCAGCCATCCA
0 CCCACTGCTCAGCCTGCCAT CTG TG ACCTGCTT CCACTGCTC GC GC

CAGCCATCCAGCTGCAGAGC GAC AC TGGATGAG GGTGACGAG CG CG
AGTGGAGAGTAGGTCTCACC C TC--- A- A T- ----------
AG
GAM33717 10386 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

1 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
GGGGAGCAGAGCTAGACTCT
GTCTC
GAM33717 11201 TGGTTGAGGCCAGGAATTCG CA-- A AGACA GCAACAAA-- - TCCCA
2 AGACAAGTCTGGGCAACAAA TGGTTGAGGC GGA TTCG AGTCTGG GT GAGA
GTGAGATCCCATCTCTACAA ATCGACTCCG CCT GGGT TCAGACC CA CTCT
AAAATTAGCCAGACTGGTGG ATTC C GG--- GATTAAAAAA T -----
GCTCCCTTAGCCTCAGCTA
GAM33717 9936 CAATGGGGGACATTTGCCAA T - CCAA T CTGT A GAGAGGT
3 GAGTTGAGAATGCTGTAATT CAA GGGGGACA TTTG GAGT GAGAATG AATTGG GGCCT

GGAGGCCTGAGAGGTGGGTC GTT TCCTCTGT AAAC CTTA CTTTTAC TTAACC CTGGG

CCAATTCTTACATTTTCCAT T C AC-- C ATTC - -------
TCCACAAACTGTCTCCTTTT
G
GAM33717 9760 AGTGGCAGGTGTGCAAATCA GT CAAA - - CCCAAACTA
4 CAACTTGGCCTCCCAAACTA AGTGGCAG GTG TCACAACTT G GCCT
AGGTACAAAGTTGTGAGTCA TCACCGTC CAC AGTGTTGAA C TGGA
CACGTCTGCCACT TG ACTG A A ---------
GAM33717 10750 GGGCTGACTTGGACTCTGAA T G CTCTGAA TT G C - AGT
7 ATGTTAAGCAACTTGCTCTC GGGC GACTT GA ATG AAGCAACTT CT TC CAGG
CAGGAGTCCTGTGAAGAAGT CCCG CTGAA TT TAC TTCGTTGAA GA AG GTCC
TGCTTCATCCTTTTGAAGTC T G TTCC--- -- - - T ---
TGCCC
GAM33717 11163 TGGAGCTGAGATTCTGTGGG AG G TT G GT AG - TGTGGGCT
9 TGAGAGAGTGGGAGAGTGTC TGG CT AGA CTGTGGGT AGAGA GGG AGTG TC
TGTGGGCTGAGCACTGGTCC ACC GG TCT GACACTCA TCTTT CCT TCAC AG
TTTCTGACTCACAGCTCTGG CG G C- G -- GG G --------
GGCCCA
GAM33718 9991 CCAATCCCCAACCCCTGCAG T C---------- T- GATTAT A- C ATGACTTA
0 TGCTTTGATTATGAGAAAGT CCAA CCCCAACCC TGCAG GCTTT GAGA AGTT TGC
TCTGCATGACTTAGCATAAC GGTT GGGGTTGGG ACGTC CGAAA TTCT TCAA ACG
TGCTCTTTTCTAAAAGCCTC T AAACCTAGATTA TC ATCTT- CG T --------
TGCAATTAGATCCAAAGGGT
TGGGGTTTGG
GAM33718 10011 CCCAACCCCTGCAGTGCTTT C---------- T- GATTAT A- C ATGACTTA
1 GATTATGAGAAAGTTCTGCA CCCAACCC TGCAG GCTTT GAGA AGTT TGC
TGACTTAGCATAACTGCTCT GGGTTGGG ACGTC CGAAA TTCT TCAA ACG
TTTCTAAAAGCCTCTGCAAT AAACCTAGATTA TC ATCTT- CG T --------
TAGATCCAAAGGGTTGGG
GAM33718 10639 GGAGAATTGCTTGAACCTGG GAA GAA-- TG AGGCA GT A - AGAT

3 GAGGCAGAGGTTGCAGTGAG GGA TTGCTT CC GG GAG TGCAGTG GC TG
CTGAGATCACGCCATTGCAC CCT AGCGAG GG CC CTC ACGTTAC CG AC
TCCAGCCTGGGCAACAGAGC AAG ACAAC GT GAC-- -- - C ----
GAGAATCC
GAM33718 10821 GTCCATCCTTTGAACATGAC CCTT ATGAC G- T T GTTCTC - GCTAATAA
4 TCCTGGTGTGTTAGTCTAGT GTCCAT TGAAC TCCT GTG GTTAG CTAGTCT ATG CT
CTGTTCTCATGCTGCTAATA CAGGTA ATTTG AGGA TAT TAATC GGTCAGA TAC GA
AAGACATACCTGAGACTGGC ---- GAGAA AA T - GTCCA- A --------
TAATTTATAAAGGAAAGAGG
TTTAATGGAC
GAM33718 10340 GAGGCAGGAGAATCGCTTGA CA AA GAA--- AAG TT A C GATC
5 ACCCGGGAAGTGGAGGTTGC GAGG GGAG TCGCTT CCCGGG TGGAGG GCAGTG GC GA

AGTGAGCCGAGATCTTGCCA CTCT CCTC AGTGAG GGGTCC ACCTCT TGTTAC CG TT

TTGTTCTCCAGCCTGGGCGA A- AA AACAGC G-- -- - - ----
CAAGAGTGAAACTCCATCTC
GAM33718 10589 GGAGAATCGCTTGAACCCGG AA GAA--- AAG TT A C GATC
6 GAAGTGGAGGTTGCAGTGAG GGAG TCGCTT CCCGGG TGGAGG GCAGTG GC GA

CCGAGATCTTGCCATTGTTC CCTC AGTGAG GGGTCC ACCTCT TGTTAC CG TT
TCCAGCCTGGGCGACAAGAG AA AACAGC G-- -- - - ----
TGAAACTCC
GAM33718 10391 GAGGGAGCCACGGTCAGATT C CAG T - TTCA TT TCT
7 TCAAGTGGTCATTTCACTCT GAGGGAG CACGGT ATT CAAGT GGTCAT CTC TCTCCC

TTCTCCCTCTGGGGGACTGA CTCCCTC GTGTTA TAA GTTCA TTAGTA GAG AGGGGG

GACATGATTAACTTGCAATA A A-- C A CA-- TC ---
ATTGTGACTCCCTC
GAM33718 10704 GGCTAAGTCATGAGAATTGC TA ATGAGAA GAA-- ATC - ----- GAGCCGAG
8 TTGAACCCAGGCATCGGAGG GGC AGTC TTGCTT CCCAGGC GGAG GT TGCAGT
TTGCAGTGAGCCGAGATTGC CTG TCAG AGCGAG GGGTCCG CCTC CG ACGTTA
ACCAATGCACTCCAGCCTGG CC ------- ACAGC A-- A TAACC --------
GCGACAGAGCGAGACTCCGT
C
GAM33718 10275 GAGAATTGCTTGAACCCAGG AA GAA-- ATC - ----- GAGCCGAG
9 CATCGGAGGTTGCAGTGAGC GAG TTGCTT CCCAGGC GGAG GT TGCAGT
CGAGATTGCACCAATGCACT CTC AGCGAG GGGTCCG CCTC CG ACGTTA
CCAGCCTGGGCGACAGAGCG AG ACAGC A-- A TAACC --------
AGACTC
GAM33719 11251 TTCTGCTGTCTATTATGAGT CT--- - - C C CTG GAAGGA
0 CTGACTGGCACAGACATCTG TTCTG GTCTAT TATG AGT TGACTGGCACAGA AT TCAAGGAA

TCAAGGAAGAAGGATTCTTT AAGAC CAGGTA ATAC TCA ACTGACTGTGTTT TG AGTTTCTT

GAGCGTATTTGTGTCAGTCA AACAC T G - A CG- ------
ACTGCATATATGGACCACAA
CAGAA
GAM33719 10780 GGTCAGTGCTTTAAGTGAAT A - AAGT A AG AATC GGAATTTGA

1 CTACTCAGAGCTGTGAAATC GGTC GTG CTTT GAATCT CTC AGCTGTGA TTGGG
TTGGGGGAATTTGACCCAGT TCGG TAT GGAA CTTGGA GAG TTGACACT GACCC
CACAGTTGAGAGAAGGTTCT G A GGT- A AG ---- ---------
GGAAGGATATGGGCT
GAM33719 9837 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33719 10978 TCCCTGTCCTGTCTTCGAGT CC C GA A TAA GGG GATCGA
3 ATTTGTTTTTAATGCTGGGT TCCCTGT TGT TTC GT TTTGTTTT TGCT TGTC
GTCGATCGAGACAACAAGCG GGGGGCA ACG AGG CG AAACGAGA GCGA ACAG
CTCAGAGCAAAGCAAGGATG TT T AA - CTC ACA ------
CATTACGGGGG
GAM33719 11150 TGCTGCATCCTGCCTGGCTC C C - --- - A CCTC - ATTTT GACAACAA
4 CCAGGAGGCCTCTCTCAGCA TGCTG AT CT GCCTGG CTC CCAGG GG TCT CAGC CT

TTTTCTGACAACAAAGCCGG ACGAC TA GA CGGACC GAG GGTCC CT AGA GTCG GA
GGCTGCAGATCCCTGGTGAG - C T TTA T - ---- C GGGCC --------
ATTCCAGGCTAGCATCAGCA
GAM33719 10487 GCTGCATCCTGCCTGGCTCC C C - --- - A CCTC - ATTTT GACAACAA
5 CAGGAGGCCTCTCTCAGCAT GCTG AT CT GCCTGG CTC CCAGG GG TCT CAGC CT
TTTCTGACAACAAAGCCGGG CGAC TA GA CGGACC GAG GGTCC CT AGA GTCG GA
GCTGCAGATCCCTGGTGAGA - C T TTA T - ---- C GGGCC --------
TTCCAGGCTAGCATCAGC
GAM33719 9838 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33719 10647 GGAGAATTGTTTGAACCCAC AA GAA--- CAT - AC - TGATACC
7 ATGGCGGAGACTGCGGTGAG GGAG TTGTTT CCCA GGC GGAG TGCGGTGA GC
CTGATACCGCGTCATTGCAC CCTC AACGAG GGGT CCG CCTC ACGTTACT CG
TCCAGCCTGGGCAACAAGAG AA AACAAC --- A -- G -------
CAAAACTCC
GAM33719 9731 AGGGAAAAAATTCATAATTC -- T AAT GA---- TC TC -- CGCCTTTC
9 AGACAGGCTCTCGGGGCTTC AGGGAAAA AAT CAT TCA CAGGCTC GGGGCT ACCA TACAA

ACCATACAACGCCTTTCTTG TCTCTTTT TTA GTA AGT GTCCGGG TTTTGA TGGT ATGTT

TATTTGGTTAGTTTTATGGG AA T CC- TGTGAG TA T- TT --------
CCTGGAGTGTTGACCATGTA
TTAATTTTCTCT
GAM33720 9674 AGAGGATTGCTTGAGCCCAG A A- GA-- --- TCAA T GATCCATG
0 GGAGGTCAAGGCTGCAGTGA AG GG TTGCTT GCCCAGGG AGG GGC GCAGT
TCCATGATTGCGCCCCTGTA TC CC AACGAG CGGGTCTC TCC CCG CGTTA
CTCTGGGCAACAGAGCAAGA - AG ACAA ATG ---- - --------
CCCT
GAM33720 10002 CCAGTATTGTGTGGGGAGTG TA - - TTTT-- TCATCTAA T T TCTTCA
2 TTTTGAGGTCATCTAATGGT CCAG TTGTGTGG GG AGTG GAGG TGG GTTG CTAT

GTTGTCTATTCTTCAGTAGC GGTC AACACACC CT TCGT CTCC ACC CAAC GATG
AACTCCAACACCCTCTACAT C- A A TTACAT CACA---- T - ------
TTGCTATCACCACACAACCT
GG
GAM33720 10593 GGAGAATCGCTTGAACCCGG AA GAA-- AGGCA GT AGC AGAT
3 GAGGCAGAGGTTGCAGTGAG GGAG TCGCTT CCCGGG GAG TGCAGTG CG
CCGAGATCGCACTACTGCAC CCTC AGTGAG GGGTCC CTC ACGTCAT GC
TCCAGCCTGGGCAACAGAGT AG ACAAC GAC-- -- CAC ----
GAGACTCC
GAM33720 9839 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33720 9840 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33720 10964 TCCACTACTGTTGTGGCTTT TACT - C - T CT---- ACTACTTTTC
7 TGCAAATTACTAAATTTCTC TCCAC GTTGT GGCTTTTG AAATTA CTAAATT CT GTG
TGTGACTACTTTTCCATTTC AGGTG TAATA CTGAAAAC TTTGGT GGTTTAA GA TAC
TTAAGTAATTTGGTTGGTTT ---- A C T T ATTCTT ----------
CCAAAAGTCAATAATGTGGA
GAM33720 10096 CTACTGTTGTGGCTTTTGCA TGTTG C - T CT---- ACTACTTTTC
8 AATTACTAAATTTCTCTGTG CTAC TGGCTTTTG AAATTA CTAAATT CT GTG
ACTACTTTTCCATTTCTTAA GGTG ACTGAAAAC TTTGGT GGTTTAA GA TAC
GTAATTTGGTTGGTTTCCAA TAATA C T T ATTCTT ----------
AAGTCAATAATGTGG
GAM33720 9841 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33721 9842 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33721 9843 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33721 9844 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33721 9717 AGGCAGGAGGATCACGTGAG C AC GA---- AGG GC GAA AGAT

3 CCCAGGAGGTGAAGGCTACA AGG AGGAGGATC GT GCCCAGG TGAAG TACAGT GTG

GTGAAGTGAGATCATGCAAC TCT TTCTCTTAG CG CGGGTCC ACTTC ATGTCA TAC
TGTACTTCAGCCTGGGCAAC - AA AGACAA G-- -- ACG ----
AGAGCAAGATTCTCTTTCT

GAM33721 10655 GGAGGATCACGTGAGCCCAG AC GA---- AGG GC GAA AGAT

4 GAGGTGAAGGCTACAGTGAA GGAGGATC GT GCCCAGG TGAAG TACAGT GTG
GTGAGATCATGCAACTGTAC TCTCTTAG CG CGGGTCC ACTTC ATGTCA TAC
TTCAGCCTGGGCAACAGAGC AA AGACAA G-- -- ACG ----
AAGATTCTCT

GAM33721 10311 GAGGATCACGTGAGCCCAGG AC GA---- AGG GC GAA AGAT

5 AGGTGAAGGCTACAGTGAAG GAGGATC GT GCCCAGG TGAAG TACAGT GTG
TGAGATCATGCAACTGTACT CTCTTAG CG CGGGTCC ACTTC ATGTCA TAC
TCAGCCTGGGCAACAGAGCA AA AGACAA G-- -- ACG ----
AGATTCTC

GAM33721 9845 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT

6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT

GAM33721 10036 CCCTGTCAGAGCTCTCCAGA - --------- AGAATA TT AGAT

7 ATATGCTTGTTGGAGATCCT CC CTGT CAGAGCTCTCC TGCTTG GG
TCAGGCAGTAAGGGAGAGTT GG GACA GTTTTGAGAGG ACGGAC CC
TTGCCTCCTTACACAGTGG T CATTCCTCC GAATG- TT ----

GAM33721 9719 AGGCCATCTTAATCGGGGCC - --- AGA C-- TCTCCCCCT

8 AGAGATGACACTCTCCCCCT AGGC CATCTTAAT CGGGGCCAG TGA AC
GTAACTCAGCCTGGCTCTGT TCCG GTAGGGTTA GTCTCGGTC ACT TG
CTATTGGGATGTGCCT T TCT CG- CAA ---------

GAM33722 10260 GACCTCAGGAAAGCTGGGTT CC AAA GAGC -- ATTAA

0 GAGCTGGGCTGAGACAATTA GA TCAGG GCTGGGTT TGGGCTGA GACA
ATGTCTGTCAGCCCAAACCC CT AGTCT CGGCCCAA ACCCGACT CTGT
GGCACTCTGACCTC CC CA- ---- GT -----

GAM33722 10775 GGTACATGTCACTACTGTTC TA T ACT --- ---- TG AACTT CTAT

1 ATAGTCTCTTTGCTGGAACT GG CA GTC ACTG TTCATAGT CTCTTTGC G GGTC
TGGTCCTATGGCCCTACTGG CC GT CGG TGAC AAGTATCG GAGAGACG C CCGG
CAGAGAGGAAGGCTATGAAA GC C ATC CCA GAAG GT ATC-- ----
CCCAGTCTAGGCCTGCGCC

GAM33722 9846 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT

4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT

GAM33722 10141 CTGAGAGGCAGAGGCTTCAG GA- GC A GA ACACCACTGCACTCC

5 TGAGCCGAGGCCACACCACT CT GAGGCAGAG TTC GT GCCGAGGCC
GCACTCCGGCCTTGGTGACA GA CTCCGTCTC GAG CA TGGTTCCGG
GAGACTCTGCCTCGAAAG AAG A- A G- ----------

GAM33722 10813 GTATAACGCAAAACACAATT ACGCAAAA ATTTCTAAATAGT TT GGCA

6 TCTAAATAGTCAAAAGTTTT GTATA CACA CAAAAGTT TCCT
TCCTGGCAAGGAGACTTTTG CGTGT GTGT GTTTTCAG AGGA
TAGACACCTACCCTGTGATC GTCTACTA CCCATCCACAGAT -- ----

```
          ATCTGTGTGC
GAM33722 11067  TGAGGCAGGAAGATCACTTG     C  AAGA     GA--      AGG    GC      ACC  ATTC
7          AGCCCAGGAGGTGGAGGCTG TGAGG AGG    TCACTT    GCCCAGG   TGGAG  TGCAGTG   CAT

          CAGTGACCCATATTCATGCC ACTCT TCC    AGTGAG    CGGGTCC   ACCTC  ACGTCAC   GTA

          ACTGCACTCCAGCCTGGGCA     C  CAG-     ACAA      G--    --      C--  ----
          ACAGAGTGAGACCCTCTCTC
          A
GAM33722 9847   AGTTTTAGGGTACATGTGCA    TTA    A  T TG   -     - G  T   T  ATAT
8          CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
          TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
          TGGTGTGCTGCACCCATTAA     TTA    C  - GT   G     C  G  C   -  ----
          CT
GAM33722 11156  TGCTTCTAGGAACCTCCATC        GAACC   -   A  CCA      T    AGCGTACCAG
9          TCATGCCATGGTGCTTCGAG TGCTTCTAG     TCCA TCTC TG   TGGTGCT CGAGG
          GAGCGTACCAGCCTTGCAGC ACGGAGGTC     GGGT AGGG AC   ACCACGA GTTCC
          ACCACAACAGGGACTGGGCT         -----    C    -  AAC      C     ----------
          GGAGGCA
GAM33723 10063  CCTGCCCACCAACTCCCAGG    CCCACCAA   C-    CTTATTCACCAACCACTC  C    TCTGACC
  CTT     TT
0          CTTATTCACCAACCACTCCA CCTG       CTC  CAGG              CA CAGC      CTGA   CTGGGG
          CCAGCTCTGACCCTGACTTC GGAC       GAG  GTCC              GT GTCG      GACT   GACTCT
          TGGGGTTCCCATCTCAGTCC    CTTCCTAC   AA    CCC---------- C    TGTCC--    CCT     --
          TCAGCCTGTGCTGCTGCCCC CCCA
          CTGAAGAGCATCCTTCCAGG

                      ----
GAM33723 10152  CTGAGTTTCCATAGGGAACT       TCCA----------       TAT       -   -    - T  GAACTA
2          ATTGGGTTTAAAGTCACCGT CTGAGTT           TAGGGAAC   TGGGTTTA AAG TCAC CG TG
          TGGAACTACACTGTGTGATC GACTCGG            GTCCCTTG   ATTCAAAT TTC AGTG GT AC
          TTATAAACTTATGTTCCCTG       TTCTTATACTATCG       T--       A   T    T  C ------
          GCTATCATATTCTTGGCTCA
          G
GAM33723 10664  GGATCGCTTGAGCCCAGGAG   A-     GA--      AGTTC   GC      AGC   GATC
3          TTCGAGGCTGCAGTGAGCTG GG  TCGCTT    GCCCAGG    GAG  TGCAGTG   TGT
          TGATCACACCACTGCACTCC CC  AGCGAG    CGGGTCC    CTC  ACGTCAC   ACA
          AGCCTGGGCAACAGAGCGAG   AG     ACAA      GAC--   --      C--   ----
          ACC
GAM33723 11005  TCGCTTGAGCCCAGGAGTTC      GA--      AGTTC   GC      AGC   GATC
4          GAGGCTGCAGTGAGCTGTGA TCGCTT    GCCCAGG    GAG  TGCAGTG   TGT
          TCACACCACTGCACTCCAGC AGCGAG    CGGGTCC    CTC  ACGTCAC   ACA
          CTGGGCAACAGAGCGA          ACAA      GAC--   --      C--   ----
GAM33723 10087  CGCTTGAGCCCAGGAGTTCG     GA--      AGTTC   GC      AGC   GATC
5          AGGCTGCAGTGAGCTGTGAT CGCTT    GCCCAGG    GAG  TGCAGTG   TGT
          CACACCACTGCACTCCAGCC GCGAG    CGGGTCC    CTC  ACGTCAC   ACA
          TGGGCAACAGAGCG          ACAA      GAC--   --      C--   ----
GAM33723 10360  GAGGCAGGAGAATTGCTTGA     A   AA     GAA--     AAGCA  GT      A  TGAATCAT
7          ACCCAGGAAGCAGAGGTTGC GAGGC GGAG  TTGCTT     CCCAGG     GAG  TGCGGTG GC
```

GGTGAGCTGAATCATGCCAC CTCTG CTTC GACGAG GGGTCC CTC ACGTCAC CG
TGCACTCCAGCCTGGGCAAC - AC ACAAC GAC-- -- - --------
AGAGCAGCACTTCGTCTC
GAM33723 10626 GGAGAATTGCTTGAACCCAG AA GAA-- AAGCA GT A TGAATCAT
8 GAAGCAGAGGTTGCGGTGAG GGAG TTGCTT CCCAGG GAG TGCGGTG GC
CTGAATCATGCCACTGCACT CTTC GACGAG GGGTCC CTC ACGTCAC CG
CCAGCCTGGGCAACAGAGCA AC ACAAC GAC-- -- - --------
GCACTTC
GAM33724 11141 TGCATGCTGGGTAAATCATT C C - AAA T --- - ---- TG ATACAG
2 CTGTCTCATTTGTCTGTTGG TG ATG TG GGT TCAT CTGTC TCATT TGTCT GT GAA
AAATACAGTTCTGGCACTAA AC TAC AC CCG GGTA GACAG AGTGG ATAGA CG CTT
GATATGGTGAACAGACAGAT T A A GA- - ACA T ATCA GT ------
GGAGGCCACAACATTCA
GAM33724 10885 GTTCTCTATGGCTAGGCAGT T-- G C A C-- ---- CATATTTT
3 AAAGAAACAGCACCCTTCAT GTTCTC AT GCTAGG AGT AAGAAA AGCA CCCTT
ATTTTAAGGGACTGTGCTAC TAAGAG TA CGGTTC TTA TTCTTT TCGT GGGAA
ATTTCTTCATTCTTGGCGAT TTT G - C ACA GTCA --------
TTTGAGAAT
GAM33724 10895 GTTTTTACTATAACATATTT TTTT TA TT- A CT A A GGTGAAGG
5 TAGAAAGCTAACAAGCTAGA GT ACTA ACATAT TAGA AG AACA GCT GAGAGAGC
GAGAGCGGTGAAGGGCTCTC CG TGAT TGTGTG GTCT TC TTGT CGA CTCTCTCG
TCAGCATGTTCCTCTCTGTC TTT- -- TCT C C- A - --------
TGTGTGTTAGTTTTGC
GAM33724 10900 TAACATATTTTAGAAAGCTA TT- A CT A A GGTGAAGG
6 ACAAGCTAGAGAGAGCGGTG TAACATAT TAGA AG AACA GCT GAGAGAGC
AAGGGCTCTCTCAGCATGTT ATTGTGTG GTCT TC TTGT CGA CTCTCTCG
CCTCTCTGTCTGTGTGTTA TCT C C- A - --------
GAM33724 10824 GTCCCCTTTCTCTTTCTACC - TT TTCTACCATA AA--- A AAAA CTGT
7 ATACCCCCAGTAAAGCTACT GTCC CC TCTCT CCCCCAGT AGCT CTT TCCT
TAAAATCCTCTGTAGGAAAG CAGG GG AGAGA GGGGGTTA TCGA GAA AGGA
AGCTGAGTAATTGGGGGCAG A T- C--------- ATGAG - ---- ----
AGATGGAGGAC
GAM33724 9848 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33725 9849 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33725 10782 GGTCGAGGTGGGTGTATCGC TG T A - A- AGT AGTC
1 TTGAGCCCAGGAGTTTGAGT GGTCGAGG GG GT TCGCT TG GCCCAGG TTG
CCAGCCTGGGCAACATAGTG CCAGTTCT TC CA AGTGA AC CGGGTCC GAC
AGACCTTGTCTTGACC GT - G T AA --- ----
GAM33725 9702 AGGAATTTGTCAGAAACTCT TTTG AAA CT GGT TAGTT
4 TTCCTGTTTTGGTTTGGAGA AGGAA TCAG CT TTCCTGTTTT TTGGAGAG
GTAGTTCTCTCTAACTAGAG TCCTT AGTT GG GAGGACAGAG AATCTCTC
ACAGGAGTGGCCTTGAAATT TTAA CC- T- ATC -----

TTCCT
GAM33725 10906 TACCTTCTTTGCTGCCTGGG -- TG C - GCT TG TTTATTTGATC
5 AGATGCTGCTATGGGCGTTT TACCTTC TT CTGC TGGG AGAT GCTA GGCG
ATTTGATCTGCTTGTGGCTC GTGGAAG AA GACG ACTC TTTG CGGT TCGT
AGTTTGCTCAGCAGTGAAAT TA GT - G ACT GT ----------
GAAGGTG
GAM33725 9645 ACCTTCTTTGCTGCCTGGGA -- TG C - GCT TG TTTATTTGATC
6 GATGCTGCTATGGGCGTTTA ACCTTC TT CTGC TGGG AGAT GCTA GGCG
TTTGATCTGCTTGTGGCTCA TGGAAG AA GACG ACTC TTTG CGGT TCGT
GTTTGCTCAGCAGTGAAATG TA GT - G ACT GT ----------
AAGGT
GAM33725 10196 CTTACCCTGTATTTCATGCA TACC - GCAATACAAAGGAAGATG G- T G T
CAA
7 ATACAAAGGAAGATGGCTGT CT CTGT ATTTCAT GCTGTTTGG GT GCCGT TC CTTAG

TTGGGGTTGCCGTGTCTCTT GA GACA TGAAGTG TGACGAACC CA CGGTA AG GAATT

AGCAATTAAGGAGATGGCTA CCAC G ---------- GA T G - ---
CAGCCAAGCAGTGTGAAGTG
ACAGCACCAG
GAM33725 10183 CTGTATTTCATGCAATACAA - GCAATACAAAGGAAGATG G- T G T CAA
8 AGGAAGATGGCTGTTTGGGG CTG TATTTCAT GCTGTTTGG GT GCCGT TC CTTAG
TTGCCGTGTCTCTTAGCAAT GAC GTGAAGTG TGACGAACC CA CGGTA AG GAATT
TAAGGAGATGGCTACAGCCA A ---------- GA T G - ---
AGCAGTGTGAAGTGACAG
GAM33726 9850 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33726 11144 TGCCTCTCTGGCACTTCCAA C---- G T CTACCTGTGAT T GAAAGTACTA
4 TCTCCTACCTGTGATAGACG TGC TCTCTG CACT CCAATCTC AGACG CTAAGT
TCTAAGTGAAAGTACTAGCT ACG AGAGAC GTGA GGTTAGGG TTTGT GATTCG
TAGTTGTTTGGGATTGGTAG ACAAA A T ---------- T ----------
TGACAGAGAAAACAGCA
GAM33726 11013 TCTCTGGCACTTCCAATCTC G T CTACCTGTGAT T GAAAGTACTA
5 CTACCTGTGATAGACGTCTA TCTCTG CACT CCAATCTC AGACG CTAAGT
AGTGAAAGTACTAGCTTAGT AGAGAC GTGA GGTTAGGG TTTGT GATTCG
TGTTTGGGATTGGTAGTGAC A T ---------- T ----------
AGAGA
GAM33726 10121 CTCTGGCACTTCCAATCTCC G T CTACCTGTGAT T GAAAGTACTA
6 TACCTGTGATAGACGTCTAA CTCTG CACT CCAATCTC AGACG CTAAGT
GTGAAAGTACTAGCTTAGTT GAGAC GTGA GGTTAGGG TTTGT GATTCG
GTTTGGGATTGGTAGTGACA A T ---------- T ----------
GAG
GAM33726 10100 CTATGCCCAGCATTGGAAAG GC ATTGG -- CC TA A C AATCAAAC
7 AGTAGAGGCCCTTACTAGCA CTAT CCAGC AAAGA GTAGAGG CT CT GCA ACCTCA
CACCTCAAATCAAACTGGGG GATA GGTCG TTTCT CGTTTTC GA GA CGT TGGGGT
TTGCAGCAGACCTTTTGCCT AA GAGA- TC CA C- - - --------
TCTTTAGAGGCTGGAAATAG

GAM33726 11017 TCTGATCCTGGAACTGCATT TC ----- CA- G GTC GGGG
9 GCTTGGTGGTCAGGAGGGGT TCTGA CTGG AACTG TTGCTTG TG AGGA
TCTTAGTAAGCAAACTCAGT AGGCT GACC TTGAC AACGAAT AT TCTT
TTAATCCCAGAGTCGGA GA CTAAT TCA G --- ----
GAM33727 10460 GCGATCTCTTAACAATTTCC GA C A- ----- AA- CC C T CATGTACTACCTCC
0 GGGCTGAACAGCCTCACCAG GC TCT TTAAC ATT TCCGGGCTG CAG TCA CAGCA GC

CATGCCATGTACTACCTCCG CG AGA AATTG TAG AGGTCCGGT GTC AGT GTCGT CG

CTTGCTGATGACTGAAGTGG A- A AG AAATC GAA -- A T ----------
CCTGGACTAAAGATGAGTTA
AAAGAAGC
GAM33727 11015 TCTCTTAACAATTTCCGGGC C A- ----- AA- CC C T CATGTACTACCTCC
1 TGAACAGCCTCACCAGCATG TCT TTAAC ATT TCCGGGCTG CAG TCA CAGCA GC
CCATGTACTACCTCCGCTTG AGA AATTG TAG AGGTCCGGT GTC AGT GTCGT CG
CTGATGACTGAAGTGGCCTG A AG AAATC GAA -- A T ----------
GACTAAAGATGAGTTAAAAG
A
GAM33727 10086 CGCTTGAGCCCAGGAGGCAG TGA AGGCA GT A- AAGAT
3 AGGTTGCAGTGAGCCAAGAT CGCT GCCCAGG GAG TGCAGTG GCC
GGCACCACTGCACTCCAGCC GTGA CGGGTCC CTC ACGTCAC CGG
TGGGCAACAGTG CAA GAC-- -- CA -----
GAM33727 10295 GAGACTCACCCGTTCTACTG -- G - - C G T--- C AAT TGAGTT
4 GCAACTGGAGTTTGTTCAAG GAGACTC ACCC TTCTACT GG CAA TGGA TT GTT AAGA ACC

AAATACCTGAGTTGGTTCTT CTCTGAG TGGG AAGGTGA CC GTT GCTT AG CAA TTCT TGG

TAACTGTCGAGTTCGATTGT GG - A T A G CTGT T --- ------
CCAAGTGGAAGGGTGGGAGT
CTC
GAM33727 10101 CTCACCCGTTCTACTGGCAA G - - C G T--- C AAT TGAGTT
5 CTGGAGTTTGTTCAAGAAAT CTCACCC TTCTACT GG CAA TGGA TT GTT AAGA ACC
ACCTGAGTTGGTTCTTTAAC GGGTGGG AAGGTGA CC GTT GCTT AG CAA TTCT TGG
TGTCGAGTTCGATTGTCCAA - A T A G CTGT T --- ------
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GAM33727 10066 CCTGGAGGCCTTTCCATATT - CCATA - GTC A TG ATAC-- TAAT
7 AGATATGTCCCCTTCTATAA CCT GGAGGCCTTT TTAGAT AT CCCTTCT TAAG CA ACT
GTGCAATACACTTAATGGTT GGA TTTTTGGAAG AATCTA TG GGGAGGG ATTC GT TGG

CCCTCTGTGCTTAGGGAGGG A ACG-- A AA- - GT CTCCCT ----
AAGTAATCTAAGCAGAAGGT
TTTTAAGG
GAM33727 9945 CACGGCTATTAAGTAGCAGA - - T ---- T- TT GATC
8 ACTGGGCTTGAATTCAGATC CACGGCTA TTA AG AGCAGA ACTGGGCT GAA CA
TGCTTCTCAGTCCAGTGTTC GTGTCGGT AAT TC TCGTCT TGACCTGA CTT GT
TCTGCTCTGTAACTGGCTGT C G - CTTG CT C- ----
G
GAM33727 9739 AGGTGATGGATGGGCATGCA ATGGAT A -- A T AT AG G CCCGAC
9 GTGAGGTCACTGTTGGATGT AGGTG GGGC TGCAGT GAGGTC CTG TGG GTC ACTG AG

CAGACTGGAGCCCGACCTCA TCCAC TCCG GTGTCA CTCCGG GAC ACT CAG TGAC TC

GTGACTCTCACCAGGGCCTC GG---- A GA - C CT -- - ------
AGACTGTGAGCCTGGCACCT
GAM33728 11074 TGAGGCAGGAGAATCACTTG CA AA GAA-- AAGA GT AA - AGAT
1 AACCCAGGAAGAGGAGGTTG TGAGG GGAG TCACTT CCCAGG GGAG TGCAGT GC CG

CAGTAAGCCGAGATCGTGCC ACTCT CCTT AGTGAA GGGTCC CCTC ACGTCA CG GC

ACTGCACTCCAGCCTGGGCA C- AG ACAAC GA-- -- C- T ----
ACAAAGTGAGATTCCCTCTC
A
GAM33728 10549 GGAGAATCACTTGAACCCAG AA GAA-- AAGA GT AA - AGAT
2 GAAGAGGAGGTTGCAGTAAG GGAG TCACTT CCCAGG GGAG TGCAGT GC CG
CCGAGATCGTGCCACTGCAC CCTT AGTGAA GGGTCC CCTC ACGTCA CG GC
TCCAGCCTGGGCAACAAAGT AG ACAAC GA-- -- C- T ----
GAGATTCC
GAM33728 10763 GGGGTATAGGCACTGAGAAG GT A-- GA AA - T-- T GAACA
3 CAAACAGGATTCATCTGAGA GGG AT GGCACTGA AGC ACAG GAT CA CTGA
ACATCGGTTGCATGTCTCTG CCC TG TTGTGACT TCG TGTC CTG GT GGCT
TGCTTCAGTGTTCAAGTCTC TC AAC -- -- T TAC T -----
CC
GAM33728 11153 TGCTGTGGCCTAACAGTTGT TG -- A AG- G-- ATA G--- A AG---- TA
5 TTTCTGAGTATATTTTCATG TGCTG GC CT AC TTGTTTTCT AGT TTTTCAT TCA AT
CAAAAG
TCAAATAGCAAAAGTAGAAC ATGAC TG GA TG GATAAAAGG TCA AGAAGTA AGT TG
GTTTTC
TTTTGGAGGAGGTGTGAAGA GT AA C AGA AGA GTG AAGA G GAGGAG --
AATGAAGAGTGACTAGAGGA GAA
AAATAGAGAGTCAGAAGTTG
CAGTA

GAM33728 10048 CCTAACAGTTGTTTTCTGAG AAC TG TCTGAG A GT AAATAG TAGAA
6 TATATTTTCATGTCAAATAG CCT AGT TTT TAT TTTTCAT C CAAAAG
CAAAAGTAGAACTTTTGGAG GGA TCA GAG GTA AGAAGTG G GTTTTC
GAGGTGTGAAGAAATGAAGA GA- GT AA---- A TG AGGAG- -----
GTGACTAGAGG
GAM33728 10026 CCCGCCTCAGCCTCTCGAGT - GCC GA- CAC ACA --- CA TGCCCAGT
8 CACTGGGATTACAGATGTGA CCC GCCTCA TCTC GT TGGGATT GATGT GAGC CCA
GCCACCATGCCCAGTTGGAT GGG CGGAGT AGAG CG ATCTTAA TTACA CTCG GGT
GCTCTAAACATTAAATTCTA T AGT AAA A-- A-- AAT TA --------
AGCAAAGAGATGATGAGGCT
GGG
GAM33728 10025 CCCGCCTCAGCCTCTCGAGT C GCC GA- CAC ACA --- CA TGCCCAGT
9 CACTGGGATTACAGATGTGA CC GCCTCA TCTC GT TGGGATT GATGT GAGC CCA
GCCACCATGCCCAGTTGGAT GG CGGAGT AGAG CG ATCTTAA TTACA CTCG GGT
GCTCTAAACATTAAATTCTA T AGT AAA A-- A-- AAT TA --------
AGCAAAGAGATGATGAGGCT
GG
GAM33729 10959 TCATAGTCTGCGTTTGTTTG CTG - T- TCT - AG TTCC

0 TGCCCATCTTTTTTGGGAAG TCATAGT CGTTT GTTTG GCCCA TTTTTG GGA TCT
TCTTTCCAGGTATTCACAGA GGTGTCG GTAAG CAAAC CGGGT AGAGAC CTT GGA
GACTTGGGCCTCAAACTGAA TA- T TC TC- A AT ----
TGATGCTGTGG
GAM33729 10158 CTGCATCACCTGTGAGAGGA ---- CT TG AG A --- T GCAGAGAAA
1 AAGAACCTTGTTTTTATAGC CTG CATCAC G AG GA AGAACCT TGT TTTATA
AGAGAAATATAAGCACAGGG GAC GTAGTG C TC CT TCTTGGA ACA GAATAT
AGGTTCTGTCACTTGCCAGT CCTA AC GT A- G GGG C ---------
GATGATCCCAG
GAM33729 9851 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33729 10874 GTGTGTCTGGTTTCCAGGAG C TT A A - TGCTGT GAGGC AAGTACC
3 GCAGGCGTGCTGTCTGAAGA GTGTGT TGGT CC GG GGCAGG CG CTGAA TTTGG
GGCTTTGGAAGTACCCCAAA TACACA ACCG GG CC CCGTCC GT GACTT AAACC
TAATTCAGTTCTTGACCTGC C -- A - A TCTT-- AAT-- -------
CCCAGGGCCACACACAT
GAM33729 10869 GTGTCTGGTTTCCAGGAGGC C TT A A - TGCTGT GAGGC AAGTACC
4 AGGCGTGCTGTCTGAAGAGG GTGT TGGT CC GG GGCAGG CG CTGAA TTTGG
CTTTGGAAGTACCCCAAATA CACA ACCG GG CC CCGTCC GT GACTT AAACC
ATTCAGTTCTTGACCTGCCC C -- A - A TCTT-- AAT-- -------
CAGGGCCACACAC
GAM33729 10226 GAAAGGGAGTCCACGGAAGC A A G G - A AG TTTG GACT
6 GTGAGAATGGAGGAAGAACA GAA GGGAGTCC CGGAA C TGAGAATGG AGGAAGA C TGC AGT

GTGCTTTGAGTGACTGCTGC CTT CTCTTAGG GTCTT G ATTTTTATT TCCTTCT G ACG TCG

AGGGTCTTCCTATTATTTTT G A - - A - GG ---- ----
AGTTCTGAGGATTCTCGTTC
GAM33729 10740 GGGAGTCCACGGAAGCGTGA A G G - A AG TTTG GACT
7 GAATGGAGGAAGAACAGTGC GGGAGTCC CGGAA C TGAGAATGG AGGAAGA C TGC AGT

TTTGAGTGACTGCTGCAGGG CTCTTAGG GTCTT G ATTTTTATT TCCTTCT G ACG TCG
TCTTCCTATTATTTTTAGTT A - - A - GG ---- ----
CTGAGGATTCTC
GAM33729 10692 GGCCATGCCTTTGTCACCCT G GTC - AA GCA A TTGTC
8 AAATACTGCACGGCCATGCC GGCCAT CCTTT AC CCTA TACT CGGCC TGCCT
TTTGTCAGGCAGGCTGAGTG CCGGTG GGAGG TG GGGT GTGA GTCGG ACGGA
ACTGGGAGTTAGGAGGGTGG - AT- A CA --- - -----
CC
GAM33729 11039 TGAGAATTGCTTGAACCCAG A---- GA-- C GGCA GT A - AGAT
9 GAGGCAGAGGTTGCAGTGAG TGAGA TTGCTT AC CAGGA GAG TGCAGTG GC CG
CCGAGATCGTGCCACTGCAC ACTCT AACGAA TG GTCCT CTC ACGTCAC CG GC
TCCATCCTGAGTGACAAAGC GTCAG ACAG A AC-- -- - T ----
AAGACTGTCTCA
GAM33730 11260 TTGCTTGAACCCAGGAGGCA GA-- C GGCA GT A - AGAT
0 GAGGTTGCAGTGAGCCGAGA TTGCTT AC CAGGA GAG TGCAGTG GC CG
TCGTGCCACTGCACTCCATC AACGAA TG GTCCT CTC ACGTCAC CG GC

CTGAGTGACAAAGCAA ACAG A AC-- -- - T ----
GAM33730 9852 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33730 9853 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33730 10633 GGAGAATTGCTTGAACCCGG AA GAA-- AGG GT A C AGAT
3 GAGGTGGAGGTTGCAGTGAG GGAG TTGCTT CCCGGG TGGAG TGCAGTG GC G
CCGAGATCGCCCACTGCACT TCTC AACGAG GGGTCC ACCTC ACGTCAC CG C
CCAGCCTGGGCAACAGAGCA AG ACAAC G-- -- C - ----
AGACTCT
GAM33730 11264 TTGCTTGAACCCGGGAGGTG GAA-- AGG GT A C AGAT
4 GAGGTTGCAGTGAGCCGAGA TTGCTT CCCGGG TGGAG TGCAGTG GC G
TCGCCCACTGCACTCCAGCC AACGAG GGGTCC ACCTC ACGTCAC CG C
TGGGCAACAGAGCAA ACAAC G-- -- C - ----
GAM33730 11233 TTATGAATCCGTTTTTATGA C - GAAA AAA CAAA
5 AATGTCCAAAATAGGCAAAT TTATGAATC GTTTTT AT TGTCCA TAGG
CTATGGACAGAAAGTAGAAA GGTGCTTAG CGAAAG TG ACAGGT ATCT
GCAGATTCGTGG A A AAAG --- ----
GAM33730 9908 ATGAATCCGTTTTTATGAAA C - GAAA AAA CAAA
6 TGTCCAAAATAGGCAAATCT ATGAATC GTTTTT AT TGTCCA TAGG
ATGGACAGAAAGTAGAAAGC TGCTTAG CGAAAG TG ACAGGT ATCT
AGATTCGT A A AAAG --- ----
GAM33731 9854 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33731 10342 GAGGCAGGAGAATCGCTTGA G AA -- AA- AGGC - T AGCCAAGATTG
1 ACCCGGGAGGCGGAGGTTGT GAGGCAG AG TCGCT TG CCCGGG GGAG GT GTGGTG

GGTGAGCCAAGATTGCGCCA CTCTGTC TC AGCGA AC GGGTCC CCTC CG TACCGC

TTGCACTCCAGCCTGGGCAA - AA CA AAC GA-- A T ----------
CAACAGCGAAACTCTGTCTC
GAM33731 10678 GGCAGGAGAATCGCTTGAAC G AA -- AA- AGGC - T AGCCAAGATTG
2 CCGGGAGGCGGAGGTTGTGG GGCAG AG TCGCT TG CCCGGG GGAG GT GTGGTG

TGAGCCAAGATTGCGCCATT CTGTC TC AGCGA AC GGGTCC CCTC CG TACCGC
GCACTCCAGCCTGGGCAACA - AA CA AAC GA-- A T ----------
ACAGCGAAACTCTGTC
GAM33731 10595 GGAGAATCGCTTGAACCCGG AA -- AA- AGGC - T AGCCAAGATTG
3 GAGGCGGAGGTTGTGGTGAG GGAG TCGCT TG CCCGGG GGAG GT GTGGTG
CCAAGATTGCGCCATTGCAC TCTC AGCGA AC GGGTCC CCTC CG TACCGC
TCCAGCCTGGGCAACAACAG AA CA AAC GA-- A T ----------

CGAAACTCT
GAM33731 10588 GGAGAATCGCTTGAACCCGG AA G GA-- GGC A T A CGAGATCAC
4 CAGGCAGAAGTTGCAGTGAG GGAG TC CTT ACCC AGGC GAAGT GCAGTG GC
CCGAGATCACGCCATTGCAC CCTC GG GAG TGGG TCCG CTTCA CGTTAC CG
TTCAGCCTGGGTGACAGAGG AG G ACAG --- A - - ---------
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GAM33731 11195 TGGTCCACATTCTACATAGT A A AC CAC GTGGACAA
5 AGCACCCTCCACACAGTGGA TGGTCC CATTCTACATAGT GC CCTC ACA
CAATGTCAAGAGGTGGCACT ACCGGG GTGGGGTGTGTCA CG GGAG TGT
GTGTGGGGTGGGGCCA - - GT AAC --------
GAM33731 10438 GCAGGCAGGGAGAGGGAGGA CAGGGAGA - A CT ACACC ATTTATGA

7 GGTGAAGGAACAAATGCTGA GCAGG GGGAG GAGGTGAAGGAACA ATG GA TGTT

ACACCTGTTATTTATGAAGC CGTCC TCCTC CTTTACTTTCTTGT TAC CT ACGA
ACTCTACATATGTTCTTTCA AAAAGTGG A A AT C---- --------
TTTCACTCCTGGTGAAAACC
TGC
GAM33731 10440 GCAGGGAGAGGGAGGAGGTG GAGA---- - A CT ACACC ATTTATGA
8 AAGGAACAAATGCTGAACAC GCAGG GGGAG GAGGTGAAGGAACA ATG GA TGTT
CTGTTATTTATGAAGCACTC CGTCC TCCTC CTTTACTTTCTTGT TAC CT ACGA
TACATATGTTCTTTCATTTC AAAAGTGG A A AT C---- --------
ACTCCTGGTGAAAACCTGC
GAM33731 10735 GGGAGGAGGTGAAGGAACAA - A CT ACACC ATTTATGA
9 ATGCTGAACACCTGTTATTT GGGAG GAGGTGAAGGAACA ATG GA TGTT
ATGAAGCACTCTACATATGT TCCTC CTTTACTTTCTTGT TAC CT ACGA
TCTTTCATTTCACTCCT A A AT C---- --------
GAM33732 9602 AACGTGTGGTGATTGATGCT G ATTGAT TCAT C TTGCCC
0 TTCATGGACTCTGTTGCCCC AACGT TGGTG GCTT GGACT TG
AAGTCCCCAAGCCTTGTACC TTGCG ACCAT CGAA CCTGA AC
AGCGTT - GTTC-- CC-- - ------
GAM33732 10609 GGAGAATCGCTTGAATCAGG AA TGAA - A GT - G TGAG
1 GAGTTGGAGGTTGCAGTGAG GGAG TCGCT TCAG GG GTTGGAG TGCAG TGA C
CTGAGGTCACCTGCATTCCA CCTC AGCGA AGTC TC CGACCTT ACGTC ACT G
GCCTGCTGACAGCGAGACTC AG C--- G - -- C - ----
C
GAM33732 10590 GGAGAATCGCTTGAACCCGG AA GAA--- AGCC GT A CGAGATCAT
4 GAGCCGGAGGTTGCAGTGAG GGAG TCGCTT CCCGGG GGAG TGCAGTG GT
TCGAGATCATGCCACTGCAC CCTC AGTGAG GGGTCC CCTC ACGTCAC CG
TCCAGCCTGGGCAACAAGAG AG AACAAC GA-- -- - ---------
TGAGACTCC
GAM33732 10961 TCATGGTTCCTGGAAGGTAA GG- CT- GGT CCACCA - TTCACA -
6 GATTGGTGGCCACCACATTC TCAT TTC GGAA AAGATTGGTGG CATTCA GTCTCC GCTAA
GTGTAG
AGTCTCCTTCACAGCTAAGT GGTA AAG CCTT TTTTAATCATC GTAAGT TAGGGG CGGTT
CGTATC
GTAGCCACATAACTATGCTT ACA TTC --- ATC--- A CAC--- T
TGGCCACGGGGATATGAATG CCACATAA
CTACTACTAATTTTTTCCCT
TGAAACAATGG

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                    --------
GAM33732 10774  GGTAAGATTGGTGGCCACCA  T-        CCACCA    -    TTCACA    -    CCACATAA
7               CATTCAGTCTCCTTCACAGC GG  AAGATTGGTGG     CATTCA GTCTCC     GCTAA GTGTAG

                TAAGTGTAGCCACATAACTA CC  TTTTAATCATC     GTAAGT TAGGGG     CGGTT CGTATC
                TGCTTTGGCCACGGGGATAT  TT        ATC---     A     CAC---    T    --------
                GAATGCTACTACTAATTTTT
                TCC
GAM33732 9609   AAGATTGGTGGCCACCACAT         CCACCA    -    TTCACA    -    CCACATAA
8               TCAGTCTCCTTCACAGCTAA AAGATTGGTGG     CATTCA GTCTCC     GCTAA GTGTAG
                GTGTAGCCACATAACTATGC TTTTAATCATC     GTAAGT TAGGGG     CGGTT CGTATC
                TTTGGCCACGGGGATATGAA         ATC---     A     CAC---    T    --------
                TGCTACTACTAATTTT
GAM33732 9604   AAGAAGAAAGAAAGCTGGCT   A-        TGG     C    GA  T  A AACAT
9               AGGGACCTCAGGATCTCAAG AAG  AGAAAGAAAGC   CTAGGGA CTCAG  TC CA G
                AACATCATGGAATTGAGTTC TTC  TTTTTCTTTTG   GGTCCCT GAGTT  AG GT C
                CCTGGGTTTTCTTTTTGCCT   CG        ---     T    A-  -  A -----
                T
GAM33733 9855   AGTTTTAGGGTACATGTGCA    TTA   A  T TG  -    -  G  T   T  ATAT
0               CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
                TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
                TGGTGTGCTGCACCCATTAA    TTA   C  - GT   G    C  G  C   -  ----
                CT
GAM33733 11080  TGAGGCAGGAGAATCATTTG    CA   AA    GA---     AGG   A  T    A-  TCAGATC
1               AACCCAGGAGGTGGAAGTTG TGAGG  GGAG  TCATTT    ACCCAGG   TGGA GT GCAGTG  GC

                CAGTGAGCTCAGATCGCACC ACTCT  CCTC  AGTAAG    TGGGTCC   ACCT CA CGTTAC  CG

                ATTGCACTCCAGCCTGGGTA    A-   AA    AACAA     G--   -  -    CA -------
                ACAAGAATGAAACTCCATCT
                CA
GAM33733 9856   AGTTTTAGGGTACATGTGCA    TTA   A  T TG  -    -  G  T   T  ATAT
3               CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
                TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
                TGGTGTGCTGCACCCATTAA    TTA   C  - GT   G    C  G  C   -  ----
                CT
GAM33733 10854  GTGGACTTAGGAGGTAGAGA    A  T  G  G  GA      TGG  --       TAAGTT
4               GTGCTTTGGGTGTAGGCCAG GTGG CT AG AG TA  GAGTGCTT   GT  GTAGGCCAGG
                GTAAGTTTCTGGTCTGCCTG TATC GA TT TC AT  TTCACGGA   CG  CGTCTGGTCT
                CATTAGGCACTTGGTAGCTG   -  -  G  G  GG      TTA  TC       ------
                TTAGCTAT
GAM33733 9857   AGTTTTAGGGTACATGTGCA    TTA   A  T TG  -    -  G  T   T  ATAT
6               CAACATGCAGGTTTGTTACA AGTT   GGGT CA G  CAC AACATG CA GT TGT AC
                TATGTATACATGTGCCATGT TCAA   CCCA GT C  GTG TTGTAC GT TA ATA TG
                TGGTGTGCTGCACCCATTAA    TTA   C  - GT   G    C  G  C   -  ----
                CT
GAM33733 10377  GAGGCAGGAGGATCGCTTGA      G  GA    GAA--     AGGCA  GT     A  -  AGAT
7               ACCCGGGAGGCAGAGGTTGC GAGGCAG AG  TCGCTT    CCCGGG    GAG  TGCAGTG GC CA

                AGTGAGCCAAGATTGCGCCA CTCTGTC TC  AGTGAG    GGGTCC    CTC  ACGTCAC CG GT
```

CTGCACTCCAGCCTGGGCAA - AG ACAAC GAC-- -- - C ----
CAGAGTGAGACTCTGTCTC
GAM33734 10840 GTGACTCCTGATATGAAATC C- - AAA A--- AG---- CT G ACGCCAGAGA
1 CATTGCCAAGGCTGACCTTA GTGACT CTGA TATG TCC TTGCCA GCTGAC TATC TCACT

TCGTCACTACGCCAGAGAAG CACTGA GACT GTAT AGG AACGGT CGACTG GTAG GGTGA

TGGGATGGAGTCAGCAGAAG AC T CA- ATAA CGAAGA AG - ----------
CTGGCAAAATAGGAACTATG
TTCAGCAAGTCAC
GAM33734 9596 AAAGGGGGGTGTAGTTATAA GG TTATAA--- - T CT G ACTTCA
3 CCAGGGTCATCTTTGATCTC AAAGGGG TGTAG CCAGGG TCATCT TGAT CATTT GAAA

ATTTGGAAAACTTCATTTCA TTTCCCC ACGTC GGTTCC GGTGGA GTTG GTAGA CTTT
AGATGGAGTTGCAGGTGGTC GA TTAGTCAGG T C AG A ------
CTTGGGGACTGATTCTGCAA
GCCCCTTT
GAM33734 9858 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33734 10387 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

5 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
GGGGAGCAGAGCTAGACTCT
GTCTC
GAM33734 10381 GAGGCGAAGAATTGCTTGAA A AA GAA-- AGG GT A CAAGATCAT
6 CCCAGGAGGTGGAGGTTGCA GAGGCG AG TTGCTT CCCAGG TGGAG TGCAGTG GC

GTGAGCCAAGATCATGCCAC CTCTGT TC AACGAG GGGTCC ACCTC ACGTCAC CG
TGCACTCCAGCCTGGGCAAC C AG ACAAC G-- -- - ---------
AGAGCAAGACTCTGTCTC
GAM33735 10739 GGGAGGCTGAGGGGGAGGAT A TGA G A A-- GA-- AGTTCAA C A - TGAT
0 CACTTGAGCCCAGGAGTTCA GGG GGC GGGG AGG TC CTT GCCCAGG GG TGCAGTG GC
CA
AGGCTGCAGTGAGCCATGAT TCC CCG CCCC TCC AG GAG CGGGTCC TC ACGTCAC CG
GT
TGCGCCACTGCACTCCAGCC G --- G C AAC ACAA GACC--- - - C ----
TGGGCAACAGAGCAAGACCC
TGCCCCGCCGCCT
GAM33735 10707 GGCTGAGGGGGAGGATCACT TGA G A A-- GA-- AGTTCAA C A - TGAT
1 TGAGCCCAGGAGTTCAAGGC GGC GGGG AGG TC CTT GCCCAGG GG TGCAGTG GC CA

TGCAGTGAGCCATGATTGCG CCG CCCC TCC AG GAG CGGGTCC TC ACGTCAC CG GT

CCACTGCACTCCAGCCTGGG CCG G C AAC ACAA GACC--- - - C ----

CAACAGAGCAAGACCCTGCC
CCGCCGCC
GAM33735 10761 GGGGGAGGATCACTTGAGCC G A A-- GA-- AGTTCAA C A - TGAT
2 CAGGAGTTCAAGGCTGCAGT GGGG AGG TC CTT GCCCAGG GG TGCAGTG GC CA
GAGCCATGATTGCGCCACTG CCCC TCC AG GAG CGGGTCC TC ACGTCAC CG GT
CACTCCAGCCTGGGCAACAG G C AAC ACAA GACC--- - - C ----
AGCAAGACCCTGCCCC
GAM33735 10454 GCCCTTCAGTCTCAGTAGCC C T ATTT-- A - CAAT
3 ACATTTCAAGTGCTCAATAG GCC TTCAGTC CAGTAGCCAC CA GTG CT
TTACATGTGCCCAGTGGCTG TGG GGGTCAG GTCGTCGGTG GT CAT GA
CTGGACTGGGTGGT T - ACCCGT A T ----
GAM33735 10039 CCCTTCAGTCTCAGTAGCCA C T ATTT-- A - CAAT
4 CATTTCAAGTGCTCAATAGT CC TTCAGTC CAGTAGCCAC CA GTG CT
TACATGTGCCCAGTGGCTGC GG GGGTCAG GTCGTCGGTG GT CAT GA
TGGACTGGGTGG T - ACCCGT A T ----
GAM33735 10388 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

5 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
GGGGAGCAGAGCTAGACTCT
GTCTC
GAM33735 10957 TCAGTTCTGTTTATCTGAAG AAG C ACCCA A TACCCAGT
6 GCTCCTACCCAGAGATTCTA TCAGTTCTGTTTATCTG GCT CT GAG TTC
CCCAGTGAAACTCCCACAGC AGTCGGGGTAGATGGAC CGA GA CTC AAG
AGCGCAGGTAGATGGGGCTG G-- C CACC- A --------
A
GAM33735 10389 GAGGCTGAGGAAAGAAGATT T GAA AAGA GAG ATTA GC A A TATGATCAT

7 GCTTGAGCCCAGGAATTAGA GAGGC GAG AG TTGCTT CCCAGGA GAG TGCA TG GC

GGCTGCAATGAGCTATGATC CTCTG CTC TC GACGAG GGGTCCT CTC ACGT AC CG
ATGCCACTGCACTCCATCCT T AGA GA-- --- AC-- -- C - ---------
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GTCTC
GAM33735 9591 AAAATAAAATAGAAATCATT AAA- T TTAT T A A A T AAATGA
8 ATTGTCTAGGCTTTTGGAGA AAAAT ATAGAAA CA TG CT GGCTTTTGG GA GCATA GCTGTGA

AGCATATGCTGTGAAAATGA TTTTG TGTCTTT GT AC GA CCGAAAATC CT CGTGT CGGCACT

TCACGGCTGTGCTCCTAAAA ACAA - ---- T - - - - ------
GCCAGTCATGTTTCTGTAAC
AGTTTT
GAM33735 9896 ATAGAAATCATTATTGTCTA T TTAT T A A A T AAATGA
9 GGCTTTTGGAGAAGCATATG ATAGAAA CA TG CT GGCTTTTGG GA GCATA GCTGTGA

CTGTGAAAATGATCACGGCT TGTCTTT GT AC GA CCGAAAATC CT CGTGT CGGCACT
GTGCTCCTAAAAGCCAGTCA - ---- T - - - - ------
TGTTTCTGT

GAM33736 10188 CTGTGATGGTTGTGTTCTAT T T ---- T G--- C GG C GCTTGTTT
1 TATAAAGTGGCACCATTGGA CTG GATGGT GTGTT CTAT ATAAA TGG ACCATT AGT TAAGGGT

GTCTAAGGGTGCTTGTTTGC GAC CTGCCG CACAG GGTG TATTT ACC TGGTAA TCA ATTCCCG

CCTTACACTAAATGGTCCCA - T TCTT - GTGA C A- C --------
AGTGTTTATGTGGTTCTGAC
ACTGCCGTCCAG
GAM33736 9859 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33736 10099 CTAGGGTGCACAGTTTTTAA CAC T A -- CTC GAC CCC ACTT
4 GAAGGCTCGCTCTCTCAGGG CTAGGGTG AGT TTTAAG AGG CTCG TCTCAGGGG CAT GC

GGACCATCCCGCACTTGCAT GGTCTCAC TTA AAATTC TCC GAGT AGAGTTCCC GTA CG

GCCCTTGAGAATGAGGTCCT --- T C TG A-- --- --- ----
CCTTAAATATTCACTCTGG
GAM33736 10447 GCATTGCTTGAGTCCAGGAG A GAG - TCAA C A T AGGTCA
6 GTCAAGGCTGCAGTGAGTCA GC TTGCTT TCCAGGA GG GG TGCAGTG G CA
AGGTCATGCCACTGCACTCC CG AACGAG GGGTCCT CC TC ACGTCAC C GT
ATCCTGGGACAGAGCAAGC - ACA A ---- - - - ------
GAM33736 9999 CCAGGCCTGCCGGTAGGTTT C CCGGTA AGA A - T AT CG TTTTGACTGGT

7 AGAATGAGGTCTGTGTCACT CCAGGC TG GGTTT ATG GG TCTGTG CACTGTGGT TA ATA

GTGGTATTACGATATTTTGA GGTCCG AC CCAAA TAC CT AGACAC GTGACACCA AT TAT

CTGGTTATTATAACCACAGT T ------ AAC - G T -- AT ----------
GTCACAGAGTCCATCAAAAA
CCCATGCCTGG
GAM33736 10776 GGTAGGTTTAGAATGAGGTC -- AGA A - T AT CG TTTTGACTGGT
8 TGTGTCACTGTGGTATTACG GGTA GGTTT ATG GG TCTGTG CACTGTGGT TA ATA
ATATTTTGACTGGTTATTAT CCGT CCAAA TAC CT AGACAC GTGACACCA AT TAT
AACCACAGTGTCACAGAGTC AC AAC - G T -- AT ----------
CATCAAAAACCCATGCC
GAM33737 10723 GGGACAGCATCCTTTTTTGG A CA- GC TTGTTTG A A ACCC
0 CATTTGTTTGTTGCGGGTGG GGG CAG TCCTTTTTTG AT TTGCGGGTGGGG GAGG TTGA

GGAGAGGATTGAACCCTTAA CCC GTC GGGAAAGAAC TG AACGCTCGCTCC CTCC AATT

CCTCACCTCGCTCGCAAGTA A CAA TA ------- A - ----
TCAAGAAAGGGAACCTGACC
C
GAM33737 10972 TCCCCTTCCTCTTTCCCTCC C- TTTCCC AGTTG ATTT- CAATGTAAT
1 CAGTTGTAAATAACATTTTT TCCCCTT CTC TCCC TAAATAAC TTTAGCAG
TAGCAGCAATGTAATCTGCT AGGGGAA GAG AGGG ATTTGTTG AAATCGTC
AAATGTTAGTTGTTTAGGGA AA TCCTGA ----- ATTGT ---------

AGTCCTGAGAAAAGGGGA
GAM33737 10033 CCCTGGAGGCAGGTGCAGAT A C G - T TGTT TG CAGGAT
2 GGAGGCTGTTTCCTGTCAGG CCCTGG GG AG TG CAGA GGAGGC TCC T
ATGTGGGACTTTGTCTTCTT GGGACC CC TT AC GTCT CTTCTG AGG G
CTGACAGTTCCCCAGGG - - G A T TTTC GT ------
GAM33737 10034 CCCTGGAGGCAGGTGCAGAT A C G - T TGTT TG CAGGAT
3 GGAGGCTGTTTCCTGTCAGG CCCTGG GG AG TG CAGA GGAGGC TCC T
ATGTGGGACTTTGTCTTCTT GGGACC CC TT AC GTCT CTTCTG AGG G
CTGACAGTTCCCCAGGG - - G A T TTTC GT ------
GAM33737 10742 GGGATGCCAAACCCTCTCCC C AACCC- C -- T C- ACTGAA
4 TGTGTTACATTAGTGCTATG GGGATG CA TCTC CTGT GTTACA TAGTG TATG
ACTGAACATAAACACTGCTG TCCTAC GT AGAG GGCA TAATGT GTCAC ATAC
TAATGGACGGTGAGATCTTC T GCTTCT T GG C AA ------
GTGTCATCCT
GAM33737 10128 CTCTTGAACCCAGGAGGTGG AA- AGG - -- GCTGAGA
5 AGGTTGGGGTGAGCTGAGAT CTCTTG CCCAGG TGGAG GT TGGGGTGA
CACTCCATTGCACTCCAGTC GAGAGC GGGTCT ACCTC CG ACCTCACT
TGGGCAACGAGAG AAC G-- A TT -------
GAM33737 10308 GAGCTGCCAGCATGGCTAGA TG CT TGAAGC A AAA G A CTTG
6 ATGAAGCAGGTAGGAGAAAT GAGC CCAGCATGG AGAA AGGT GGAG TTGGA AGACT GA

TGGAGAGACTAGACTTGTTG TTCG GGTCGTACC TCTT TCTA CCTC GACCT TCTGA TT

AGTCTTCCAGCCTCCATCTT TA C- ------ - C-- - G ----
TCTCCCATGCTGGATGCTT
GAM33737 10529 GGAATCTTGCTTTGTAGCCC ATC T T C -- T T ---- TCTTGGC
7 AGGCTGGAGTGCAGTGGTGT GGA TTGCTT G AGCC AGGCT GGAG GCAG GGT GTGA

GATCTTGGCTCACGGCAACC CCT GACGAA C TCGG TCTGG CCTC CGTC CCA CACT
TCTGCCTCCCGGGTCTAGGC CTT - - A GC - T ACGG -------
TCAAGCAGTTCTCC
GAM33737 10528 GGAATCTTGCTTTGTAGCCC CT T T C -- T T ---- TCTTGGC
8 AGGCTGGAGTGCAGTGGTGT GGAAT TGCTT G AGCC AGGCT GGAG GCAG GGT GTGA

GATCTTGGCTCACGGCAACC TCTTG ACGAA C TCGG TCTGG CCTC CGTC CCA CACT

TCTGCCTCCCGGGTCTAGGC -- - - A GC - T ACGG -------
TCAAGCAGTTCT
GAM33737 10985 TCCTCTCCACGCTTTACTTT C TTTACTTTTA AA- TG- T A CT- ACCACAGC
9 TAGGTAACTGCTTTTGTTGT TCCTCT CACGC GGT CTGCTTT TTG GC GGGA GGTGT
GCAGGGACTGGTGTACCACA AGGGGA GTGCG CCA GACGAAA GGT CG CCCT CCACA

GCACACCTCCTCCCGCCTGG A ---------- GTC TGA C - CCT --------
AGTAAAGCAGCTGACCGCGT
GAAGGGGA
GAM33738 10599 GGAGAATCGCTTGAACCTGA AA GAA--- GAG - GT - A CAAGATC
0 GAGGCGGAGGTTGCGGGGAG GGAG TCGCTT CCT AGGC GGAG TGCGG GG GC
CCAAGATCGCACCATTGCAC CCTC AGCGAG GGG TCCG CCTC ACGTT CC CG
TCCAGCCTGGGCAACAAGAG AA AACAAC --- A -- A A -------
CGAAACTCC

GAM33738 10981 TCCTACAACTTGAGTCTTTG ACAA A CTT TACT T -- TCTA ATACGTCAAC
3 ATACTGGTGTCACTTTCAGG TCCT CTTG GT TGA GG GTCACT TTCAGGAGC AGA
AGCTCTAAGAATACGTCAAC AGGA GAAC CA ACT CC CAGTGG GAGTCTTCG TCT
TCTCGCTTCTGAGTTGGTGA AA-- - --- C--- - TT C--- ----------
CCCCTCAACCAAGAAAGGA
GAM33738 10731 GGGAGCAAGTTTAGGGGTCA CA TA--- T-- G TT CCC AAATCA
4 GGTAGTGCTCCTCTTTTCCC GGGAG AGTT GGGGTCAGG AGT CTCCTC TTC TG
CTGAAATCACACAAGAATGA CCCTC TCAG TTTCAGTCC TCG GAGGAG AAG AC
GGAGGGCTTTCCCTGACTTT CC AAACG CTT G T- AAC ------
GCAAAGACTCCCTCCC
GAM33738 11125 TGAGGTAGGAGAATCGCTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
5 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCGCTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33738 10603 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

6 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33738 10999 TCGCTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

7 AGGCTGCAGTGAGCCAAGAT TCGCTT CTCGGG GGAG TGCAGTG
CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33738 9978 CATAATGAGTCCACAGCCTC A- GT- ACA -- - G CT TGTAGAATTGATTT
8 GGGGGACGATTGTTCCTGTT CAT ATGA CC GCCTC GG GGGAC ATTGTTC GTTTC
TCTGTAGAATTGATTTGAAA GTA TACT GG CGGAG TC CCCTG TAATAAG CAAAG
CTTGAATAATGTCCCACTGG AA AGT AA- GG A - TT ----------
GAGGCAAGGTGATCATAAAT
G
GAM33738 9912 ATGAGTCCACAGCCTCGGGG GT- ACA -- - G CT TGTAGAATTGATTT
9 GACGATTGTTCCTGTTTCTG ATGA CC GCCTC GG GGGAC ATTGTTC GTTTC
TAGAATTGATTTGAAACTTG TACT GG CGGAG TC CCCTG TAATAAG CAAAG
AATAATGTCCCACTGGGAGG AGT AA- GG A - TT ----------
CAAGGTGATCAT
GAM33739 10007 CCATGCTAAATAAAGGAGAG A AA AAGG G A AG GA--- TG - CAGAGAA
0 CTTAGGTAGACAGACTTGAC CC TGCT ATA AGA CTT GGT ACAGACTT CCT GAGA GGC

CTTGGAGAGGCCAGAGAAGC GG ATGA TGT TCT GAA TCG TGTTTGAA GGA CTCT CCG

CTTCTCTGAGGACAGAAAGT - A- GAAG - G -- AGACA GT T -------
TTGTGCTGAAGTCTGAAGTG
TAAGTAGG
GAM33739 9673 AGAGCTTAGGTAGACAGACT G A AG GA--- TG - CAGAGAA
1 TGACCTTGGAGAGGCCAGAG AGA CTT GGT ACAGACTT CCT GAGA GGC
AAGCCTTCTCTGAGGACAGA TCT GAA TCG TGTTTGAA GGA CTCT CCG

AAGTTTGTGCTGAAGTCT - G -- AGACA GT T -------
GAM33739 10627 GGAGAATTGCTTGAACCCAG AA GAA--- ACG GT C A - AGAT
3 GACGTGGAGGTTGCCATGAG GGAG TTGCTT CCCAGG TGGAG TGC ATG GC TG
CTGAGATCACGCCATTGCAC CCTC AGCGAG GGGTCC ACCTC ACG TAC CG AC
TCCAGCCTGGGCAACAAGAG AA AACAAC G-- -- T - C ----
CGAAACTCC
GAM33739 9952 CACTTGAACCTGGAAGGCAG AA- GGA A T A TGAGATTGT
4 GGGTTGCAGTGAGCTGAGAT CACTTG CCT AGGC GGGGT GCAGTG GC
TGTGCCATTGCACTCCAGCC GTGAAC GGG TCCG CCTCA CGTTAC CG
TGGGCAACAAGTG AAC --- A - - ---------
GAM33739 11126 TGAGGTAGGAGAATCGCTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
5 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCGCTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33739 10604 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

6 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33739 11000 TCGCTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

7 AGGCTGCAGTGAGCCAAGAT TCGCTT CTCGGG GGAG TGCAGTG
CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33739 11124 TGAGGTAGGAGAATCACTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
9 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCACTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33740 10563 GGAGAATCACTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

0 GAGGGGAGGCTGCAGTGAGC GG TCACTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33740 10564 GGAGAATCACTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

1 GAGGGGAGGCTGCAGTGAGC GG TCACTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG CAG- ACAAC GA- -- ----------
TGAGACCC
GAM33740 10949 TCACTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

2 AGGCTGCAGTGAGCCAAGAT TCACTT CTCGGG GGAG TGCAGTG

CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33740 10956 TCAGTCCCTTTGGGTGTGAC T CT G A - CA TT C CATCTTCAGTTTT
3 TGCTGTACACATTTTCATGT TCAG CC TTG GTGTG CTGCT GTA CATT CATGTTAC ATTGA

TACCATTGACATCTTCAGTT AGTT GG GAT TATAC GACGA TAT GTAA GTGTAGTG TAACT

TTTCAATGTGATGTGTAATG - T- G - A AC T- - ----------
CATATAAGCAGCATATGTAG
TGGTTGA
GAM33740 10151 CTGAGGCAGGAGAATTGCTT AGAA - A- A- TGAA T A- GAGAT
5 GTACCCGGGAGGTGAAGGTT CTGAGGCAGG TTGCT TGT CCCGGG GG GGT GCAGTG GCC

GCAGTGAGCCGAGATGGTGC GACTTTGTCC AACGA ACA GGGTCC CC TCA CGTCAC TGG

CACTGCACTCCAGCCTGGGC CGG- G AC GA ---- - CG -----
AACAGAGCAAGGCCCTGTTT
CAG
GAM33740 9860 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
7 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33740 11232 TTAGGAAAGTAGTTTTAATC AA TTTAA GCCC- TG CCTG
8 TCATAGGCCCCCAGTGGGGA TTAGG AGTAGT TCTCATAG CCAG GGGATCC
TCCCCTGGGATCCTCTGGCC GATCC TCGTCA AGAGTGTC GGTC TCCTAGG
ATGCTGTGAGAACTGCTAGC GA ----- GTACC -- ----
CTAG
GAM33740 11127 TGAGGTAGGAGAATCGCTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
9 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCGCTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33741 10605 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

0 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33741 11001 TCGCTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

1 AGGCTGCAGTGAGCCAAGAT TCGCTT CTCGGG GGAG TGCAGTG
CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33741 11056 TGAGGCACGAGAATCGCTTG C AA G GAA-- AGGC GC A AGAGATCAC
3 AACCCAGGAGGCGGAGGCTG TGAGGCA GAG TC CTT CCCAGG GGAG TGCAGTG GC

CAGTGAGCAGAGATCACGCC ACTCTGT CTC AG GAG GGGTCC CCTC ACGTCAC CG

ACTGCACTCCAGCCTGGGCA - AG G ACAAC GA-- -- - ---------
ACAGAGGGAGACTCTGTCTC
A
GAM33741 9986 CATGTTGGCCAGACTGGTCT T - GACT CT - CA T TCT CACCTT
4 GTAACTCCAGACTTCAGGTG CATG TGGC CA GGTCTGTAA CCAG ACTT GG GA GCC

ATCTGCCCACCTTGGCCTCC GTAC ACCG GT CCGGACATT GGTC TGAA CC CT CGG
CAAAGTGCTGGGATTACAGG C A ---- AG G A- - C-- ------
CCTGAGCCACCATG
GAM33741 11128 TGAGGTAGGAGAATCGCTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
5 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCGCTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33741 10606 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

6 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33741 11002 TCGCTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

7 AGGCTGCAGTGAGCCAAGAT TCGCTT CTCGGG GGAG TGCAGTG
CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33741 10123 CTCTGTCACCCAGGCTGGAG TC CC--- A -- T GAT - C-- CCT
8 TGAGTGTGATCTTGGCTCAC CTCTG AC AGGCTGG GT GAG GT CTTGG CTCA GGCAA

GGCAACCTTTGCCTCCTGGG GAGAC TG TCCGATC CG CTC TA GAACT GGGT CCGTT

TTCAAGCAATTCTCCTGCCC GA AGCCC C TC T AC- T CCT ---
TAGCCTCCCGAGTAGCAGAG
GAM33741 11239 TTCAGGTTTTCAGACACCTG GG ACC TAG---- - A - CT GGACAA
9 CAGTAGTAGAACAGAATATT TTCA TTTTCAGAC TGCAG TAGAAC AGA TATTT TAGCT GA

TTAGCTCTGAGGACAATCTA AAGT AGAGGTTTG ACGTT GTCTTG TCT ATAAG ATTGA CT

AGTTATGAATAGTCTGGTTC AA AT- TAGGAAT G G T AT ------
TGTAAGGATTTGCATAGTTT
GGAGAAATGAA
GAM33742 10693 GGCCCAGCGTGGCTCCTGAC CT CC--- AA A- AAG---- GTTAAA
0 CTGGAGGATAACAATGATAA GGCCCAGCGTGG CCTGA TGGAGGAT CAATGAT ATGG TGCT

TGGAAGTGCTGTTAAAAGTA CCGGGTCGTGCC GGACT ACTTTTTG GTTATTG TATC ATGA

AGAATGACTATGAGTTATTG AC CGTCT A- AG AGTAAGA ------
AGTTTTTCATCTGCTCAGGC
ACCGTGCTGGGCC

GAM33742 11023 TCTTCATTATCCTCTATATC A-- -- TATC- CT -- - CGG
1 ATTGCTATGCCCTGGTGTTG TCTTC TTATCC TCTA ATTG ATGCC CTG GTGTTGTGCC

TGCCCGGGGTACAACACGTA AGAAG AATAGG GGGT TAGC TGTGG GAT CACAACATGG

GTAGGTGTTCGATAAACTTG GTA TT TCAAA T- AT G ---
GGTTGGATAAATGGAAGA
GAM33742 10665 GGATGGCTTGAGTCCAGGAG ATG- GA-- AGG GT - AGA
4 GTGGAGGTTGCAGTGAACAG GG GCTT GTCCAGG TGGAG TGCAGTGA ACAG
AGATTGTGTCACTGCACTCT CC CGAG CGGGTCC ATCTC ACGTCACT TGTT
AGCCTGGGCAACAGAGCGAG AGAG ACAA G-- -- G ---
ACC
GAM33742 10509 GCTTGAGTCCAGGAGGTGGA GA-- AGG GT - AGA
5 GGTTGCAGTGAACAGAGATT GCTT GTCCAGG TGGAG TGCAGTGA ACAG
GTGTCACTGCACTCTAGCCT CGAG CGGGTCC ATCTC ACGTCACT TGTT
GGGCAACAGAGC ACAA G-- -- G ---
GAM33742 9861 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33742 10289 GAGACAGGAGAATCGCTTGA G AA G - A- - - A T AGCCAA
8 ACCTGGGAGGCAGAGGTTGC GAGACAG AG TC CT TG ACCTG GGAG GCAG GGT GCGGTT

GGTTAGCCAAGATTGTGCCA CTCTGTC TC AG GA AC TGGGT CCTC CGTC CCG TGTTAG

CTGCACTCCATGGGTGACAC - AG A C AG A A A - ------
AGAGAGACTCTGTCTC
GAM33742 10097 CTAGAGTCCCCCTCAGCTGT CCT TGT- - CTTTC T A - GAGA
9 GGGGGAGCTTTCAAATTTGA CTAGAGTCCC CAGC GGGGG AG AAATT GAA TC AG
AATCAGGAGACTCGAATTCC GATTTCAGGG GTCG TCCCC TC TTTGA CTT AG TC
AGTTTTTCCTACCCCTTAGT T-- TGAT A CTT-- C A C ----
GCTGTGGGACTTTAG
GAM33743 10845 GTGATTCAGCCAGACGTGAT GA CAGACG---- GA GG-- TAT T-- T G
CTTGAAC
0 GGAGGAAATGGTGGTATCTT GT TTCAGC TGATG GGAAAT TGG CT GTGT ATTAA CA
GTGTTATTAAGCACTTGAAC TA AAGTCG ACTAT CCTTTA ATC GA CACG TAGTT GT
TTGGTTGATGCACTGCAGTC AG TACAAGAAGA AA AATA TCT CGT - G -------
TCTAATAAATTTCCAATATC T
AAGAAGAACATGCTGAAGAA
T
-
GAM33743 11237 TTCAGCCAGACGTGATGGAG CAGACG---- GA GG-- TAT T-- T G CTTGAACT

1 GAAATGGTGGTATCTTGTGT TTCAGC TGATG GGAAAT TGG CT GTGT ATTAA CA
TATTAAGCACTTGAACTTGG AAGTCG ACTAT CCTTTA ATC GA CACG TAGTT GT
TTGATGCACTGCAGTCTCTA TACAAGAAGA AA AATA TCT CGT - G --------
ATAAATTTCCAATATCAAGA
AGAACATGCTGAA
GAM33743 10954 TCAGCCAGACGTGATGGAGG CAGACG---- GA GG-- TAT T-- T G CTTGAACT

2 AAATGGTGGTATCTTGTGTT TCAGC TGATG GGAAAT TGG CT GTGT ATTAA CA
ATTAAGCACTTGAACTTGGT AGTCG ACTAT CCTTTA ATC GA CACG TAGTT GT
TGATGCACTGCAGTCTCTAA TACAAGAAGA AA AATA TCT CGT - G --------
TAAATTTCCAATATCAAGAA
GAACATGCTGA
GAM33743 11136 TGATGGAGGAAATGGTGGTA GA GG-- TAT T-- T G CTTGAACT
3 TCTTGTGTTATTAAGCACTT TGATG GGAAAT TGG CT GTGT ATTAA CA
GAACTTGGTTGATGCACTGC ACTAT CCTTTA ATC GA CACG TAGTT GT
AGTCTCTAATAAATTTCCAA AA AATA TCT CGT - G --------
TATCA
GAM33743 9862 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
5 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33743 11164 TGGAGCTGCTGGGTAAAATA C CT AA A A T CTT CT- CAAGTT
7 ATGTGTACTTGTCTTAGTTT TGGAG TG GGGTA ATA TGTGT CT GT AGTTTGCT TTTC
GCTCTTTTCCAAGTTGAAGT ACCTC AC CCCGT TGT ACACG GA CA TTAGACGG GAAG

CTGGCAGATTTCACCAGAGC C C- C- G A C CT- TCT ------
ACAGTGTCTGCCCCCACCTC
CA
GAM33743 11129 TGAGGTAGGAGAATCGCTTG A AGAA GAA-- AGG GC
AGCCAAGATCACACAC
8 AACTCGGGAGGGGAGGCTGC TGAGGT GG TCGCTT CTCGGG GGAG TGCAGTG
AGTGAGCCAAGATCACACAC ACTCTA CC AGTGAA GGGTCC CCTC ACGTCAC
CACTGCACTCCAGCCTGGGC C CCAG ACAAC GA- -- ----------
AACAAAGTGAGACCCCCATC
TCA
GAM33743 10607 GGAGAATCGCTTGAACTCGG AGAA GAA-- AGG GC AGCCAAGATCACACAC

9 GAGGGGAGGCTGCAGTGAGC GG TCGCTT CTCGGG GGAG TGCAGTG
CAAGATCACACACCACTGCA CC AGTGAA GGGTCC CCTC ACGTCAC
CTCCAGCCTGGGCAACAAAG AG-- ACAAC GA- -- ----------
TGAGACC
GAM33744 11003 TCGCTTGAACTCGGGAGGGG GAA-- AGG GC AGCCAAGATCACACAC

0 AGGCTGCAGTGAGCCAAGAT TCGCTT CTCGGG GGAG TGCAGTG
CACACACCACTGCACTCCAG AGTGAA GGGTCC CCTC ACGTCAC
CCTGGGCAACAAAGTGA ACAAC GA- -- ----------
GAM33744 9734 AGGGGTTGTCCTTAAGTTCC CCTTAA CC T C - G T TTG
1 CTCTGCCTGCAGTCCTGCTT AGGGGTTGT GTT C CTGC TG CA TCCTGCTT GTT
TGTTTTGGACAAGTAGGAGT TTCCCGACA CGA G GACG AC GT AGGATGAA CAG
GACAAGCAGGTCAGCACAGC ------ CT - A A G - ---
CCTT
GAM33744 10764 GGGGTTGTCCTTAAGTTCCC CCTTAA CC T C - G T TTG
2 TCTGCCTGCAGTCCTGCTTT GGGGTTGT GTT C CTGC TG CA TCCTGCTT GTT
GTTTTGGACAAGTAGGAGTG TCCCGACA CGA G GACG AC GT AGGATGAA CAG
ACAAGCAGGTCAGCACAGCC ------ CT - A A G - ---
CT

GAM33744 10772 GGGTTGTCCTTAAGTTCCCT CCTTAA CC T C - G T TTG
3 CTGCCTGCAGTCCTGCTTTG GGGTTGT GTT C CTGC TG CA TCCTGCTT GTT
TTTTGGACAAGTAGGAGTGA CCCGACA CGA G GACG AC GT AGGATGAA CAG
CAAGCAGGTCAGCACAGCCC ------ CT - A A G - ---
GAM33744 10986 TCCTGACGGGGTCCTCTGGC AC------ T CT TTTA ACA- A- CCCCG
5 TGCATTTAGGAACAAGGAGC TCCTG GGGG CCTCTGG GCA GGA AGG GCT
TCCCCGAGTAACCTGAAGTC AGGAC CCCC GGAGACC CGT CCT TCC TGA
CACTCTGCCCAGAGGCCCCA ATTCAACA - -- CTCA GAAG AA -----
CAACTTACAGGA
GAM33744 10556 GGAGAATCACTTGAACCCGG AA GAA--- AAGGC GT A - AGAT
6 GAAGGCGGAGGTTGCAGTGA GGAG TCACTT CCCGGG GGAG TGCAGTG GC CG
GCCGAGATCGTGCCACTGCA CCTC AGTGAG GGGTCC CCTC ACGTCAC CG GC
CTCCAGCCTGGGCAACAAGA AG AACAAC GA--- -- - T ----
GTGAGACTCC
GAM33744 10946 TCACTTGAACCCGGGAAGGC GAA--- AAGGC GT A - AGAT
7 GGAGGTTGCAGTGAGCCGAG TCACTT CCCGGG GGAG TGCAGTG GC CG
ATCGTGCCACTGCACTCCAG AGTGAG GGGTCC CCTC ACGTCAC CG GC
CCTGGGCAACAAGAGTGA AACAAC GA--- -- - T ----
GAM33744 10205 CTTGAACCCGGGAAGGCGGA AA- AAGGC GT A - AGAT
8 GGTTGCAGTGAGCCGAGATC CTTG CCCGGG GGAG TGCAGTG GC CG
GTGCCACTGCACTCCAGCCT GAAC GGGTCC CCTC ACGTCAC CG GC
GGGCAACAAG AAC GA--- -- - T ----
GAM33744 9863 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33745 11145 TGCCTGAATAAAGCTAGACG AATAAAGCTA - TCATT A- C -- ACCCC
0 TTCATTGACCAGCAGAGTCT TGCCTG GAC GT GACCAGC GAGT TTTTAT AACT
TTTATAACTACCCCAGTTCC ACGGAC CTG CA CTGGTCG TTCA AAGGTG TTGA
GTGGAAAACTTGGGCTGGTC ---------- T TGAAT GG A CC -----
TAAGTACTGTCCAGGCA
GAM33745 10753 GGGCTTTTGCCCTAGATGGA T- T TG A T -- CTCAGTCAC
2 CAAGTTCAAATCCTGGCTCA GGGC TTTGCCC AGA GACA GT CAAA TCCTGG
GTCACTTAGGAAATTTGGCT CTCG GAACGGG TCT TTGT CG GTTT AGGATT
GTTTGTCTTGGGCAAGTTGC TT T GT - - AA ---------
TC
GAM33745 11096 TGAGGCAGGAGAATCGGTTG A AA---- G- AA AGGCA - T AGC AGAT
3 AACCCAGGAGGCAGAGGTTG TGAGGC GGAG TC GTTG CCCAGG GAG GT GTGGTG CG

TGGTGAGCCGAGATCGTACC ACTCTG CCTC AG CAAC GGGTCC CTC CG TACCAT GC

ATTGCACTCCAGCCTGGGCA - AAAACG AA -- GAC-- A T --- ----
ACAAGAGCAAAACTCCGTCT
CA
GAM33745 10350 GAGGCAGGAGAATCGGTTGA A AA---- G- AA AGGCA - T AGC AGAT
4 ACCCAGGAGGCAGAGGTTGT GAGGC GGAG TC GTTG CCCAGG GAG GT GTGGTG CG

GGTGAGCCGAGATCGTACCA CTCTG CCTC AG CAAC GGGTCC CTC CG TACCAT GC
TTGCACTCCAGCCTGGGCAA - AAAACG AA -- GAC-- A T --- ----

CAAGAGCAAAACTCCGTCTC
GAM33745 11068 TGAGGCAGGACAATCACTTG CAATCA GAA-- A TT GC A CGAGATCAC
6 AACCCAGGAGTTTGAGGCTG TGAGGCAGGA CTT CCCAGG GT GAG TGCAGTG GC

CAGTGAGCCGAGATCACGCC GCTCTGTTCT GAG GGGTCC CA CTC ACGTCAC CG
ACTGCACTCCACCCTGGGCA AGAAC- ACAAC - C- -- - ---------
ACAGAGCAAGATCTTGTCTC
G
GAM33745 10324 GAGGCAGGACAATCACTTGA CAATCA GAA-- A TT GC A CGAGATCAC
7 ACCCAGGAGTTTGAGGCTGC GAGGCAGGA CTT CCCAGG GT GAG TGCAGTG GC
AGTGAGCCGAGATCACGCCA CTCTGTTCT GAG GGGTCC CA CTC ACGTCAC CG
CTGCACTCCACCCTGGGCAA AGAAC- ACAAC - C- -- - ---------
CAGAGCAAGATCTTGTCTC
GAM33745 9907 ATGAAGTGAGTCACATTGGC A- A CA---- CTAC TG GA - TG- TGAGACTGAT
8 TACTGGTGAGGAAGGAGCAG ATG AGTG GTCA TTGG TGG AGGAAG GCAGA GTTG GGC

AGTTGTGGGCTGAGACTGAT TAC TCAC CAGT AACC ACT TCCTTC TGTCT CGAC TCG
GCTGTTCAGCATCTGTCTTC GA - AGATAC ---- GT -- A TTG ----------
CTTGTCACCAACATAGATGA
CCACTAGCAT
GAM33745 9759 AGTGAGTCACATTGGCTACT A CA---- CTAC TG GA - TG- TGAGACTGAT
9 GGTGAGGAAGGAGCAGAGTT AGTG GTCA TTGG TGG AGGAAG GCAGA GTTG GGC

GTGGGCTGAGACTGATGCTG TCAC CAGT AACC ACT TCCTTC TGTCT CGAC TCG
TTCAGCATCTGTCTTCCTTG - AGATAC ---- GT -- A TTG ----------
TCACCAACATAGATGACCAC
T
GAM33746 10944 TCACTTAAACCCGGGAGGTG AA-- AGG GT A GGAGATGGT
0 GAGGTTGCAGTGAGTGGAGA TCACTT ACCCGGG TGGAG TGCAGTG GT
TGGTGCCACTGCACTCCAGC AGTGAG TGGGTCC ACCTC ACGTCAC CG
CTGGGTGACAGAGTGA ACAG G-- -- - ---------
GAM33746 10683 GGCATCTGTAATCCCAGCTA AT- - G A GGG G CGAGAAT
1 CTCGGGAGGCTGAGGCACGA GGC CTGTAATC CCA CT CTC AGGCT AGGCA
GAATTGCTTGAGCCTGGGAG CTG GACGTTAG GGT GA GGG TCCGA TTCGT
GTGGAGATTGCAGTGAGTC AGT A G - --- G -------
GAM33746 10632 GGAGAATTGCTTGAACCCAG AA GAA--- A- T- A - AGGT
2 GAGGTTGCAGTGAGCCGAGG GGAG TTGCTT CCCAGG GG TGCAGTG GC CG
TTGCGCCATTGCACTCCAGC CCTC AGCGAG GGGTCC CC ACGTTAC CG GT
CTGGGCAACAAGAGCGAAAC AA AACAAC GA TC - C ----
TCC
GAM33746 10080 CGAAGGCAGCATGGAAGAAT AG-- A----- ATA T G G A AGGA
3 AGGCAGTATTGGATTTGAAA CGA GCAGC TGGAAGA GGCAG ATT GATTT AA TC
TCAGGAGACTTGGAATTGAA GTT TGTCG ACCTTCT CCGTC TAA TTAAG TT AG
TTCTGCCTCTTCCACTACCA AAAG ACCATC --- T G G C ----
GCTGTGAAATTG
GAM33746 10434 GCAGCATGGAAGAATAGGCA A----- ATA T G G A AGGA
4 GTATTGGATTTGAAATCAGG GCAGC TGGAAGA GGCAG ATT GATTT AA TC
AGACTTGGAATTGAATTCTG TGTCG ACCTTCT CCGTC TAA TTAAG TT AG
CCTCTTCCACTACCAGCTGT ACCATC --- T G G C ----
GAM33746 9864 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT

5 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33746 9865 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33746 10399 GAGGTCATAATGTGAATGTT CATA A G T- CATGT AGAACA
9 GTATGCAGTGGCCATGTCAT GAGGT ATGTG ATGTT TATGCAG GGC CATC
CAGAACAGGTGTGCCAGCCC CTTCG TACAT TACAA GTACGTC CCG GTGG
CCTGCATGGAACATGTACAT ---- G G CC ACCGT ------
GCTTC
GAM33747 10142 CTGAGAGGTGAGATTCCACA GA AT--- A CCC G C--- -- AGTG G
0 TCCCAAGTTGCACAGCTGGG CT GAGGTGAG TCC CAT AAGTT CA AGCTGGGGAG AGAC
TCAG ACAG
GAGAGACAGTGTCAGGACAG GA CTTTACTT AGG GTA TTCGA GT TCGACCCCTC TCTG
AGTC TGTC
TATCGCCTGTGCTGAGGTCT A- ATTTT A T-- A CAGA GA G--- G
AGCTCCCCAGCTAGACTGAA TATCGC
GCTTTATGAGGATTTTATTC
ATTTCAAG

GAM33747 10234 GAACTGGGTCATTTATCAAA TG -- T TA GTTTA G AA ATCCCTC
2 CTCTGTGTTTATGTGGCCTT GAAC GGT CA T TCAAACTCTGT TGTG CCTTTAG TATT
TAGAATATTATCCCTCAGTA TTTG TCA GT G AGTTTGAGGTA ACAC GGAGATT ATGA
AGTTAGAGGCACAGATTAAT GT CT T GA ATTAG - GA -------
GGAGTTTGAAGGTTGTCACT
TGGTTT
GAM33747 9866 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33747 11082 TGAGGCAGGAGAATCGCTTG G AATC GAA--- AGGC - T GA AAGAT
6 AACCCAGGAGGCGGAGGTTG TGAGGCAG AG GCTT CCCAGG GGAG GT GTGGT GCG

TGGTGAGCGAAGATCGTGCC ACTCTGTC TC CGAG GGGTCC CCTC CG TACCG TGC

ATTGCACTCCAGCCTGGGCA - AAAA AACAAC GA-- A T -- -----
ACAAGAGCAAAACTCTGTCT
CA
GAM33747 9867 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
7 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33747 9618 AATCAAAAAGGTTTGAGCAA A A - A C ACAGTC
8 AGGATGAACACAATCTACAG AATCAA AAGGTTTG GCAAAGGA TGA CA AATCT

TCAGATTATGTCACTCCTTT TTAGTT TTCCAGAC CGTTTCCT ACT GT TTAGA
GCCCAGACCTTCTTGATT C C C - A ------
GAM33747 10143 CTGAGCAGGGAGAATCTCGG - AGAAT GGGAT A- TCAA C A CACAATTTT

9 GATCCCAGGAGGTCAAGGCT CTGAG CAGGG CTC CCCAGG GG GG TGCAGTG GC

GCAGTGAGCCACAATTTTGC GACTC GTCCC GAG GGGTCC CC TC ACGTCAC CG
CACTGCACTCCAGCCTGGGC T AGAAC ACAAC GA ---- - - ---------
AACAGAGCAAGACCCTGTCT
CAG
GAM33748 9868 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
0 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33748 9589 AAAAATGAAAGGAAAAGGAG - GA - ATGACC
1 GGGAGGCAGATGGGAAGATG AAAAAT GAAAGGAAAAGGAGGGGAGGCA TG GGAAG

ACCCTTTTACAAATGTTTCT TTTTTG CTTTCTTTTTCCTCTTCTTTGT AC TTTTC
TCTCCTTTTTCTTTCTGTTT T AA A ------
TT
GAM33748 10602 GGAGAATCGCTTGAACCTGG ATC GAA--- GGG - C T A- CAAGATC
2 GGGGCGGACGTTGCAGTGAG GGAGA GCTT CCT GGGC GGA GT GCAGTG GC
CCAAGATCGCACCATTGCAC CCTCT CGAG GGG TCCG CCT CA CGTTAC CG
TCCAGCCTGGGCAACAAGAG AAA AACAAC --- A - - CA -------
CAAATCTCC
GAM33748 11016 TCTGAGTCAGTGGGCTGAGA A -- -- GAAAGGC- TTCATCT
5 AAGGCTGCCCACCTTTCATC TCTG GTCAG TGG GCTGA TGCCCACCT
TAGGTGGGCACAACGTAATC AGAC CAGTT ACC CGACT ACGGGTGGA
AGCTGCCAGCTTGACCAGA - CG GT AATGCAAC -------
GAM33748 11051 TGAGATTTCTAAGGCACTGC TTCTA---- GC A AA- ACT AGTGG
6 TTCTAAGTAGGAATCACACT TGAGAT AGGCACT TTCT AGTAGG TCAC GC
GCAGTGGGTTAGTGACACCC ACTTTG TCCGTGG AAGA TCGTCC AGTG TG
TGCTCAGAAATGGTGCCTGT TAAAACGTG TA C CAC AT- -----
GCAAAATGTTTCA
GAM33748 9637 ACATTATTAGGAATTTCAAG TA AT AG G ATG G TG G- A ACTTAGGA
8 AGCTGGGCATGTTGGAGTAT ACATTAT GGA TTCAAG CT GGC TT GAGTA CCT TG TCTCAGTT

GCCTGTGATCTCAGTTACTT TGTGATG TCT GAGTTT GG CCG GA TTCAT GGA AC GGAGTCGG

AGGAGGCTGAGGCAGAAGGA -- -- GA A --- G TA AG - --------
TTACTTGAGGCCAGGAGTTT
GAGTCTGTAGTGT
GAM33748 11166 TGGAGGAGGAGGCTGGTGCT AG - C TAAATA- CTAAATCAAACCACA
9 GGTTAAATACAACCTAAATC TGGAGG GAGGCTGG TG TGGT CAAC
AAACCACAGTTGACCAACCA ACCTTC CTTCGACC AC ACCA GTTG
CCACATCCAGCTTCTCCTTC CT T - CCAACCA ----------
CA
GAM33749 10282 GAGACAGGACCTGGCTTCAG C- CCT A- -- C CT--------- T CCTG
0 GACTGTGGACTGGGCTGCTG GAGA AGGA GGCTTCAGG CTGT GGA TGGG GC GG

GCCTGCTTGCTTCCTCCCTT CTCT TCCT CCGGAGTCC GACG CCT ACCC CG TC
CCCCATTCCTAGCAGGGCCT TC C-- GG AT T CTTCCCTCCTT T ----
GAGGCCCTCCTCTTCTC
GAM33749 10738 GGGAGGCCAAGGTGGGAAGA CA AAG - A- TGG GAGACA
5 TTGCTTGAGCCCTGGAGGTT GGGAGGC AGGTGGG ATTGCT TG GCCC AGGTT
GAGACAAGCCTGGGCAACAT TTCTTTG TTTACCC TAACGA AC CGGG TCCGA
AGCAATACCCCATTTGTTTC -- CA- T AA --- ------
TT
GAM33749 10552 GGAGAATCACTTGAACCCAG AA GAA-- A- CGAA T A- TAAGATC
6 GAGGCGAAGGTTGCAGTGAG GGAG TCACTT CCCAGG GG GGT GCAGTG GC
CTAAGATCGCACCACTGCAC TCTT AGTGAG GGGTCC CC TCA CGTCAC CG
TCCAGCCTGGGCAACAGAGT AC ACAAC GA ---- - CA -------
GACATTCT
GAM33749 10144 CTGAGCTTAGATCTTATGTG AGA AT G C - GT- CC-- CTGTTCATC
7 GCCTTTCTGGTCTGTGTATC CTGAGCTT TCTT GT GC TTTCT GGTCT GTATC AGGA
CCAGGACTGTTCATCTCCTA GACTCGGA AGAA CA TG AGAGA CCAGA CGTAG TCCT
TGTGATGCTGAAGACCAAGA --- C- G - A AGT TGTA ---------
GAGTGACCAAGAAGGCTCAG
GAM33749 10031 CCCTGAACTCAGGGGCTTCG AA--- A C T T AA TACGA CTGCG
8 CCACTGATTGTCCAAACGCA CCCTG CTC GGGGCTT GCCAC GAT GTCCA CGCAATTCTTG GT

ATTCTTGTACGAGTCTGCGG GGGAC GGG CCTCGAG CGGTG CTA CAGGT GTGTTAAGAGC
CG
CCAACCGAGAATTGTGGCTG AACGC - T T - CG CAAC- -----
GACATCTGTGGCTGAGCTCC
GGGCGCAACAGGG
GAM33749 10452 GCCCTGAACTCAGGGGCTTC TGAACTCA C T T AA TACGA CTGCG
9 GCCACTGATTGTCCAAACGC GCCC GGGGCTT GCCAC GAT GTCCA CGCAATTCTTG GT

AATTCTTGTACGAGTCTGCG CGGG CCTCGAG CGGTG CTA CAGGT GTGTTAAGAGC CG

GCCAACCGAGAATTGTGGCT -------- T T - CG CAAC- -----
GGACATCTGTGGCTGAGCTC
CGGGC
GAM33750 10106 CTCAGGGGCTTCGCCACTGA A C T T AA TACGA CTGCG
0 TTGTCCAAACGCAATTCTTG CTC GGGGCTT GCCAC GAT GTCCA CGCAATTCTTG GT

TACGAGTCTGCGGCCAACCG GGG CCTCGAG CGGTG CTA CAGGT GTGTTAAGAGC CG

AGAATTGTGGCTGGACATCT - T T - CG CAAC- -----
GTGGCTGAGCTCCGGG
GAM33750 10758 GGGGCTTCGCCACTGATTGT C T T AA TACGA CTGCG
1 CCAAACGCAATTCTTGTACG GGGGCTT GCCAC GAT GTCCA CGCAATTCTTG GT
AGTCTGCGGCCAACCGAGAA CCTCGAG CGGTG CTA CAGGT GTGTTAAGAGC CG
TTGTGGCTGGACATCTGTGG T T - CG CAAC- -----
CTGAGCTCC
GAM33750 9869 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----

CT
GAM33750 10020 CCCAGTGACCCACAGGTAAG T ------ GTA AA TTCCAG - GTGGCTCA
7 AACCTTGTGTTTTCCAGATT CCCAG GA CCCACAG AG CCTTGTGTT ATTC TGAGT
CTGAGTGTGGCTCAGCTCGT GGGTT CT GGGTGTC TC GGAACACGG TAAG GCTCG

GAATGCAGTGGCACAAGGCA - AGGTGA --- AC TGACG- T --------
CTCTGTGGGAGTGGATCTTG
GG
GAM33750 10013 CCCACAGGTAAGAACCTTGT GTA AA TTCCAG - GTGGCTCA
8 GTTTTCCAGATTCTGAGTGT CCCACAG AG CCTTGTGTT ATTC TGAGT
GGCTCAGCTCGTGAATGCAG GGGTGTC TC GGAACACGG TAAG GCTCG
TGGCACAAGGCACTCTGTGG --- AC TGACG- T --------
G
GAM33751 10363 GAGGCAGGAGAATTGCTTGA G AA GAA-- A- C AAGT GC AGAT
0 ACCCAGGAGGCAGAAGTTGC GAGGCAG AG TTGCTT CCCAGG GG AG TGCAGTGA CG

AGTGAGCCGAGATCGCATCA CTCTGTC TC AGCGAG GGGTCC CC TC ACGTTACT GC

TTGCACTCCAGCCTGGGCAA - AG ACAAC GA - ---- AC ----
CAGAGCGAGACTCTGTCTC
GAM33751 9974 CAGGTGTGCGCCACCACACG CGCC C A -- CTG ATGGC
1 TGACTGGGAAGCCTTCTGGT CAGGTGTG ACCACA GTG CTGGGAA GCCTT GTTTTAAG

TTTAAGATGGCTTTAGAATG GTCTACAC TGGTGT CAC GATCCTT CGGAA TAAGATTT
AAAGGCAGTTCCTAGCACCT TAAC C - GA AG- -----
GTGGTCAATCACATCTG
GAM33751 10523 GGAACGAGAATTGCTTGAAC GA AA- TG GA-- - CAAA T A T AGATCA
2 CCAGGAGGCAAAGGTTGCAG G ACGAG T CTT ACCCAGG AGG GGT GCAGTG G CA
TGAGTCAAGATCATGCCACT C TGTTC A GAG TGGGTCC TCC TCA CGTCAC C GT
GCACTCCTGCCTGGGTGACA TC CAG GT ACAG G ---- - - - ------
GAGTGAGACCTTGTCTC
GAM33751 10065 CCTGCTGTATGCTAGGCATT - -- CT- C A- GGGC
5 GTGCAAGGTGTTAGGGCTGA CC TGCTGT ATG AGG ATTGTGC AGGTGTTA
TGCTTGAGCACAGTACCTCC GG ATGACG TAC TCC TGACACG TTCGTAGT
ACATCTGCAGTATGG T TC ACC A AG ----
GAM33751 10088 CGCTTGCAACTGAAAGGCGG GCAAC AA- - GT AACCAAGATCGCAC
6 AGGTTGCAGTGAACCAAGAT CGCTT TG AGGC GGAG TGCAGTG
CGCACCACTGCACTCCAGCC GCGAA AC TCCG CCTC ACGTCAC
TGGGCAACAAAAGCG AACA- GGG A -- ----------
GAM33751 9946 CACTAGGCTAGACATACAAA T GC ATACAAAG - GCC G T AAATATA TCAT
8 GACCCCTTGCCCGTGGCTCC CAC AG TAGAC ACC CCTT CGTG CTCCCAT TC TC
CATTTCAAATATATCTCATG GTG TC ATTTG TGG GGAG GCAC GAGGGTG GG AG
ACCAGGGTGTGGGAGCACGA - AA AGAA---- A ACA - T GACC--- ----
CAGAGGAGGTAAGAGTTTAA
ACTGTG
GAM33752 10038 CCCTTATGGGATTCTGGAAG TTAT--- TC A TG - A - TGAGT AAAAA
0 TGGTGGCTACACGGATGTAC CCC GGGAT TGGA G GTG GCT CACGGA TGTACA GTGA

ATGAGTGTGAAAAAATCATT GGG TCCTA GTCT T CAT CGA GTGTCT GTATGT TACT
AAACTGTATGCTCTGTGAAG TAATCCT TT A GT T A C CAAAT -----

CTTACTGTATCTGTTATCCT
TCCTAATGGG
GAM33752 9956 CAGACCCTCTCTCTTTCCCA GACCC C- CCA G A-- CACCTGAGA TGAATT

1 GGCTTCCTGTCCTTCAGCAA CA TCT TCTTTC GGCTTCCT TCCTTC GCAAGGC AC
GGCCACCTGAGAACTGAATT GT AGA AGAAAG TCGGAGGA GGGAAG CGTTCCG TG

GTAAATTCCAGCCTTGCAAG AAAT- AC --- G GAA ACCTTAAA- ------
GAAGGGGAGGAGGCTGAAAG
ACAAGATAAATG
GAM33752 11011 TCTCTCTTTCCCAGGCTTCC C- CCA G A-- CACCTGAGA TGAATT
2 TGTCCTTCAGCAAGGCCACC TCT TCTTTC GGCTTCCT TCCTTC GCAAGGC AC
TGAGAACTGAATTGTAAATT AGA AGAAAG TCGGAGGA GGGAAG CGTTCCG TG
CCAGCCTTGCAAGGAAGGGG AC --- G GAA ACCTTAAA- ------
AGGAGGCTGAAAGACAAGA
GAM33752 11025 TCTTTCCCAGGCTTCCTGTC CCA G A-- CACCTGAGA TGAATT
3 CTTCAGCAAGGCCACCTGAG TCTTTC GGCTTCCT TCCTTC GCAAGGC AC
AACTGAATTGTAAATTCCAG AGAAAG TCGGAGGA GGGAAG CGTTCCG TG
CCTTGCAAGGAAGGGGAGGA --- G GAA ACCTTAAA- ------
GGCTGAAAGA
GAM33752 10744 GGGATTACAGGCACCTGCTG TA CACC CT A TTTT ATTTTTAATA GGG
4 CCAAGTCTGGCTAATTTTTG GGGAT CAGG TG GCCA GTCTGGCTAAT GT GAGAC
TATTTTTAATAGAGACGGGG CTCTA GTCC GC TGGT CGGACCGGTTG CG CTTTG
TTTCGCTATGTTGGCCAGGC -- TCAA TC - TAT- ---------- ---
TGGTCTCGAACTCCTGATCT
C
GAM33752 10478 GCTCCTGCTTGCATATGCAT G TG G A - C AACT
5 GGGTACACAGCCTGTAACTA GCTCCT CT CATAT CATGGGT CACA GC TGT
CATGTGTGTGAGCCTGTGGG TGAGGG GA GTATG GTGTCCG GTGT TG ACA
TATGTGAGGGGAGT - GT G A G T ----
GAM33752 10233 GAACCTTTGATGTTACTCTA A TA T C - TC GTGAGGG
6 TCGTCTGGATCTCTTTTGCC GAACCTTTG TGT CTC AT GTCTGGAT C TTTTGCCT
TGTGAGGGAGGCAGAGAGGT TTTGGAGAC ACG GAG TA CGGATTTA G GAGACGGA

ATTTAGGCATGAGGCAGCAG G -- - - T GA -------
AGGTTT
GAM33752 10521 GGAACAGCAGGGCTAGAAAG C - GC AG-- C TCTG
8 CCAGAGAGACAGGGGCTCTG GGAA AGCAGG GCTAGAAA CAG AGA AGGGGC
GCCCTTTCTGATGCTGTTTT CCTT TCGTCC CGATTTTT GTC TCT TTCCCG
TAGCACCTGCTTTCC - A -- GTAG - ----
GAM33752 9696 AGCGGTGAAGACCAAGGCCA A C AGCT CTC GTCATTCAA
9 GAGCTTAAACTCATAGGGGT AGCGGTG AGACCAAGG CAG TAAA ATAGGG
CATTCAACTCTGTTTTTATT TTGTCAT TTTGGTTCC GTT ATTT TGTCTC
AGTTGTCCTTGGTTTATACT A T GATT T-- ---------
GTT
GAM33753 10057 CCTCCTCCATCCGTCTCCCA - ATC CCAGGGT G GAA A TTTCAAT
0 GGGTGCCTTTGTTTTGAATC CCTCCT CC CGTCTC GCCTTT TTTT TC TTTTTGA
ATTTTTGATTTCAATTTAAG GGAGGA GG GCAGAG CGGAGA AGAA AG AAGAATT
AAGAGAAAGAAGAGGCTGAG A AA- T------ - AG- - -------
ACGAAGGAAGGAGG

GAM33753 9870 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33753 9871 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33753 9872 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33754 10365 GAGGCAGGAGAATTGCTTGA G AG AA TG GAA-- AGG GT A - AGAC
1 ACCCAGGAGGTGGAGGTTGC GA GC GAG T CTT CCCAGG TGGAG TGCAGTG GC TG

AGTGAGCTGAGACCATGCCA CT TG TTC A GAG GGGTCC ACCTC ACGTTAC CG AC
TTGCACTCCAGCCTGGGCAA G G- AG GT ACAAC G-- -- - T ----
CAGAGTGAGACTTGGTGTC
GAM33754 10274 GAGAATTGCTTGAACCCAGG AA TG GAA-- AGG GT A - AGAC
2 AGGTGGAGGTTGCAGTGAGC GAG T CTT CCCAGG TGGAG TGCAGTG GC TG
TGAGACCATGCCATTGCACT TTC A GAG GGGTCC ACCTC ACGTTAC CG AC
CCAGCCTGGGCAACAGAGTG AG GT ACAAC G-- -- - T ----
AGACTT
GAM33754 9873 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33754 9874 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33754 10561 GGAGAATCACTTGAACCTGG AA A- ACC GG- - GT A - AGAT
5 GAGGCGGAGGTTGCAGTGAG GGAG TC CTTGA TG AGGC GGAG TGCAGTG GC CG

CCGAGATTGAGCCATTGCAC CCTC AG GGACT AC TCCG CCTC ACGTTAC CG GT
TCCAGCCTGGACATCAGGGC AG CG --- AGG A -- - A ----
GAGACTCC
GAM33754 10019 CCCAGGTTTCAGTTTGGTAG GT TTG- AG A TTAGCATTTAGT TC TTTTGGT

7 CATGAATCCTTAGCATTTAG CCCAG TTCAGT GT CATG ATCC GAC CAG
TGACTCCAGTTTTGGTCTGC GGGTC GGGTTA CG GTAC TAGG CTG GTC
TGTCTTTCTTAAATGGATGC AT CCAA GA G TAAATTCTTT-- TC -------
ATGAGGCAACCATTGGGTAC
TGGG
GAM33754 11085 TGAGGCAGGAGAATCGCTTG G A AA GAA-- GGCAA CT A- TGAGATC

8 AACCCAGGTGGCAAGGCTTG TGA GC GGAG TCGCTT CCCAGGT GG TGCAGTG GC

CAGTGAGCTGAGATCGCACT ACT CG CCTC AGCGAG GGGTCCG CC ACGTCAT CG
ACTGCACTCCAGCCTGGGCA - A AG ACAAC A---- TC CA -------
ACAGAGCGAGACTCCAGCTC
A

GAM33754 10586 GGAGAATCGCTTGAACCCAG AA GAA-- GGCAA CT A- TGAGATC

9 GTGGCAAGGCTTGCAGTGAG GGAG TCGCTT CCCAGGT GG TGCAGTG GC
CTGAGATCGCACTACTGCAC CCTC AGCGAG GGGTCCG CC ACGTCAT CG
TCCAGCCTGGGCAACAGAGC AG ACAAC A---- TC CA -------
GAGACTCC

GAM33755 11062 TGAGGCAGGAAAATGGCTTG A AAATG GAA--- AGG GT A- TGAGATT

2 AACCCGGGAGGTGGAGGTTG TGAGGC GGA GCTT CCCGGG TGGAG TGCAGTG GC

CAGTGAGCTGAGATTGCGCC ACTCTG CCT CGAG GGGTCC ACCTC ACGTCAC CG
ACTGCACTCCAGCCTGGGCA - CAAAA AACAAC G-- -- CG -------
ACAAGAGCAAAACTCCGTCT
CA

GAM33755 9639 ACCAGTGGTTAGCAGATGAG AG TT CA GA GA GG A--- CTG GATGAA

3 GTGAAAGAGATGGGACAGTG ACC TGG AG GATGAGGT AA GATG AC GTGACTGTAT TTCT

ACTGTATCTGTTCTGATGAA TGG ACC TC TTACTTCA TT CTGC TG CATTGACGTG GAGG

GGAGATTGTGCAGTTACATG -- T- -- AA A- AA CGTA TTA ------
CGTAACGTCATTAAACTTCA
TTCTTCCAGGT

GAM33755 10418 GATGAGGTGAAAGAGATGGG GA GA GG A--- CTG GATGAA

4 ACAGTGACTGTATCTGTTCT GATGAGGT AA GATG AC GTGACTGTAT TTCT
GATGAAGGAGATTGTGCAGT TTACTTCA TT CTGC TG CATTGACGTG GAGG
TACATGCGTAACGTCATTAA AA A- AA CGTA TTA ------
ACTTCATT

GAM33755 10375 GAGGCAGGAGAGTTGCTTGA GGAGAG TG GAA-- AAGC GT - TGAGATT

5 ACCCAGGAAGCGGAGGTTGC GAGGCA T CTT CCCAGG GGAG TGCAGTGAG C
AGTGAGCTGAGATTGCCTCA CTCTGT A GAG GGGTCC CCTC ACGTCACTC G
CTGCACTCCAGCCTGGGCAA AACAA- GT ACAAC GA-- -- C -------
CAGAGTGAAACAATGTCTC

GAM33755 10202 CTTGAACCCAGGAAGCGGAG GAA-- AAGC GT - TGAGATT

6 GTTGCAGTGAGCTGAGATTG CTT CCCAGG GGAG TGCAGTGAG C
CCTCACTGCACTCCAGCCTG GAG GGGTCC CCTC ACGTCACTC G
GGCAACAGAG ACAAC GA-- -- C -------

GAM33755 9715 AGGCAGGAGAATTGCTTGAA CA AA GAACC G- A T A A - AGAT

8 CCTGTGAGGCAGAGGTTGCA AGG GGAG TTGCTT TGT AGGC GAGGT GC GTG GC TG

GTGAGCTGAGATCATGCCAC TCC CCTC AGCGAG GCG TCCG CTTCA CG CAC CG AC

AGCACTTCAGCCTGAGCGAC A- AG ACA-- AG A - A - T ----
AGAGCGAGACTCCACCT

GAM33756 9875 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT

6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC

TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33756 11224 TGTTCAGAAAGTCTGTTGTT CA- - T T T CCC GTAAGACACAGCTA
7 GTAAACATCCCCGACTGGAA TGTT GAA AGTC GT GT GTAAACATC GACTGGAAGCT
GCTGTAAGACACAGCTAAGC ACAG CTT TCGG CA CG CGTTTGTAG CTGACTTTCGA
TTTCAGTCAGATGTTTGCTG ACA A C T T A-- ----------
CTACCGGCTATTCACAGACA
GAM33756 10227 GAAAGTCTGTTGTTGTAAAC - T T T CCC GTAAGACACAGCTA
8 ATCCCCGACTGGAAGCTGTA GAA AGTC GT GT GTAAACATC GACTGGAAGCT
AGACACAGCTAAGCTTTCAG CTT TCGG CA CG CGTTTGTAG CTGACTTTCGA
TCAGATGTTTGCTGCTACCG A C T T A-- ----------
GCTATTC
GAM33756 9756 AGTCTGTTGTTGTAAACATC T T T CCC GTAAGACACAGCTA
9 CCCGACTGGAAGCTGTAAGA AGTC GT GT GTAAACATC GACTGGAAGCT
CACAGCTAAGCTTTCAGTCA TCGG CA CG CGTTTGTAG CTGACTTTCGA
GATGTTTGCTGCTACCGGCT C T T A-- ----------
GAM33757 10765 GGGTACCAGATGTGCTTCCT CC CTT CTC A A- G TG C TATCT
0 GTCCTCAGTAAAGAACTTGG GGGTA AGATGTG CCTGTC AGTA AGA CTTGGAGTAT T TTC
TCAAA
AGTATGTTGTTCCTCAAATA CCTAT TTTACAT GGACAG TCAT TTT GGACCTCGTG G AAG AGTTT

TCTTTTGATGAATGGGTGCT -- C-- --- C GA - GT T -----
CCAGGAGTTTCTACTGACAG
GCTACATTTTATCC
GAM33757 9684 AGATGTGCTTCCTGTCCTCA CTT CTC A A- G TG C TATCT
1 GTAAAGAACTTGGAGTATGT AGATGTG CCTGTC AGTA AGA CTTGGAGTAT T TTC TCAAA

TGTTCCTCAAATATCTTTTG TTTACAT GGACAG TCAT TTT GGACCTCGTG G AAG AGTTT

ATGAATGGGTGCTCCAGGAG C-- --- C GA - GT T -----
TTTCTACTGACAGGCTACAT
TT
GAM33757 10069 CCTGTCCTCAGTAAAGAACT CTC A A- G TG C TATCT
2 TGGAGTATGTTGTTCCTCAA CCTGTC AGTA AGA CTTGGAGTAT T TTC TCAAA
ATATCTTTTGATGAATGGGT GGACAG TCAT TTT GGACCTCGTG G AAG AGTTT
GCTCCAGGAGTTTCTACTGA --- C GA - GT T -----
CAGG
GAM33757 9876 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33757 11071 TGAGGCAGGAGAATAGCTTG G AATA GAA--- AGG GT A - AGAT
4 AACCCAGGAGGTGGAGGTTG TGAGGCAG AG GCTT CCCAGG TGGAG TGCAGTG GT CG

CAGTGAGTCGAGATTGCACC ACTCTGTC TC CGAG GGGTCC ACCTC ACGTTAC CA GT

ATTGCACTCCAGCCTGGGCA - AAAA AACAAC G-- -- - C ----
ACAAGAGCAAAACTCTGTCT

CA
GAM33757 10286 GAGACAGGAGAATCGCTTGA A AA GAAC-- AGG - T AGCCGAGATTG
5 ACCCCAGAGGTGGAGGTTGT GAGAC GGAG TCGCTT CCCAG TGGAG GT GTGGTG

GGTGAGCCGAGATTGCACCA CTCTG CCTC AGCGAG GGGTC ACCTC CG TACCAC
TTGCACTCCAGCCTGGGCAA - AA AACAAC CG- A T ----------
CAAGAGCGAAACTCCGTCTC
GAM33757 9877 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
6 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33757 9878 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33757 10373 GAGGCAGGAGAATTGCTTGA G AA TG GA-- AGGC AT A - AGAT
9 GCCCAGGAGGCGGAGATTGC GAGGCAG AG T CTT GCCCAGG GGAG TGCAGTG GC CG

AGTGAGCCGAGATCGTGCCA CTCTGTC TC A GAG CGGGTCC CCTC ACGTCAC CG GC

CTGCACTCCAGCCTGGGCAA - AG GT ACAA GA-- -- - T ----
CAGAGTGAGACTCTGTCTC
GAM33758 10912 TAGACTTGGGAGGGAACCTT T-- - GA -------- - CTACTCCAGC TTACA
0 ACAGTCCTCTACTCCAGCTC TAGACT GG GAGG ACCT TA CAGTCCT TCCCTGATT
CCTGATTTTACAGATCGGGG GTCTGA CC CTTC TGGA AT GTCGGGA AGGGGCTAG
ACCCACCATTCAGGGCTGAT CTC A TC CTCAAACA A CTTACCACCC -----
AACAAACTCAGGTCTCTTCA
CCCTCAGTCTG
GAM33758 9608 AAGAGGCCTAAAAGTTTAAT CCT- TTTAATGCCA CCTT -- A G G - ATGT
1 GCCAGACCTTAGGGGCAGGA AAGAGG AAAAG GA AGG GGCAGG TGGA CAGG CTAAA
AG
TGGAGCAGGGCTAAAAGATG TTTTCC TTTTC CT TCC TCGTCC GTCT GTCC GGTTT TC

TCTCTTTGGGCCTGTCTGCC TTTC ---------- TCCT TT - - G C ----
TGCTTTCCTTCCTTCCTTTT
CTTTCCTTTT
GAM33758 10209 CTTGACACCTCCTGTCCAGT G CCTG A - T C C AA- TGACT
4 ACTGTCTTGATGCCTGCCCC CTT ACACCT TCCAGT CTG TC TGATGC TGCCC AT AG
ATAAAGTGACTCTGCGATGG GAA TGTGGG AGGTTA GAC AG ATTGTG ACGGG TA TC

GCAAGTGTTATGATCAGATT A ---- - T T A - GCG -----
GGAGGGTGTAAAG
GAM33758 9629 ACACCTCCTGTCCAGTACTG CCTG A - T C C AA- TGACT
5 TCTTGATGCCTGCCCCATAA ACACCT TCCAGT CTG TC TGATGC TGCCC AT AG
AGTGACTCTGCGATGGGCAA TGTGGG AGGTTA GAC AG ATTGTG ACGGG TA TC
GTGTTATGATCAGATTGGAG ---- - T T A - GCG -----
GGTGT
GAM33758 10411 GAGTTTGAGATCTGTCTGGG -- A T CT A T AA - C----- AACAA

6 CAACATGCTGAAACCCCAGC GAGT TTG GA CTGT GGGCA CA GCTG AC CCCAGCT TGTA

TCTGTAAACAATACAAAAAT CTCA GAC CT GACA TCCGT GT TGGC TG GGGTCGA ACAT

TAGCTGGGCGTGGCGGTCTG TC C - -- - C GG C TTAAAA -----
TGCCTACAGTCCCAGCTACT
C
GAM33758 10186 CTGTCTGGGCAACATGCTGA CT A T AA - C----- AACAA
7 AACCCCAGCTCTGTAAACAA CTGT GGGCA CA GCTG AC CCCAGCT TGTA
TACAAAAATTAGCTGGGCGT GACA TCCGT GT TGGC TG GGGTCGA ACAT
GGCGGTCTGTGCCTACAG -- - C GG C TTAAAA -----
GAM33758 11235 TTCACGCTTGAACCTGGGAG G AA- TG AGG GT A CGAGATCAT
8 GTGGAGGTTGCAGTGAGCCG TTCAC CTTG CC GG TGGAG TGCAGTG GC
AGATCATGCCATTGCACTCC AAGTG GAAC GG CC ACCTC ACGTTAC CG
AGCCTGGGCAACAAGAGTGA A AAC GT G-- -- - ---------
A
GAM33758 9879 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33759 11122 TGAGGTAGGAGAATCACATG GT G AA CA- AA- A- GAGGT A CGAGACCAC

0 AACCCGGGAGGTGGAGGTTG TGAG AG AG TCA TG CCCGGG GGTG TGCAGTG GC

CAGTGAGCCGAGACCACGCC ACTC TC TC AGT AC GGGTCC CCAC ACGTTAC CG
ATTGCACACCAACCTGGGCA TG - AG CAG AAC AA ----- - ---------
ACAGACTGAGACTCTGTCTC
A
GAM33759 11247 TTCCGATAAAAGAGTTGCCA AAAAGAG CCA --- AA A A G - - TGTC
1 AGACCCTTGGAAGCTCCACA TTCCGAT TTG AGAC CCTTGG GCTCC CAGT AT GGT GTCTT
TCGG
GTAATGGGTGTCTTTCGGTG GAGGTTG AAC TTTG GGAGCT CGGGG GTCG TG TCA TAGAG
AGTC
TCCTGATGAGATGACTGGTG ------- --- AGA C- - G G G T ----
GCTGGGGGCCTCGAGGAGAG
TTTCAAGTTGGAG
GAM33759 10877 GTGTTGAGATCCTTTCACAG TG - C --- T ACAATTACGTTCACA
2 TTGTGGTTACAATTACGTTC GTGT AG AT CTTTCA CAG TGTGGTT
ACAAGCTACACCTGCCATGA CACG TC TA GAGAGT GTC ACATCGA
GAGAATACTTGGCAC GT A A ACC C ----------
GAM33759 9880 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33759 9881 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
4 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----

CT
GAM33759 9882 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
5 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33759 11053 TGAGGCAAGAGAATCGCTTG AA AA GAA--- AGGCA GTTGA A - AGAT
7 AACCCAGGAGGCAGAGGTTG TGAGGC GAG TCGCTT CCCAGG GAG AGTG GC CG

AAGTGAGCCGAGATCGTGCC ACTCTG CTC AGCGAG GGGTCC CTC TTAC CG GC
ATTGCACTCCAGCCTGGGCA C- AA AACAAC GAC-- ACG-- - T ----
ACAAGAGCGAAACTCCGTCT
CA
GAM33759 10315 GAGGCAAGAGAATCGCTTGA AA AA GAA--- AGGCA GTTGA A - AGAT
8 ACCCAGGAGGCAGAGGTTGA GAGGC GAG TCGCTT CCCAGG GAG AGTG GC CG
AGTGAGCCGAGATCGTGCCA CTCTG CTC AGCGAG GGGTCC CTC TTAC CG GC
TTGCACTCCAGCCTGGGCAA C- AA AACAAC GAC-- ACG-- - T ----
CAAGAGCGAAACTCCGTCTC
GAM33759 10908 TACTTGTGCAGGTTTGTTAA GCAGG TAAA TT AA GAG TTCT ATCC
9 ATGGGTTTATTGTGTAATGC TACTTGT TTTGT TGGGT ATTGTGT TGCT ATTTGGGC AATG

TGAGATTTGGGCTTCTAATG ATGGATA AGATA ATCCA TGATACA ACGA TGAACCCG TTAC

ATCCCATTGCCCAAGTAGCA ACTA- ---- -- A- --- ---- ----
AACATAGTACCTAATAGAAT
CAATAGGTA
GAM33760 10425 GCAAAGCACTTACTTCTTTG A TT -- T ATAGTTACAAA
1 CAGATGAGACTGAGACATAG GC AAGCACTTAC CT TTGCAGA GAGACTGAGAC
TTACAAAGTCTCAGTTTCCT CG TTCGTGAATG GA AACGTCT CTTTGACTCTG
CTGCAAACAGTTGTAAGTGC A TT CA C ----------
TTAGC
GAM33760 9610 AAGCACTTACTTCTTTGCAG TT -- T ATAGTTACAAA
2 ATGAGACTGAGACATAGTTA AAGCACTTAC CT TTGCAGA GAGACTGAGAC
CAAAGTCTCAGTTTCCTCTG TTCGTGAATG GA AACGTCT CTTTGACTCTG
CAAACAGTTGTAAGTGCTT TT CA C ----------
GAM33760 11275 TTGGAGTTAGGATCCCCAGG TG TT- TCCCC T- - TGG- TCTGG
5 TTCTAGTCCTGAGTCTGGAC T GAG AGGA AGGTTC AGTC CTGAGTC AC
TCTGGGTAAGTGACTCAGCG A TTC TCCT TCCAAG TTAG GACTCAG TG
ATTCTGAACCTTGTTTCCTT GT TAT TTGT- TC C TGAA -----
ATCTTTGA
GAM33760 9923 ATTACTAGGTTTAAATAAGA ATAAGAA TGC TC- TTAG GCCTCTG
6 ACAGATGCTTGCTTTGGTTC ATTACTAGGTTTAA CAGA TTGCTTTGGT AAG GCAT
AAGTTAGGCATGCCTCTGAT TGATGATTCAGATT GTCT AACGGAACCA TTC CGTA
GCATTTCTTAATACCAAGGC CGGGA-- CTA TAA TTTA -------
AAATCTCTGAGGGCTTAGAC
TTAGTAGT
GAM33760 11093 TGAGGCAGGAGAATCGCTTG G AATC GAA TG AGG GT TG A - AGAT
7 AACCTGGGAGGTGGAGGTTG TGAGGCAG AG GCTT CC GG TGGAG TG GTG GC CG

TGGTGAGCCGAGATCGCGCC ACTCTGTC TC CGAG GG CC ACCTC AC TAC CG GC

ATTGCACTCCAGCCTGGGCA - AAAA AAC GT G-- -- GT - C ----
AGAGCAAAACTCTGTCTCA
GAM33760 10347 GAGGCAGGAGAATCGCTTGA G AATC GAA TG AGG GT TG A - AGAT
8 ACCTGGGAGGTGGAGGTTGT GAGGCAG AG GCTT CC GG TGGAG TG GTG GC CG
GGTGAGCCGAGATCGCGCCA CTCTGTC TC CGAG GG CC ACCTC AC TAC CG GC
TTGCACTCCAGCCTGGGCAA - AAAA AAC GT G-- -- GT - C ----
GAGCAAAACTCTGTCTC
GAM33761 9883 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33761 10796 GGTGGTGAGAGGGGCCTGGG GG AG - - C - GGA T GTTCTTTG
4 GCGTGGTGTGGAGGGTCGAG GGT TG AGG GG CCTGGGG GTGG TGT GGG CGA
TTCTTTGTCGTCCCACAGTC CCG GC TCC CC GGACCCC CACT ACA CCC GCT
ACCCCCAGGACCACCTTGCG AA GT A A - G --- T --------
AAGCC
GAM33761 11243 TTCCAAGTGAAAATAGACTT --- A GACTTT- G CAGAA TCTTGGTATCTT
5 TCTGGAGGAGCAGAAAGGAC TTCC AAGTG AAATA CTGGAG AG AGGACAGC
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CCTGAGAACTGCTCCAGTTA AGA G ATAAATT G AAGAG ----------
AATATATTTGTATTTAGAGG
AA
GAM33761 10849 GTGCATTTCTATTTCTAGTT AT- AT- TC A- CAGGCAATTCA
6 TTTCACGGAACTGACCAGGC GTGC TTCT TTCTAGTTTT ACGG ACTGAC
AATTCAGTCAGTAGCTGTCA CACG AAGA GAGGTCAAAA TGTC TGACTG
AAACTGGAGTCCAGAACAGG GAC CCT C- GA ----------
CAC
GAM33761 11262 TTGCTTGAACCCGGGAGGCA GAA-- AGGCA GT A TGAGATGGT
7 GAGGTTGCAGTGAGCTGAGA TTGCTT CCCGGG GAG TGCAGTG GC
TGGTGCCACTGCACTCCAGC AACGAG GGGTCC CTC ACGTCAC CG
CTGGGCAACAGAGCAA ACAAC GAC-- -- - ---------
GAM33761 9884 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33762 9984 CATGAAATTTAGTGTGATTA ATT----- - TTTTTTCTACTTTT
0 TTTTTTCTACTTTTTAATCA CATGAA TAGTG TGATTA
TCATTATTTTGAAGTTTATG GTATTT ATTAC ACTAAT
GAAGTTTT T ----------
GAM33762 9885 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
1 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
TATGTATACATGTGCCATGT TCAA CCCA GT C GTG TTGTAC GT TA ATA TG
TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33762 9886 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
2 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
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TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----

CT
GAM33762 9887 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
3 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
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TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
CT
GAM33762 10220 CTTTTCCACCATCTAAGAGA CCATC AA-- AA CA CTTA
4 AAGGAAGTTCAGAGCCTTAG CTTTTCCA TAAGAGA GG GTT GAGC
CTTCAACACCACAATTTCTT GAAAAGGT ATTCTTT CC CAA TTCG
AACTGGAAAAG CA--- AACA A- C- ----
GAM33762 11094 TGAGGCAGGAGAATCGCTTG G AA GAA-- GTG - - TT AGCTGAGATCG
5 AAGCCGTGAGGTGGAGGTTT TGAGGCAG AG TCGCTT GCC AGG TGGAG GT TGGTG

TGGTGAGCTGAGATCGCGCC ACTCTGTC TC AGCGAG CGG TCC ACCTC CG ACCGC

ATTGCACTCCAGCCTGGGCA - AA AACAA G-- G A TT ----------
ACAAGAGCGAAACTCTGTCT
CA
GAM33762 10661 GGAGTATCGCTTGAACCTGC A GAACC G- - GT A- CGGGATC
6 GAGGCGGAGGTTGCAGTGAG GGAGT TCGCTT TGC AGGC GGAG TGCAGTG GC
CCGGGATCGCACCACTGCAC CCTCA AGTGAG ACG TCCG CCTC ACGTCAC CG
TCCAGCCTGGGCAACAGAGT G ACA-- GG A -- CA -------
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GAM33762 11104 TGAGGCAGGAGAATGGCGTG A AATG G- AA- AGGC CT A - AGAT
7 AACCCGGGAGGCGGAGCTTG TGAGGC GGAG GC TG CCCGGG GGAG TGCAGTG GC CG

CAGTGAGCCGAGATCGCGCC ACTCTG CCTC TG AC GGGTCC CCTC ACGTCAC CG GC

ACTGCACTCCAGCCTGGGCA - AGAG AG AAC GA-- -- - C ----
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A
GAM33762 9888 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
8 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
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TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
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GAM33762 9889 AGTTTTAGGGTACATGTGCA TTA A T TG - - G T T ATAT
9 CAACATGCAGGTTTGTTACA AGTT GGGT CA G CAC AACATG CA GT TGT AC
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TGGTGTGCTGCACCCATTAA TTA C - GT G C G C - ----
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GAM33763 9712 AGGCAGAAGAATTGCTGGAA A AA GAA-- AGGC GT A- CAAGATC
0 TCTAGGAGGCGGAGGTTGCA AGGCAGA G TTGCTG TCTAGG GGAG TGCAGTG GC

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TGCACTCCAGCCTGGGCAAC - AG ACAAC GA-- -- CG -------
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GAM33763 10574 GGAGAATCGCTTGAACCCAG AA GAA-- AGGCA GT A CAAGATCAT
1 GAGGCAGAGGTTGCAGTGAG GGAG TCGCTT CCCAGG GAG TGCAGTG GC
CCAAGATCATGCCACTGCAC CCTC AGTGAG GGGTCC CTC ACGTCAC CG

TCCAGCCTGGGCAACAGAGT AG ACAAC GAC-- -- - ---------
GAGACTCC
GAM33763 9675 AGAGGGAGAATTGCTTGAGC G AA GA-- ATTTC GC AGCTATGATCACAC

2 CCAGGATTTCGAGGCTGCAG AGA GGAG TTGCTT GCCCAGG GAG TGCAGTG
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GCACTCCAGCCTGGGCAACA G AG ACAA GAC-- -- ----------
GAGCAAGACTCTGTCT
GAM33763 10390 GAGGGAGAATTGCTTGAGCC G AA GA-- ATTTC GC AGCTATGATCACAC

3 CAGGATTTCGAGGCTGCAGT GA GGAG TTGCTT GCCCAGG GAG TGCAGTG
GAGCTATGATCACACCACTG CT TCTC AACGAG CGGGTCC CTC ACGTCAC
CACTCCAGCCTGGGCAACAG G AG ACAA GAC-- -- ----------
AGCAAGACTCTGTC
GAM33763 10612 GGAGAATCTCTTGAACCCGG AAT-- AA- AGG GT G A - AGAC
4 GAGGTGGAGGTTGGGGTGAG GGAG CTCTTG CCCGGG TGGAG TG GGTG GC CG

CCGAGACCGCGCCATTGCAC CCTC GAGAAC GGGTCC ACCTC AC TTAC CG GC
TCCAGCCTGGGCAACAAGAG AGAGT AAC G-- -- G - C ----
TGAGACTCC

GAM NAME	GAM RNA SEQUENCE	PRECUR SEQ-ID	SOURCE REF-ID	GAM POS
GAM25	AATTGCTTGAACCCAGGAAGTG	10361		A
GAM31	TCAAGTAATCCAGGATAGGCTG	10712		A
GAM44	AAGGTGGTGTCATGTTTTGGGG	10225	THC1430784	A
GAM55	CTGCCATTTCCAGGAGATCACC	9654	THC1550782	A
GAM55	GGTGGGTTTCCTTAATGGCATC	9654	THC1550782	B
GAM66	TTTGCACCTGAGACAGATAGCC	9890	THC1596213	A
GAM83	AAGGTGGTGTCATGTTTTGGGG	9594	THC1430784	A
GAM99	TGGAGAGATAAGCCAAGTATCC	10072	THC1481711	A
GAM106	ATTAGCTATAGCAAAAGGCTTA	11185	THC1578040	A
GAM112	TGATATATAATCAGCCCATGAT	9976		A
GAM144	CTGTGCCTGTGACGAGGGATGA	10844	THC1576207	A
GAM175	GACCCTGTGTTCAAGGTTAGGG	11029	THC1505396	A
GAM189	CATTGCACTCCAGCCTGGGCAA	10243		A
GAM193	TATTGCTAAGAATTCAGGTAGT	10490	THC1461697	A
GAM205	GTGGAGTTCTCTGCTAGTCCTA	10955	THC1489754	A
GAM206	TGCACTTGTCTTTACCCTAGAG	9626	THC1555962	A
GAM206	TTTCTGGAGGGCAAGTGCAGGG	9626	THC1555962	B
GAM240	TGGCACATAGTAAGTGTTCAGT	11204	THC1514987	A
GAM240	ATCACTATTAATGTGTGCTAGT	11204	THC1514987	B
GAM259	GTCAGCAAGGAGGGGTGGACAA	9934	THC1497034	A
GAM269	CATTGCACTCCAGCCTGGGTGA	10396		A
GAM270	AAGGTAGATAAAGGCTTCACGT	9919	THC1472192	A
GAM281	CACTGCACTCCAGCCTGGGCAA	10402	THC1476894	A
GAM282	TGAGAGAGCAAGTGAATTTCCC	10716	THC1528843	A
GAM282	CTGGCTCTACCCTCTCACTTCA	10716	THC1528843	B
GAM291	AGATAGTTCTCTGTTGTTGGGG	11179		A
GAM317	TAGGAAGTATTTTTTAAAAACA	10674	THC1503708	A
GAM329	TCATAAACTGGCAAGCACTACC	10797		A
GAM330	ACTGCACTCCAGCCTGGGTGAC	10273	THC1430517	A
GAM335	CCCCAGTCAATGCTTCTCTCCA	9932	THC1525711	A
GAM347	TCATTGCAACCTCCACCTCCTG	9752	THC1459051	A
GAM347	CTCCTAGGCTGGAGTGCAGTGG	9752	THC1459051	B
GAM354	ACACAGGCCCAGAGAGGCAGTG	10673		A
GAM361	CATTGCACTCCAGCCTAGGCAA	11098		A
GAM367	TGAGGTAAGTATGTTATTGGAA	11120	THC1534183	A
GAM388	TGTGCACAACATGCAGGTTTGT	9776	THC1432163	A
GAM401	TCACTGCAACCTCTGCCTTCCG	9669		A
GAM408	CTGGGATGGAGGAGAATTAGAG	10542	THC1542346	A
GAM426	TCTGGATTTGAGAGGCTTTACT	10058	THC1532849	A
GAM492	CCGTAAAATGTTCAAATGTTTT	11209	THC1425133	A
GAM492	AAAGCTTTGTTCATTGTATCTG	11209	THC1425133	B
GAM495	AAAATGCTTACAGGCAGTAGCC	10024		A
GAM507	GAGAGAGGTAGAGGGGAGCAGA	10728	THC1464659	A
GAM519	TGTGGCTTAGGTGAGCATGTGA	9641	THC1560312	A
GAM519	TCCCACAGCTTCCTAGCCACAG	9641	THC1560312	B
GAM520	TCTGGTTTGAGAGACAATGACA	10809	THC1534497	A
GAM550	TTTGCACACTTTCCAAGTTGCC	10897		A

GAM569 ACACAGGCCCAGAGAGGCAGTG 10404 A
GAM572 TAAGTGAGTAGGCATTGTTCT 9658 THC1456344 A
GAM584 GGCCCCTTTGTGAGGCACGCTT 10146 THC1588098 A
GAM588 TCCAGTGAAACAGGTCTCTTTG 9928 THC1541093 A
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GAM604 GTGGCATTGGTGGTGGCATTGG 10098 THC1442048 A
GAM640 GGCGTGATCTTGGCTCACCACA 10481 THC1549049 A
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GAM667 TGTAGGTGGTTGAGAGAATGAA 10851 A
GAM674 TGAGATCATCGTTACAAGCAGC 9938 THC1521438 A
GAM689 ACTGCACTCCAGCCTGGGCAAC 10321 A
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GAM772 GCCAGGATGAAGAGGAGGAGAA 11168 THC1436688 A
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GAM785 AGAAGATCCCTGCTCTGAGTCA 10027 THC1539612 A
GAM801 TTGTGCTTGTACTGACCATGTA 10252 THC1464135 A
GAM807 TAAGTGCTGCTGATTTTGGAAA 11034 THC1542535 A
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GAM933 TTAGGGCAGGCATGAGAGAACT 9643 THC1526006 A
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GAM1193 CACCCAGGCTGGAGTGCAGTGG 10309 A
GAM1197 TGTCAGTTTTTTAAATACTCAG 9685 THC1581606 A
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GAM1217 TATTACATTCATTTTGATGGTT 9644 A
GAM1221 TTCCAGATGGGTAGGAATACCT 11031 THC1586339 A
GAM1234 TGTCTTCATCCAGGAACCACAT 11221 THC1407182 A

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GAM1447 TGCTGTGCTAAAGGAAGGATTA 10818 THC1585180 A
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GAM1502 TATATGTCTGGTATTCTTGGGG 9980 A
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GAM1543 ATTGCACTCCAGCCTGGGTGAC 10622 THC1588979 A
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GAM1617 TTGCCCAGGCTGGAGTGCAGTG 9897 A
GAM1650 TCCAAAAGTGGAGAGGAATATG 11198 THC1441934 A
GAM1650 ATTTTTCTGCATTTGTATTGGA 11198 THC1441934 B
GAM1653 TGGAGCAGAAAGGCAGGAGTCC 10791 A
GAM1698 CTTGGCCCTGTGAGGCTTCACC 10870 A
GAM1735 TGAGATGAACCAGGTATCTCAG 10829 A
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GAM1896 TTCCTCTGCCACGTCTTTCCCT 10004 THC1424734 A
GAM1914 TTCTACTAGTGGTTGATGGCCT 10416 THC1548235 A
GAM1937 TGAGTATTCACCAGGTGCTGGG 9624 THC1590719 A

GAM1942	AGCAAGATGGTAGCATTGGAGA	10777		A
GAM1961	CAAAGTGCTGAGATTACAGGCA	10694	THC1587276	A
GAM1975	TTCCAAGCCTTCCCCGGGATCA	9905	THC1498867	A
GAM1975	TGGTGGGGAGAGGCTTGGGAAG	9905	THC1498867	B
GAM1976	CTGGCTCCCTCTCTTCTCTCCC	10517		A
GAM1997	ACTCAGAGCCATTCCGCTCAGG	10825	THC1410841	A
GAM1997	AGCGGAGACCTGAGCTATGAGT	10825	THC1410841	B
GAM2010	CATTGCACTCCACCCTAGGCAA	9634	THC1453894	A
GAM2014	GCTTCTCCTGTCCCCTCCCTAC	10682	THC1469417	A
GAM2022	GTTGGGTGTGAGGGGGGTCCCA	10258	THC1596797	A
GAM2027	CATGGTACTGCCACAGAAGAGT	10467	THC1430335	A
GAM2033	TCAAGCTCATTCCTCTAACCTC	10236	THC1566321	A
GAM2051	GAACAGCTCCAGTCTACAGCCC	9948		A
GAM2058	TGAAAGAGATGTGGTGTGTGAA	10513	THC1440062	A
GAM2062	CCCAGGAGGCGGAGGTTGCAGT	11181	THC1486208	A
GAM2098	TTGAGCACAGTTTGAGGAGTGT	10197		A
GAM2171	GGCAATATTCCAGGATAGGCTG	10110		A
GAM2221	TCCAAAGACTCAACAGTTAGAC	9920		A
GAM2223	TCTTAGATTGAGAAGATGTGGC	11022	THC1449211	A
GAM2233	GGACTGCAGTCACACTCTAAGA	9755	THC1555864	A
GAM2233	TCTTTCTACACCTCTGCCAGTG	9755	THC1555864	B
GAM2251	GATTCCTCCTCTTTAAAATGGT	11172	THC1481584	A
GAM2251	ACCCACCCTCTGTGAGGAGGAT	11172	THC1481584	B
GAM2260	GGGCATGATGATGGCACTAGCG	10524		A
GAM2262	TGAGGTAGGATGATTGCTAGCT	9724		A
GAM2263	TTATCCTAAATGTGTTTTGAAG	9619	THC1454581	A
GAM2263	AATTTAGAATCGTTTCTGATAG	9619	THC1454581	B
GAM2270	ATCACATTGCCAGTGATTACCC	10841	X	A
GAM2272	TCTGCTGTGATGGACACTTGT	9891	THC1581432	A
GAM2290	TGTTATTTTGTCCAAGAGAGAG	9630	THC1489192	A
GAM2300	TTAGCAGTTGTGAGACCCTAGA	9665	THC1524612	A
GAM2300	TTTGGGGTCTCCCCAGCATGCA	9665	THC1524612	B
GAM2306	TGGGTTAGTGGTTGAATAGTTT	11288		A
GAM2309	AGTTCCATGGAAAACAACAAAG	10021	THC1531218	A
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GAM2391	TTAGCAGTTGTGAGACCCTAGA	10853	THC1524612	A
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GAM2393	AATGAAGCCACAGAGATTTGCT	9775	THC1456561	A
GAM2398	ATCTAGAGAGGCAGTCTGGCCA	9611	THC1481765	A
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GAM2440	ACTGCACTCCAGCCTGGGTGAC	11256		A
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GAM2519	ACTGCAGCTTCAGGGACTTGTG	9913		A
GAM2543	TTAATGCTAATCGTGATAGGGG	11152		A

GAM2565	ATGACACAGTGGGGCCAGTTGG	10306	THC1413987	A
GAM2591	ACCACAGTGTCACAGAGTCCAT	10044	THC1523079	A
GAM2608	TAAGGTGCATCTAGTGCAGTTA	10221	X	A
GAM2618	TGGGAAGATGCTGGCAAGGTGC	11220		A
GAM2624	TCTGAGCCCAGGAGTTTGAGGC	9903	THC1408939	A
GAM2624	GCACTCAAGCCTGGGTTACAGA	9903	THC1408939	B
GAM2628	TCCCTTTGAAGCCAGGTTCCAG	10846	THC1504686	A
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GAM2640	ATGCCTGTAATCCCAGCATTTT	11205	THC1446810	A
GAM2672	TGTGACACGTTCATTCTGCAAG	10457		A
GAM2732	ATCACTTTGCAGGGATTACTAA	10785	THC1524958	A
GAM2762	CACACAGTCGTGTAGTTTTGCG	10200	THC1427725	A
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GAM2780	TGAGTGACAGAGCAACACTCTG	10174	THC1434204	A
GAM2799	TTGCCCAGGCTGGAGTGCAGTG	9754		A
GAM2799	CACTGCAACCTCCACCTCCTGG	9754		B
GAM2807	AATCTCCATTTGTAAATGTGAC	9926		A
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GAM2817	TGATTGTATGATATATGAGTTT	10420	THC1503496	A
GAM2839	GGGTCTCAAATGAGGGACATTT	10129	THC1414413	A
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GAM2846	TATTAGTTGATTCCAAGGGACC	10104	THC1460148	A
GAM2868	TGGAATGGCTGAAGACTGTGAA	10046	THC1479162	A
GAM2887	GGCCTGAGGTCAGCAGTAGAGG	10789	THC1565280	A
GAM2908	CCACTGCACTCCAGCACTCCAG	10680	THC1551777	A
GAM2911	GACACAGGCCCAGAGAGGCAG	10165		A
GAM2920	GCTGAGACCACCCTTGCCTGCC	10706	THC1537468	A
GAM2920	GGCTGGGCATGGTGGCTCACGC	10706	THC1537468	B
GAM2927	ATAAAGCAGGTTAACAAAGCTG	10001	THC1533857	A
GAM2931	TGGAGAGAGCAGGTTGCTAAGA	10668		A
GAM2950	AGGCCAGAGAGGACTCTCTTTT	10005	THC1595210	A
GAM3004	TATTTGTTTTTAATGCTGGGTG	10037	THC1562045	A
GAM3028	TTCTGGTGAATTCAGGATGGTA	9743		A
GAM3057	GGCATGATTCAGCAGAGGAGAG	10217	THC1540352	A
GAM3061	TTAAAGATCACTTGACATGGAC	10250		A
GAM3064	TTTAAGCTATAGTTCCAGGCCC	10671	THC1413273	A
GAM3065	GACATGATGTAGCAGATGATGG	10649	THC1561193	A
GAM3077	TTACCATGTTGGCCAGGCTGGT	9975	THC1482310	A
GAM3081	CTGGGATTACAGGTGTGAACCA	10054	THC1486336	A
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GAM3091	TGGGAGGCTACACGTTTCTCCA	10253	THC1583417	A
GAM3123	CTTCAATGCTTGAGAAGTCGTA	10050	THC1538938	A
GAM3126	TGAGATCATCGTTACAAGCAGC	11212	THC1521438	A
GAM3132	TAAGTGCTGCTGATTTTGGAAA	9697	THC1542535	A
GAM3138	TGGTCTCTTGAAAGAGGCTCTT	9652		A
GAM3140	TGGAGCAGAAAGGCAGGAGTCC	9763		A
GAM3143	CAGAGGATGCGGCTGGGAACGG	10699	THC1438390	A
GAM3157	GTGAAGGTAGGTTTCAGGTTTG	11285	THC1518042	A
GAM3163	CACTGCAATGACTGTCAGAACA	11019	THC1420983	A

GAM3174 TTTGATGCATGTGACCTGGGAT 9656 THC1562314 A
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GAM3190 CATTGCACTCCAGCCTGGGCAA 10415 A
GAM3195 TGAGGGCAGGTGTGAAAATGCT 10884 A
GAM3211 TCTCATATAGCTGGGTTGCAGC 10984 THC1551612 A
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GAM3236 TTCAAGAAAGCCAAGATGGCTG 10435 A
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GAM3350 TGCAGATACATGTGTAACTGAA 10894 THC1572440 A
GAM3368 GATTTTCATAGGAGCAGAAACC 10953 THC1586053 A
GAM3414 TGGAGAAATTATATTTTACTAA 9917 A
GAM3422 TCTTTTTTGGGAGACGGAGTCG 10760 THC1481240 A
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GAM3946 TTGCCCAGGCTGGAGTGCAGTG 10833 THC1586614 A
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GAM4011	TGTGTTGGAGCAGAGGCAGGGG	9765	THC1541347	A
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GAM4020	AGCTGTGAGCCTGCCTTCCAGT	9615	THC1452346	B
GAM4027	TTCCTGGTGGAGGCATTCGGAG	11191	THC1482663	A
GAM4064	TGGTCCAGAGGAGGAATGAGGG	10022	THC1476990	A
GAM4074	TACGCTGTGCTGTGACATGGTA	10140		A
GAM4085	TGTAAACATCCCACACACTCAG	9711		A
GAM4130	GGGCCATGACAGGGAGATAGGC	10199		A
GAM4136	CCAAAGTGCTAGGATTACAGCC	9668	THC1588241	A
GAM4142	TCTTTGATCTCTTCCGGGGCTT	10081	THC1445449	A
GAM4147	AATCTCCATTTGTAAATGTGAC	11207		A
GAM4152	ATGACCAGGAATTGAGAGACTG	10154		A
GAM4188	GGAAGAATGTGCTTTTGTTGTT	9909		A
GAM4189	GTCCAGTGCTCACTGCCGACAT	9666	THC1493174	A
GAM4199	GGGGGATGATAGCAGCCAG	10173	THC1472943	A
GAM4199	CCTCTCCATGTACCCATTCCCC	10173	THC1472943	B
GAM4205	TCAGGTTCCTGATTGGAGTTCT	10494	THC1562945	A
GAM4238	AGAGATAAAGAGGTTTAGGCAG	10112	THC1595205	A
GAM4243	AAAGGCAGACGGTGAATGCCTT	9595	THC1535339	A
GAM4298	TGGCAAGGTGTGGGCTAGAGAT	10843	THC1441053	A
GAM4315	TAGCACCTTCTGAAATAACGTG	9960		A
GAM4364	AGGGTTGTTAGTTTTTTGGTTG	9623	THC1454247	A
GAM4376	GAGGTAGAGGTTGCAGTGAGTC	10325	THC1549027	A
GAM4377	CCCTGGGCTGGTGTTTGACTTG	10976	THC1566325	A
GAM4377	GAGTACAAATGAAGTCTGTGGG	10976	THC1566325	B
GAM4382	TGACTGGAGGAAGGGAGGTAAG	9983		A
GAM4398	ATAGAAGAGCAGTGGGGTAGAA	11199	THC1449412	A
GAM4408	TTTGGATTCCTGGTTCCTACAG	9746	THC1595183	A
GAM4423	AAAGGAGTTTGTGACATTGACA	10486	THC1488043	A
GAM4426	GAAGTTTGAAGCCTGTTGTTCA	11283	THC1456099	A
GAM4429	CGACTCTTGACCATGGCTGGGG	10859	THC1500843	A
GAM4432	CAGGTGCAAGTGTTAAAGGGTA	9931	THC1504877	A
GAM4446	GTCGGGAGGAAAAGAAAGAAGA	10969	THC1555513	A
GAM4446	TTTTTATCTTTTTCTCCAGATG	10969	THC1555513	B
GAM4448	TCTTTGCTGGAAGGTGCCTCCC	9953	THC1463380	A
GAM4459	TGACAAGATACAGGGTAGTGAA	10240		A
GAM4516	GGCATGATGGAGAGGGTGGAGA	10651	THC1428232	A
GAM4538	GAAACTAGTGTTGGGACAAAGG	10975	THC1501655	A
GAM4544	GGTGATGCATTTAAAAGGGCAG	10926	THC1553853	A
GAM4557	TATTACATTCATTTTGATGGTT	11230		A
GAM4561	AGTAGACAGTGGCAACATAGTC	9992	THC1510400	A
GAM4571	CCTGGAGTGACAGGTGTAGCCT	9771	THC1427370	A
GAM4571	GCTGCTGCCTCAACATTTTAGG	9771	THC1427370	B
GAM4633	TCTTTTTGTTGTAGCTGTATGG	11142	THC1437961	A
GAM4650	ACTGCACTCCAGCCTGGGTGAT	10553		A
GAM4656	AAGGCACTTGCCCAGAGCTGCA	10921	THC1539180	A
GAM4671	ACCAGCTGCATCCTGCAAACTT	10032	THC1472112	A
GAM4671	CACTTTCAGAGATGCCCTGAGT	10032	THC1472112	B

GAM4685	AGACTGGCCTCAAGCTCCCAGA	11293		A
GAM4690	TCTGTCATTTTTCTCTTTCCAT	10888		A
GAM4707	CATTGCACTCCAGCCTAGGCAA	10352		A
GAM4709	CAGCAGTGTTGCGAATCATCAC	10157	THC1534017	A
GAM4733	TCCCCAAGCCTTGTACCAGCGT	9593	THC1586272	A
GAM4738	TTAATGCTAATCGTGATAGGGG	9729		A
GAM4769	CGCTATGTTGGCCAGGCTGGTC	10176	THC1416609	A
GAM4796	TACTCATTTATGCATTGTTTTG	10896	THC1471744	A
GAM4800	GGAAAACAAGTACCCCTGGAAC	10690	THC1585438	A
GAM4803	ATGGGCAAATACTGGGAGCTGG	11165	THC1452742	A
GAM4814	TTGCCCAGGCTAGAGTGCAGTG	10992	THC1564358	A
GAM4814	CACTGCAACCTCTGCCTCCTGG	10992	THC1564358	B
GAM4821	TATGTGAGACACTGTCCTAGGC	10930	THC1410801	A
GAM4821	GCCTGGCCTTCCTGTGTTTTAC	10930	THC1410801	B
GAM4844	TGATTGTATGATATATGAGTTT	11226	THC1503496	A
GAM4895	GCTGCTCCTGCTCTCCCTCTCC	10116	THC1589309	A
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GAM4913	TATAACAGCCAGCTTGGATTCA	9599		A
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GAM4946	TGAGATGAACCCGGTACCTCAG	10922	THC1592088	A
GAM4969	AGCAGAGCCACCAAATTTAGTG	10491	THC1501266	A
GAM4971	TTCCTTCAGTTCAGGGAACCCT	10965	THC1443612	A
GAM4975	TTCCCTCATTCTCCACCCAGTC	9993	THC1536309	A
GAM4986	TCTGCTGTGATGGACACTTGTA	9981	THC1581432	A
GAM5000	CAGTGCTGAGTATGAAAGGCCC	10518	THC1507051	A
GAM5008	CCTGGAGTGACAGGTGTAGCCT	10156	THC1427370	A
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GAM5011	CATATCTCCAGGTTCTGCTGGA	10837	THC1482318	A
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GAM5035	AGGTCCTCACACACAGCTCTGC	10820	THC1549688	A
GAM5035	GCAGGCTGGTTGGTGAGGCAAA	10820	THC1549688	B
GAM5048	TTTACAGATGGCAAAGATCTGG	10510		A
GAM5058	ACTGCACTCCAGCCTGGGTGAC	10645	THC1529894	A
GAM5082	TAGAGTTATATGATGTGCTAGT	10778		A
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GAM5090	CGGCAAGATGCCGGAGTGCTGG	10160	THC1554616	A
GAM5127	TCCAGGGTGGGCCTCAGACCCT	10734	THC1558776	A
GAM5142	CACCCAGGCTGGAGTGCAGTGG	9751	THC1502117	A
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GAM5209	CCAGCCTGAGGTTCCTGGAGGG	10525	THC1457464	A
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GAM5222	TCCTCATCTTTGAGTCCCAGCG	9898	THC1412192	A
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GAM5254	TGAGTGTATGTGTGAGAGAGAA	11132		A
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GAM5270	TCAGTGCAAACTAAGCAGGGCA	10016		A
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GAM5272	CTCACCAGTTACTCTCCAGTTG	10727	THC1504618	B
GAM5278	TACCCCGATAGGGAGGGTGGGG	10980		A

GAM5278	ACCATCTTCCCTTTCTCGAGTA	10980		B
GAM5292	GCCCTGTTGACCAGAATTTGTT	11143	THC1549749	A
GAM5324	GATATCATGGGAAGGTGTACTT	10951	THC1448850	A
GAM5329	AGCAAGATGGTAGCATTGGAGA	11139		A
GAM5340	TGATTGGCAATGGTTATGACGG	9709	THC1540166	A
GAM5342	GTTCTGCTGAGATACGTGCTCT	9601	THC1551467	A
GAM5354	TACAGCTCTGCTTCTGGCTCAC	11223	THC1577776	A
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GAM5371	CTCACTGCAACCTCCGCCTCCC	9757	THC1471364	A
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GAM5374	TACTCATTTATGCATTGTTTTG	9987	THC1471744	A
GAM5385	TCACAGTGAACCGGTCTCTTTC	9977		A
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GAM5422	ATGAGAGTAGGAGTTTGGGCTC	10860		A
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GAM5486	TGAGGAAGGTGTGAGAAATGAG	10210		A
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GAM5526	AATGCTGTGCCAGAGCTGCACC	10393	THC1592424	A
GAM5560	TGAAATGCTTTTAGGACACTGC	11007		A
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GAM5615	AAATCCAGAATCTAGACTGAAT	10117	THC1518024	A
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GAM5703	GTCCAGTGCTCACTGCCGACAT	10256	THC1493174	A
GAM5728	GGCATGTGTGAGCAGCTGCAGG	10119		A
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GAM5798	GAAAGTAGTAAGTTGTATAGTT	10000		A
GAM5800	AGTATTACAGCAGGTACTGGTT	11225		A
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GAM5809	GACAAGAGGCACAGACAGCAGG	11252	THC1448987	A
GAM5814	TGCAAGTCTGTGATTTTGTGTT	9664	THC1515190	A
GAM5823	GGAAAGTTAAAGATGTATGTAT	10909	THC1569880	A
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GAM6700	TCAGAGTAGGCTTGATGTAATC	9606	THC1411123	A
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GAM6836	ACTGCACTCTAGCCTAGGTGAT	10334	THC1516956	A
GAM6840	GCTGAATTTTGACTCCATCTCC	10967	THC1410381	A
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GAM6982	GAAGGCAGTAGGTTGTATAGTT	9985	THC1562390	A
GAM6994	TTGCCTAGGCTGGAGTGCAGTG	11149		A
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GAM7017	TCTGCTGTGATGGACACTTGTA	10244	THC1581432	A
GAM7022	TTGGTTGCTGATGAGCTTTGAG	10767	THC1416555	A
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GAM7095	TGTGAGAGAAATGGCAAGTTGG	10960		A
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GAM7140	TACAGGCAGGCACAGAGGCAGT	10443		A
GAM7146	TGCTGTAGTATGTATATAGTAT	9924		A
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GAM7166	AGGGAGTTTACATGTTTTCTAA	10492	THC1458161	A
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GAM7199	TGGCAAAGAAGGCAGTACAGTT	10669	THC1599986	A
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GAM7241	CTCAGTGTGAAGAACTACGGGT	9910	THC1530062	A
GAM7250	GAAGAGCTGTGTGCTGTGATGT	9971	THC1555889	A
GAM7255	TGGTCTCTTGAAAGAGGCTCTT	10218		A
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GAM7260	ATGTCAGTGAAGAGGTCTGGCA	10138	THC1520561	A
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GAM7272	CTGGGCAGTAATGTAGTTGAGA	10040	THC1485240	A
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GAM7320	GGTTCTCAAATGAGGGACATTT	10130	THC1414413	A
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GAM7350	CTAATTGTTCCTGCAGGTAGTA	10828	THC1413248	A
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GAM7366	TATTGCACTCCAGCCTGGGCAA	10635		A
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GAM7374	CAGATCTGGGATACAGCTGTGG	10056	THC1530397	B
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GAM7546	TGATGCTTGAGCACAGTACCTC	10064	THC1551816	A
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3352	BACE	GCCAGTGCGAGCCCAGAGGGCCCGAAG
3353	BACE	GCCAGGGACGGACGTGGGCCAGT
3354	BACE2	GCCAGAATTCACTAGGA
3355	BACE2	GCCTTCTCCCCTCCCGCGAGCC
3356	BACE2	GCCTGAGCCCGGCGAGGGTGGGGAGGG
3357	BACE2	GGTGCGCGCCCATCCCTGCCCGCAGCCCCG
3358	BACE2	GTGGGTTTCTCTGTGCTCTGA
3359	BACE2	CTTGTCTTAATCGTCCTGCTGCTGC
3360	BACE2	GATGGTCCTCACAAGCCTCTTCTG
3361	BACE2	GATGGCAGGAGAATCAGCCTGG
3362	BACE2	CCGCTCAGTCTTTGAGCGAGCCCA
3363	BACE2	CCTGCTGCTGCTGCCGTTCCGG
3364	BACE2	CTCCCAGATGCCTTCTAGATT
3365	BACE2	CTGAGCCCGGCGAGGGTGGGG
3366	BACE2	CGTCTGTGGAGCCATCCTCCT
3367	BACE2	AACCAAAACAGAGTGGATTGGGCTGCA
3368	BACE2	AGACCTGGAACCAGAGCCACAG
3369	BACE2	AGCCAGAATTCACTAGGA
3370	BACE2	AGCCTCCTCCCCTCCCGCGA
3371	BACE2	ACCGGCTAGGCTGGGCGCGCCCCCC
3372	BACE2	ACAGGAAGCTTTTTGTAT
3373	BACE2	ACCAACATAAAACAAAAC
3374	BACE2	AATGATGAGTCCTCTCTGGTCAGACAT
3375	BACE2	CCCTCCCGCGAGCCTCCTCCCC
3376	BACE2	CCCTCACCCAAAAGAATTATCATC
3377	BACE2	CCAGGGTCCTGTGCCTGGA
3378	BACE2	CCAGGAAGAGTTCTATCCCCAAGCTGG
3379	BACE2	CCAAAACAGAGTGGATTGGGCT
3380	BACE2	CAGGAGAATCAGCCTGGGGCCTGGGGA
3381	BACE2	TGTGCCTGGATGGGGGTG

3382	BACE2	TTGCCCAGGGTCCTGTGCCTGG
3383	BACE2	TTGCCCAGGGTCCTGTGCCTGGATG
3384	BACE2	TTGCCCAGGGTCCTGTGCCTGGATGG
3385	BACE2	TGTCCCCGCTCAGTCTTTGAG
3386	BACE2	TCTGTTCTGCTCCCAGATGCCTTCTAG
3387	BACE2	TCTGCTCCCAGATGCCTTCTAGATTCA
3388	BACE2	TAATTGCCTTTGAGGTTAT
3389	BACE2	GTTCTCTTCTCTCTTCAATCTCT
3390	BACE2	TAGGAGGTCATCAACCGATG
3391	BACE2	TCAATGATGAGTCCTCTCTGGTCAGA
3392	BACE2	TCTCTGTTCTGCTCCCAGATGCCTTC
3393	BAX	TCACCATCTGGAAGAAGATGGG
3394	BAX	TGTGTTTTTCCTCCATAAATTAT
3395	BAX	ATCTACCCTGCTGACCTCCC
3396	BAX	AGGGGTGGGGATTGGGGGACATGGGC
3397	BAX	AGTGCCTTCTGCCCTCCCTGGAGCCT
3398	BAX	CCTTCTGCCCTCCCTGGAGCC
3399	BAX	GATTCATCTACCCTGCTGACCT
3400	BAX	GACCCTCTGACCCTAGCTCT
3401	BAX	GGTCTTGAGGGGGTAATAAACCTCC
3402	BAX	GGCCTCCTCTCCTACTTTGGGA
3403	BAX	GCATTTTTCTTACTTTTGTAA
3404	BCHE	GCCTGGTTCAATTTCTTTCTTTCCTTA
3405	BCHE	GTCCAATTTACAGGCTGGAGCAGCAGCTG
3406	BCHE	GAGATATTAAAATAAGCACAGAA
3407	BCHE	CTCCTTGCAAACTTTACCATCTTTGTTGCAG
3408	BCHE	AGATATTAAAATAAGCACAGAAAAT
3409	BCHE	TTATGTAGCTGAAACAAAAATG
3410	BCHE	TTATGTAGCTGAAACAAAAATGCCAGA
3411	BCHE	TAGTATTTTACCTAGCATTTCA
3412	BLMH	TCCTAGAGTAGAGTGGAGGGAGGGTGG
3413	BLMH	TCATCTCTAACAGCTCAGGAT
3414	BLMH	TTAGCATTTTAATTAGATGTAATTGTT
3415	BLMH	TTCCAGTCTCCACCAGGAA
3416	BLMH	CCTTGTTCCTAGAGTAGAGTGG
3417	BLMH	GAGGGAGGGTGGCCTAAGAGTTGAGC
3418	BLMH	GCCCTCCAGCTCTTTCCTCCTTCCA
3419	BLMH	GCCAAAGTTATGCAAGGGACTGTGTG
3420	CASP3	GCATGGTCAAAGGCTCAA
3421	CASP3	GTCAATGACAGTTTCTTTTT
3422	CASP3	GGCATGGTCAAAGGCTCAAACCTT
3423	CASP3	GAATTTTTATGATATTCCCCC
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3427	CASP3	CTCCAGGCCTCAGCAGGTGCG
3428	CASP3	CTCTCATTTTGACCTACTCTCAT
3429	CASP3	CTACCTCAAACTTCCAGTCA
3430	CASP3	CTCAGCAGGTGCGGAGCCGTCACTGCA
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3432	CASP3	AGCCTGTTCCATGAAGGCAGAG
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3445	CAV1	TGCTGCCAGAACCTTGGGGA
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3455	CAV1	CCCTGCTCAGTAAAGCACTTG
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3457	CAV1	CAGCAAACTCTTTTCCCACTGT
3458	CAV1	CCAACAACCTCAACTGCCTA
3459	CAV1	ATACAAGATCTTCCTTCCTC
3460	CAV1	AACCAACAACCTCAACTGCCTA
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3467	CAV1	AGATGGGGGAGGAGGCAGTAATAA
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3469	CAV1	CCTCCCAGCCACCGCCCCCCTC
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3476	CAV1	GAACTCAAACTGAGGAATTTCA
3477	CAV1	GAGGGGCTGTAAAATGGAGGC
3478	CAV1	GAGGCTCCCTCCCAGCCACCGCCCCCC
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3482	CAV1	GCTTTTTATTCCTCCTGCTCATA
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3484	CAV2	GCACTGTTCTGATTATGTAAGCATTTG
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3486	CAV2	GATTGGGATACTGTAATACT
3487	CAV2	CTTTGGAAATAAAAGATAAAAG
3488	CAV2	CTTGGACCCCAGGTCTGGAG
3489	CAV2	CGGGACGGCCGGGCTGGGAGCTGG
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3495	CAV2	AAGATGTTTCATTTTACTGTATAT
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3497	CAV2	AGTATACATTTTATAATGATGAACTT
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3506	CHAT	CCAGCGCACAGCCTGGGCAG
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3521	CLU	CGCCCAGCCTCTCCCCGCTCTGGAT
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3524	CLU	AGAACAGAATTGCTCC
3525	CLU	ACCGCAAAAAGCACCGGGA
3526	CLU	AACCAGGCCCCAGCCTCCAGGC
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3528	CLU	CCCCGCTCTGGATCCTGCACT
3529	CLU	TCCAGGCCCCCAACTCCGCCC
3530	CNTF	TCTCTCTTCCTTGCTTTCTCTTCT
3531	CNTF	GTTGATTTAAACTCTTAGA

3532	CNTF	TGGCTAACTTTTATTATCTTCTATAT
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3534	CNTF	TCTGAACTTTGGAAGCTGGGGA
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3561	CRAT	GCCACTGCCACCTGCCTCC
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3736	DHCR24	GAAGCATCTGTCTTGTCATTCCA
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3756	DLST	GGGCTGAGGAGGCAGTTTTTGT
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3781	DLST	TTCAGTTAAGTTGCTGTAAGCA

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3783	DLST	TTCATTCTCCGTTGTCATTGACTTCA
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3785	DLST	TTGCCTTGAGCTTTTCAGTTAA
3786	DLST	TTGTCTCTTCCTCTGCAGGACA
3787	DSCR1	TGTGGAGGTGGCTGGTC
3788	DSCR1	TGTTGTAGGAAAAGCTGTTC
3789	DSCR1	TGCATGCTTTGGAAATTTGGAA
3790	DSCR1	TGCGGAACTCTTCCTGGAATGC
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3792	DSCR1	TGCTTTGGAAATTTGGAAGATGGT
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3795	DSCR1	TAGGTATTATATTTTGGCCTTAC
3796	DSCR1	ACAGGAAGCCGCCTAGTGCAG
3797	DSCR1	ACTCTTTGCAACAGCACTTGCT
3798	DSCR1	AGCAGTTTCACTGCCAACTTTT
3799	DSCR1	AGGACGCATTCCAAATCATACTC
3800	DSCR1	AGGAAAGCGTTTGGAAAACGTATCA
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3802	DSCR1	ATGCAGTGCCTTTCCCCATTCA
3803	DSCR1	ATCAGTGAGCTCAGGAGAGAGCT
3804	DSCR1	ATCATACTCACGGGAGGAATC
3805	DSCR1	GGGAGCCGGTTTGGGAGAGACCA
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3813	DSCR1	CCTGTTTCTAAGTGGCCTGCAGG
3814	DSCR1	CCTGCAGGGGCCACTCTCTA
3815	DSCR1	CTTTTCTGGTAGGTTCTGTCTGTGCCA
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3817	ESR2	AGAAGGCAAGGCCGGTGTGTTTAT
3818	ESR2	TGCAGGGCGAAGAGCAGGCGGCGAGC
3819	FHL2	TCTGTAACCTCCCGTTGCGTC
3820	FHL2	TGTCGCCCAGGCTGGAGTGCAG
3821	FHL2	TGTCGCCCAGGCTGGAGTGCAGT
3822	FHL2	TCACTGCAAGCTCTACCTCTT
3823	FHL2	TACAGGTTGCTGAAAAGCCAGGA
3824	FHL2	TCTCACCCAGGCAATCTTGCCT
3825	FHL2	TCGCCCAGGCTGGAGTGC
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3827	FHL2	TCGCCCAGGCTGGAGTGCAGTG
3828	FHL2	TTCAACACAGAGAAGTTGCTGCT
3829	FHL2	TTTCTCTCACTGTCTATTTA
3830	FHL2	TTTGTCGCCCAGGCTGGAGTGC
3831	FHL2	TTTGTCGCCCAGGCTGGAGTGCAGTG

3832	FHL2	AGCCTCCCAAGTAGCTGGGACT
3833	FHL2	AGCTCACTGCAAGCTCTACCTC
3834	FHL2	AGCTCACTGCAAGCTCTACCTCTTGGT
3835	FHL2	ACGATCTCAGCTCACTGCAAGCT
3836	FHL2	AACCAAGATTATGTGACTTGCA
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3838	FHL2	AGGCTGGAGTGCAGTGGCACGAT
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3840	FHL2	CCCAGGCTGGAGTGCAGTG
3840	PRND	CCCAGGCTGGAGTGCAGTG
3841	FHL2	CCCAGGCTGGAGTGCAGTGG
3842	FHL2	CCAGGCTGGAGTGCAGTGG
3842	IGF1	CCAGGCTGGAGTGCAGTGG
3843	FHL2	CCAGCCGCCCGCGCCCTCCAGCCCCG
3844	FHL2	CCAGGGAAAGAGAAAACTCGCCCT
3845	FHL2	CCATTCTCCTGCCCCAGCCTCCC
3846	FHL2	CCCAGCCTCCCAAGTAGCTGGG
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3854	FHL2	GCCCAGGCTGGAGTGCAGT
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3855	FHL2	GGAGAGGGGAGCAGAGCCGGA
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3909	FLNB	TGCCTTCAGAAATAAGTCCTAGA
3910	FOS	TGAGCCAGGCCTGGGTCTGTG
3911	FOS	TCTGACATTAACAGTTTTCCAT
3912	FOS	TGCTTCACAGCGCCCACCTGTCT
3913	FOS	GTGTCTCTTTTCTCTTTCTCCTTA
3914	FOS	TATCTGTGCGTGAAACACAC
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3916	FOS	TGTTCTGACATTAACAGTTTTCCATGA
3917	FOS	AGCAGTGACCGTGCTCCTACCCAG
3918	FOS	AGGCAGCCGGCACCCACAAGTGCCACT
3919	FOS	ACACTTCAGAGAGCTGGTAGTTAGTAG
3920	FOS	ATTTAAGCATTGTTTGCTTATT
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3925	FOS	GCCCGAGCTGGTGCATTACAGA
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3927	FOS	CTTTTCTCTTTCTCCTTAGTC

3928	FOS	GAGAAACACATCTTCCCTAGAGGGTT
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3938	FPRL1	CATTCCTGCCTGACAGGACCA
3939	FPRL1	CCAGAGAGAGGCCAAGGCTGAT
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3942	FPRL1	CCCACTGCATTTGCAGCCTTGAGG
3943	FPRL1	CACAGGTTGTAGAGATAGAGATGG
3944	FPRL1	ATGGATTTGCACCCACTGCATTTGC
3945	FPRL1	ACACTCCTAAATTTAGAGTCAA
3946	FPRL1	AATAAACCACACTTAGTCCTGAT
3947	FPRL1	AGAGGTGGGGAACAAGTAAAAGCT
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4219	HTR2A	CCAGAAGCTCAAGGCTGCAGTGA
4220	HTR2A	AAAATGTTCTGACAGCATTTCA
4221	HTR2A	AAATGTTCTGACAGCATTTCA
4222	HTR2A	ACCAAATGCCTTT
4223	HTR2A	ACTATTGCTGCTTTCTCTTCTACTTCT
4224	HTR2A	ACTGCCATTTCCTCCTGGG
4225	HTR2A	AGACCAACCTGGGTAACAAAGT
4226	HTR2A	CTGTGGTCCCAGCTACAGGGGA
4227	HTR2A	GCAATTGCTTCTCTAAAACAGCACT

4228	HTR2A	CTCAGGTTTCCGGCTACTGA
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4230	HTR2A	GCAGTGAGCCAAGTTCACACC
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4232	HTR2A	GGAGGCTGAGACGCAAGGATCA
4233	HTR2A	GGAGGCTGAGATGGGAGGATCA
4234	HTR2A	GGTGACTTTCCTATGACACTC
4235	HTR2A	GGTATTTGGTAACTTGCTGT
4236	HTR2A	GGCTCGTGCATGTAATCCTAG
4237	HTR2C	GGCAGAACCTAGTCTTGTTGTTCAT
4238	HTR2C	GGTTTTGATCTCAGCATCCTG
4239	HTR2C	GTCAGTGAGTCAGAGGCAGA
4240	HTR2C	GCTTTGCAACCTTGTACTTT
4241	HTR2C	GCTGCAGCTAATTTGTGAAAGTG
4242	HTR2C	CTCACAGCACATTTGTTAAT
4243	HTR2C	CGCTAGTGGGTTATCAGCTAACACCCG
4244	HTR2C	CCTTTGTCAAATGGTATTTTT
4245	HTR2C	CCTTTCTCTCTTTCTTTTGTGC
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4247	HTR2C	CCGCCGAGGCGCGAGGTTGCGGCGCGCAG
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4249	HTR2C	GAAGAAGAAAGAAGACGCGAT
4250	HTR2C	GAAGTAGTGTGAGTGTTAGA
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4252	HTR2C	CTTACACACCTGAGAATGTGC
4253	HTR2C	CTTCAAAAACAACTAAAGGATGA
4254	HTR2C	CTGCCTGGTCTTCCTCCCGGACGCTA
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4256	HTR2C	AGGACTGAAGAAAATCCTTCAG
4257	HTR2C	AATTAAAAAGACACTTTTAC
4258	HTR2C	ACACAGTAAGATAGGTTCTGCTT
4259	HTR2C	ACAAGTGTTTCTAGTAACAGTATT
4260	HTR2C	ACAAGTGTTTCTAGTAACAGTATTTC
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4262	HTR2C	AATATAAATCACAGATTTCCA
4263	HTR2C	AACATAGTGGTATTTTAACATAGCAG
4264	HTR2C	CATGCATTCAGATCTGAAGTAG
4265	HTR2C	CAGCATCCTGGAAATTTGT
4266	HTR2C	CAGCATCCTGGAAATTTGTG
4267	HTR2C	CAGCATCCTGGAAATTTGTGTGCTT
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4269	HTR2C	CACACAACTGTGGATAAATTTT
4270	HTR2C	AGGCGCGAGGTTGCGGCGCGCAGC
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4274	HTR2C	TGAGTGTTAGAAAAAACTGGAA
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4276	HTR2C	TCTTCTGTCTGTACATCGTTGTC
4277	HTR2C	TGGAAACATCTGATTTCTGAA

4278	HTR2C	GTTTTGATCTCAGCATCCTG
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4281	HTR2C	TCAGTGAGTCAGAGGCAGA
4282	HTR2C	TGTGTGCAGAGTATACAAGTGT
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4284	HTR2C	TTGTACTTTACAATCATGCC
4285	HTR2C	TTTGGTTGCTTAAGACTGAAGCAA
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4289	IAPP	TGTCTTCAATTAAAAGACCACAGACTT
4290	IAPP	TCCAGCCTGGGTGGCAGAGTG
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4293	IAPP	TGACCAACGTGGTGAAACCCTGTCTCT
4294	IAPP	TGCCTGTAATCCCAGCTACTCAG
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5080	PRND	TCCAGTTTTTTGCCACTGCAA
5081	APPBP2	TCCGAGTAGCTGGGATTACAGG
5081	PRND	TCCGAGTAGCTGGGATTACAGG
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5492	THOP1	TCTCCTCTCTGGGAAACGTCCC
5493	THOP1	CGGCTGTCTTGCCTCTTGTC
5494	THOP1	GCGGCTGTCTTGCCTCTTGTC
5495	THOP1	GCACTGCGACTGCCCAGTCTGGCC
5496	THOP1	GGTGGAAGGAGGGAGGGAGCCGC
5497	THOP1	GGTGGAAGGAGGGAGGGAGCCGCAGGCG
5498	THOP1	GGCACAGTGCCTGGGACTGGC
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5500	THOP1	GGGGCAGGCTCTGGCACAGTGCCTGGGA
5501	TNF	GCTCCCCAGGGGAGTTGTGTC
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5503	TNF	CCTGGCCTCTGTGCCTTCTTTTGAT
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5505	TNF	CTGGAATCTGGAGACCAGGG
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5520	TNF	TGCTGGCAACCACTAAGAATTCA
5521	TNF	TTCCTTGAGACACGGAGCCCAG
5522	TNFRSF5	TGGCTCCAACACTGCTGCTCCA
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5524	TNFRSF5	TCCTGGCTCCAACACTGCTG
5525	TNFRSF5	TCACCCAGGAGGATGGCAAAG
5526	TNFRSF5	TCACCCAGGAGGATGGCAAAGAGAGTC
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5528	TNFRSF5	AGTGGGCTGCACCCACCCAG
5529	TNFRSF5	AGTTTGAGACAGGAGACCTGGCACTG
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5531	TNFRSF5	CAGGAGACCTGGCACTGGA
5532	TNFRSF5	CAGGAGAGACAGTGAGGCTGCA
5533	TNFRSF5	GAGACAGGAGACCTGGCACTGGA
5534	TNFRSF5	GCGTGAGGGTGAGGGGCTGG
5535	TNFRSF5	GGGGCAGGGGAGTCAGCAGAGGCCTCG
5536	TNFRSF5	GGCTCCAACACTGCTGCTCCA
5537	TNFRSF5	GGTGAGGGGCTGGCACTGACTGGGCATAGC
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5539	TNFRSF5	GTCACCCAGGAGGATGGCAAAGAGAGT
5540	TNFRSF5	GGTCACCCAGGAGGATGGCAA
5541	TNFRSF6	GTGAAAAACAACAAATTCAGTTCTGA
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5543	TNFRSF6	GGCAAGACTGCCCTTAGAAATTCTAG
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5545	TNFRSF6	GCCAGCCCTGGCTGCCCAGGCGGAG
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5559	TNFRSF6	TCCTCAAGGACATTACTAG
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5569	TNFSF5	AGTTCTCTTCTTTCCACCCTGTCCCTA
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5574	TNFSF5	CTATGAAAAGACAAGGCCAT
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5576	TNFSF5	CTCTGCCAGAAGATACCATTT
5577	TNFSF5	CTTGCAGGCTGTGGTGGAGCTGA
5578	TNFSF5	GCAGAAGGGAAATGGGGAGCCTCAGC
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5581	TRPM2	GGCTGTGTGACGGCTGCCTGAA
5582	TRPM2	GGGCACTGTCTGAACTCCTGAC
5583	TRPM2	GGGAGGGAGCTCTTTCTCTGGCCCTGCAG
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5586	TRPM2	GGCCTGGCTGGCTCTTCTGTGCTTTCCACAAA
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5630	TRPM2	TTCTCCTCTGACCCATCAGCT
5631	UBB	TTACTCTGCACTATAGCCATTTG
5632	UBB	TTACTCTGCACTATAGCCATTTGCCCCA
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5634	UBB	TGTGGGTGGACGTGGTTGGTGAT
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5636	UBB	AACCTGTTCAAAATGTTAATA
5637	UBB	ATGGCATTCGCAGTGCCCAGTGATG
5638	UBB	GCATTACTCTGCACTATAGCC
5639	UBB	GTGGGTGGACGTGGTTGGTGAT
5640	UBB	GTGGGTGGACGTGGTTGGTGATTGGC
5641	VLDLR	CACATTCTACTTCAGCTTTGG
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GAM NAME GAM RNA SEQUENCE TARGET REF-ID TARGET UTR TARGET BS-SEQ (UPPER:GAM;LOWER:TARGET) BINDING-SITE POS DRAW GAM

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TTAGCGAATTTGGGTCCT CAC
C

GAM25 AATTGCTTGAA CCCAGGAAGTG MME NM_007288.1 3 GGCTTCCTGCAAT - CC--- G A
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T TTAAC G

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TCT A-----

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-- AGC TC
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GAM281 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM281 CACTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC CT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
GAM281 CACTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM281 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
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GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM281 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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GCA
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GAM282 TGAGAGAGCAA APLP1 NM_005166.2 3 GGAAATTCTTATT A C-- -- A
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- CCC TT
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TT TCTCTCGTTCA TAAAGGG
TTTCCGG GAG
GAM282 CTGGCTCTACC APBB2 NM_173075.1 5 GAAGTTAGAGGGT CT--- -- C B
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CCGAGA TGGGAGA TGAAG
CCACC AA T
GAM282 CTGGCTCTACC PLAU NM_002658.1 3 TGCATGGGCTCGA A ----- CTTC B
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GACCGAGA GGGA GGGT
- AGCTC ACGT
GAM291 AGATAGTTCTC APBB2 NM_173075.1 5 CCTCAGCCAGAGA AGA----- TT A
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AAGACGAG --
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TC GTCG AGAGACA CAACTT
- TTGA -
GAM291 AGATAGTTCTC PRND NM_012409.1 3 CTCTTTGGAACAA TTCT ---- A
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TCTATC GACAACAA TCTC
---- GGTT
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GAM317 TAGGAAGTATT ADAM17 NM_021832.1 3 GTTTTTAAAATAT ---- T T A
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GTCC TTC TA AAAATTTTTG
AGTT - T
GAM317 TAGGAAGTATT APPBP2 NM_006380.2 3 TGTTTTTAAAAAA TA---- GT- A
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A TTTT TAAAAAATTTTTGT
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GAM317 TAGGAAGTATT GYPA NM_002099.2 3 TGTTTTTTAAAAG G T A
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A T
GAM317 TAGGAAGTATT IL1A NM_000575.3 3 CATTTTGGTAAAA - AC A
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GTTCTTCATAAAA GGTTTT
T AC
GAM329 TCATAAACTGG APPBP2 NM_006380.2 3 GACGTACTTGCAG G C TAC A
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AGTATTTGAC GTTC TG
- A CAG

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T GTAT ATCGTTCGTGGTGG
TTTCCATTC ---
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TGACGTGAGGTCGGACCCGCTG

GAM330 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
GCCTGGGTGAC GAGTGCAGT ACTGCACTCCAGCCTGGG GAC
TGACGTGAGGTCGGACCC CTG
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CGTAAA G TGA
GAM335 CCCCAGTCAAT DLST NM_001933.2 3 CTGGAGGACGTGG A C CC A
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GAM335 CCCCAGTCAAT TNFRSF5 NM_152854.1 3 GGTGAGGGGCTGG C----- AT---- T A
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TAGC GGGTCAGT CGGGGAG GG
CGATAC CACGGT T
GAM335 CCCCAGTCAAT TRPM2 NM_003307.1 5 TGGAGAGAGGACT - T- ATG A
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GGG GTC GT GGAGAGAGGT
A CT CA-
GAM347 TCATTGCAACC IAPP NM_000415.1 3 CAGGAGGCGGAGG A A
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GAM347 CTCCTAGGCTG ACE NM_152831.1 3 CCATTGCACTCCA G B
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GAM347 CTCCTAGGCTG ADAM17 NM_003183.3 3 CCACTACACTCCA T C B
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T CT- G
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CTT A
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T- G
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G GGGTCCGACCTCACGTCACC
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C GTGTTCGGGTCT CTCC GTC
C CACCA T C-
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CTGTTC GTGTTCGGGTCT CTCC GT
CTTGTC CACCA T
T
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C
C
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A- GGC GGCCA
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CGACTC TA AA
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GTGTTC GTCTCTCC CAC
C TA AA
GAM354 ACACAGGCCCA MAPT NM_173727.1 3 CACTGGGACTCGT - - AGG A
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TGTGTCCGG GT CTC GTCAC
T G AGG
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TGTCCGGGTC CTCC GTCAC
TC C AAG

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AGAT TGTCCGGGTC CTCC GTCAC
TAGACTC C AAG
GAM354 ACACAGGCCCA S100B NM_006272.1 3 ATTCTTTCTGCTA -------- CAGT A
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T TGTGTCCGG GTCTTTCT
ATTATATC TA--
GAM354 ACACAGGCCCA SLC17A7 NM_020309.1 3 ATTGCCTCTCAGG A----- AG A- A
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GTG TGGG CTCTCCGTTA
GTCGAA A- GA
GAM354 ACACAGGCCCA SNCB NM_003085.2 3 GCAACCCCCTCGG - A A CA- A
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TGTGTCCG GG CTC CC CG
A - C CAA
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GTGACGTGAGGTCGGA CCG
C C
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C CT
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GACG GGTCG GATCCGT
TTGTG GTC AG
GAM361 CATTGCACTCC IGF1 NM_000618.2 3 CTGTCCCCCAGGC A--- A A
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CCCC C
GAM361 CATTGCACTCC IGF1 NM_000618.2 3 TGTCCCCCAGGCT A--- A
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GTGACGTGAGGTCGGA CTGT
CCCC
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GTACGGC C
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TCCGT CATATA ATAACCT
GAA C TTAA
GAM388 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM401 TCACTGCAACC ACE NM_152831.1 3 TGGGAGCCGGAGG A C A
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C C
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GAM401 TCACTGCAACC NCKAP1 NM_013436.2 5 CGGAAGGCAGGAG TCA--- - A - A
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GCGCGG C C G
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GAM408 CTGGGATGGAG IGF1 NM_000618.2 3 TCTTTATTCTGCC C----- A - T- A
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GAM426 TCTGGATTTGA CRAT NM_004003.2 5 GGTGAAGCCTCTG T T- G A
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AG CCT GG TCTCCGAAGTGG
T TC G
GAM426 TCTGGATTTGA DHCR24 NM_014762.1 3 AGTAAGCCTCTCC TTT T A
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GAM492 CCGTAAAATGT CAV2 NM_001233.2 3 AAGATGTTTCATT CC----- TTC A
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GAM492 AAAGCTTTGTT PRND NM_012409.1 3 CAGATACACAAGT TTG --- B
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GAM495 AAAATGCTTAC BACE NM_012104.2 3 GCTAGTACCTGTA CAG A
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ATG

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ATG T
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AA GAC
GAM495 AAAATGCTTAC CAV2 NM_001233.2 3 GCACTGTTCTGAT A ------- A C A
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G ATTAGTC - -
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TACATG ATTAGTC
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GC
CG
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A TCT TCCGT CCCTCGTCT
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G TCC
GAM519 TGTGGCTTAGG CRYAB NM_001885.1 5 TCACACTCACCTA T------- T CA A
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CACCGA TCCACTC ACACT
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GAM519 TCCCACAGCTT CNTF NM_000614.2 3 CTGAACTTTGGAA A TAGCCA B
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- TTTCAA
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CCTAGCCACAG GCTGTGGTTTTCT CCACAGCT CCT GCCACAG
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GAM520 TCTGGTTTGAG BACE NM_138972.1 3 TTCATTGTCTCTA TC-- --- C A
AGACAATGACA TCTGAACCACCCT TGGTTTG AGAGACAATGA
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TCCC CTA T
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GAM520 TCTGGTTTGAG THOP1 NM_003249.2 3 TGTCATTGTCTGT T--- TTT-- G A
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T GGCC CT TCTGTTACTGT
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GAM550 TTTGCACACTT ADAM17 NM_003183.3 3 CTGACTTAAGTGT TCC C A
TCCAAGTTGCC GCAAA TTTGCACACTT AAGTTG
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GAM550 TTTGCACACTT B2M NM_004048.1 3 GGCAACTTAGAGG A--- CC A
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GAM550 TTTGCACACTT CTNND2 NM_001332.1 3 GTTAACTTGGAAA ACAC CC A
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ACT- TG
GAM550 TTTGCACACTT CTNND2 NM_001332.1 3 TTAACTTGGAAAT ACAC C A
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ACT- T
GAM550 TTTGCACACTT IGF1 NM_000618.2 3 GGCAATATAAGGA CA- AA-- A
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CTA AATA
GAM550 TTTGCACACTT PRNP NM_000311.1 3 GTAATTAAAAAAT TT ------ C A
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C CACCA T C-
GAM569 ACACAGGCCCA AVP NM_000490.2 5 CCTGTCCTCACCA A----- ----- - A
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CTTGTC CACCA T
T
G
C
C
GAM569 ACACAGGCCCA CRAT NM_144782.1 5 GCTGCCTCTACCG AC GC- ----- A
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A- GGC GGCCA
GAM569 ACACAGGCCCA CTSB NM_001908.2 3 CACAACCTCTCTG A----- CC CA A
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C GTGTTC GTCTCTCC CAC
CGACTC TA AA

GAM569 ACACAGGCCCA CTSB NM_147782.1 3 CACAACCTCTCTG A CC CA A
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GTGTTC GTCTCTCC CAC
C TA AA
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T G AGG
GAM569 ACACAGGCCCA NCSTN NM_015331.1 3 CACTGGAACCTCC AC A --- A
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TC C AAG
GAM569 ACACAGGCCCA NCSTN NM_015331.1 3 CACTGGAACCTCC AC----- A --- A
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TAGACTC C AAG
GAM569 ACACAGGCCCA S100B NM_006272.1 3 ATTCTTTCTGCTA -------- CAGT A
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T TGTGTCCGG GTCTTTCT
ATTATATC TA--
GAM569 ACACAGGCCCA SLC17A7 NM_020309.1 3 ATTGCCTCTCAGG A----- AG A- A
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GAM569 ACACAGGCCCA SNCB NM_003085.2 3 GCAACCCCCTCGG - A A CA- A
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TGTGTCCG GG CTC CC CG
A - C CAA
GAM572 TAAGTGAGTAG IGF1 NM_000618.2 3 GGAACAATGCTTT TGAGT- A
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GAM584 GGCCCCTTTGT TRPM2 NM_003307.1 3 GAGGTGCCTCAAC C TTTG G A
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CCG GG ACTCCGTG GAG
A TACA -
GAM588 TCCAGTGAAAC BACE NM_012104.2 3 GAAGAGACCAAGC TC T ----- A
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TC C TCGAA
GAM588 TCCAGTGAAAC TNFRSF5 NM_152854.1 3 ACAGGAGACCTGG AAA TG A
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G-- CA
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GAM593 ACAGCAAGTCT HTR2A NM_000621.1 3 GGTATTTGGTAAC CTT GT - A
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GAM593 ACAGCAAGTCT VLDLR NM_003383.1 3 AGGTTTGCAAAGA GCA T G A
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GA CTCGT
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CACCG ACCG CCACCGTAGCC
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GAM604 GTGGCATTGGT CRAT NM_144782.1 3 CCAATGCCACAGC CA G A
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CG A
GAM604 GTGGCATTGGT CTNND2 NM_001332.1 3 TTGTGTATATTAC GTG--- TG A
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CGCCGTAACCAC TGTG
ATTATA TT
GAM604 GTGGCATTGGT DHCR24 NM_014762.1 3 CCAGCCACCACTG CA TG AT A
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TG GT --
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TGGGATT -- GT AC
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C CCGTAACCAC CTGT CC
- AT TGT
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AC CCGT
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CG CCG AACCACCACC GTGG
TC - C A
GAM640 GGCGTGATCTT ACE NM_152831.1 3 GCAGTGAGCCAAG C CAC A
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CC CGCTAGAACCGAGTG
A ACG

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CC CACT GAACCGAGTG
A T ACG
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TTGT CTA GTC GAGTGGTG
C T- A
GAM640 GGCGTGATCTT MTNR1A NM_005958.2 3 TGTGGTGAGCCGA A
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T TA AG
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T G-
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ACAT CCACCAAC CT TTT CT
TG A A C
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GCT TAGT ATGTTCGT
G TGAC A
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TA G G
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ACGGTA G G
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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ATG T
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AA GAC

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ACGGT CAT TG
GAM760 AGTCAGACGTT GFAP NM_002055.2 3 GCCACTGCCACAC A----- T ACA A
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CAGTCTGCA ACCGT CG
CTCTCC C CAC
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- GATTG A T
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- - A G
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A G A-
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C CG TCCTACTTCTTCT CCTC
ATCC CAA C
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CTTGTC CACCA T
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A- GGC GGCCA
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CGACTC TA AA

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GTGTTC GTCTCTCC CAC
C TA AA
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T G AGG
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TC C AAG
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TGTGTCCG GG CTC CC CG
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A-- G
GAM828 ACACATCTAAT BLMH NM_000386.1 3 TTAGCATTTTAAT AC----- GGCT A
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-- C CT
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GAGACA - C
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GAM933 TTAGGGCAGGC IL1A NM_000575.3 5 GTTCTCTTCTCTA CAT--- A
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AGGCTTCACGT AAATATCTT AAGGTA AGGCTTCA GT
TTCTAT TCCGAAGT CA
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TC T - G
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TCT -
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A G CGT
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G ACTG
GAM1089 GTGTGGGCAGG PRND NM_012409.1 3 TGAGCCACCACGC T C-- - C B
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C CATCCGTCCCG CAC GAG
T CAC C T
GAM1089 GTGTGGGCAGG TGFB1 NM_000660.1 3 GGGAGGAGTTCCT T CCGTG B
GCCGTGCTCCC GCCCACC G GTGGGCAGGG CTCCC
C CACCCGTCCT GAGGG
- TGAG-
GAM1099 CTGTTCAGATC HTR2C NM_000868.1 3 CATGCATTCAGAT - T T A
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GAT AAGTCTAGAC TACGTA
G T C
GAM1144 TCTTGGTGCTT APBB2 NM_173075.1 5 TCATCCAGCCCAG GCTTTT A
TTGCTGGATGA AAACCAAGA TCTTGGT GCTGGATGA
AGAACCA CGACCTACT
AAGACC
GAM1144 TCTTGGTGCTT APOC1 NM_001645.2 5 CCTCCAGCAAGGA TGC TG A
TTGCTGGATGA TTCAGGA TCTTGG TTTTGCTGGA
AGGACT GGAACGACCT
TA- CC
GAM1144 TCTTGGTGCTT CHAT NM_020986.1 5 CATCCCTGCACCA ---- TT T- A
TTGCTGGATGA GGACTCACCAAGA TCTTGGTG CT TGC GGATG
AGAACCAC GA ACG CCTAC
TCAG CC TC
GAM1144 TCTTGGTGCTT CLU NM_001831.1 3 ACCGCAAAAAGCA - T ATG A
TTGCTGGATGA CCGGGA TCTTGGTGCTTTT GC GG
AGGGCCACGAAAA CG CC
A - A--
GAM1163 CTGCATGGAGG ACE NM_152831.1 3 TCATGGCCACCTC CTGCA----- T A
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ACCTCCACC GGTACT
AGAAACAGGG -
GAM1191 CTGGGCGTGTG ACHE NM_015831.1 5 CATCGGCCGCCTC C GT - A
AGGCGGCTGTG CAGCTCCCGG CTGGG GT GAGGCGGCTG TG
GGCCC CG CTCCGCCGGC AC
T AC T

GAM1191 CTGGGCGTGTG FHL2 NM_001450.2 5 CCAGCCGCCCGCG CT-------- TGA T A
AGGCGGCTGTG CCCTCCAGCCCCG GGGCGTG GGCGGCTG
CCCGCGC CCGCCGAC
GCCCCGACCT --- C
GAM1191 CTGGGCGTGTG MME NM_000902.2 5 GCAGCCGCCCAAC TG C G A A
AGGCGGCTGTG TCCTGG C GG GT TG GGCGGCTGT
G CC CA AC CCGCCGACG
GT T - -
GAM1191 CTGGGCGTGTG PSEN1 NM_007318.1 5 CTCCGCGCCTCAC C GCTGT A
AGGCGGCTGTG GCCCCGG CTGGG GTGTGAGGCG
GGCCC CGCACTCCGC
- GCCTC
GAM1191 CTGGGCGTGTG SERPINA NM_001085.2 3 GAAGCTCTCACAC G GC GT A
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GAC CGCACACTC TCGA
A -- AG
GAM1191 CTGGGCGTGTG SERPINA NM_001085.2 3 TGAAGCTCTCACA G GC GTG A
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GAC CGCACACTC TCGA
A -- AGT
GAM1191 CTGGGCGTGTG SNCB NM_003085.2 5 CGCAGCCGCCGCT C T -- A
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GACCC TAC CT CCGCCGACGC
C - CG
GAM1193 CACCCAGGCTG ACE NM_152831.1 3 CCATTGCACTCCA CA------ G A
GAGTGCAGTGG GCTGGGAGACACA CCCAG CTGGAGTGCAGTGG
G GGGTC GACCTCACGTTACC
GACACAGA -
GAM1193 CACCCAGGCTG ADAM17 NM_021832.1 3 CCACTACACTCCA C A
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GTGGGTCCGACCTCAC TCACC
A
GAM1193 CACCCAGGCTG FLNB NM_001457.1 3 CAAAGCCCTCCAG C-- T AG A
GAGTGCAGTGG CCTGTTTGTG CAC CAGGCTGGAG GC TG
GTG GTCCGACCTC CG AC
TTT C AA
GAM1193 CACCCAGGCTG FPRL1 NM_001462.1 5 CCACTGCATTTGC C-- - - - A
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T TGG GT CCGAC TTTACGTCACC
TAC A T G
GAM1193 CACCCAGGCTG IAPP NM_000415.1 3 CCACTGCACTCCA A
GAGTGCAGTGG GCCTGGGTG CACCCAGGCTGGAGTGCAGTGG
GTGGGTCCGACCTCACGTCACC

GAM1193 CACCCAGGCTG TGFB1 NM_000660.1 3 CCAGGCATTTGAG C----- ----- AG A
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ACATA TGGGTCCGACC TTACG A
ATACAA AGAGT G-

GG

CC

GAM1197 TGTCAGTTTTT MPO NM_000250.1 3 CTGAGTATGTGGA CA A A
TAAATACTCAG AGGCAGCA TGT GTTTTTTA ATACTCAG
ACG CGGAAGGT TATGAGTC
A- G
GAM1197 TGTCAGTTTTT SOD2 NM_000636.1 3 CTGAGTATGTTAA T- GTTT--- - A
TAAATACTCAG GCTCTTTATGACT GTCA TTTAA ATACTCAG
G CAGT GAATT TATGAGTC
GT ATTTCTC G
GAM1216 TACAGGCAGGC ADAMTS5 NM_007038.1 3 AAACCTTTGACTG GCA CAG A
ACAGAGGCAGT CCTGTA TACAGGCAG CAGAGG
ATGTCCGTC GTTTCC
A-- AAA
GAM1216 TACAGGCAGGC APBA2 NM_005503.2 3 GCTGCCTCTGCCA TA G GCA A
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GTC GTC GTCTCCGTCG
AC A ACC
GAM1216 TACAGGCAGGC DLST NM_001933.2 3 CAGCCTCTGTCCT G C AG A
ACAGAGGCAGT GGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - AC
GAM1216 TACAGGCAGGC DLST NM_001933.2 3 GCAGCCTCTGTCC G C AGT A
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GTGTC GTCC TGTCTCCG
G - ACG
GAM1216 TACAGGCAGGC NGB NM_021257.2 3 TTGCTCTGTGCTG GCA G A
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GTGTC TCGTGTCTC GTT
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GAM1216 TACAGGCAGGC NGB NM_021257.2 3 TTTGCTCTGTGCT GCA G T A
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GTGTC TCGTGTCTC GTT
AG- - T
GAM1216 TACAGGCAGGC SNCG NM_003087.1 5 CTGCGAGCTCCGT TA-------- C A --- A
ACAGAGGCAGT CCTGCCTGCAGCA CAGGCAGG AC GAG GC
GCACA GTCCGTCC TG CTC CG
ACACGACGAC - C GAG

AG
TC

GAM1216 TACAGGCAGGC TFCP2 NM_005653.2 5 GCTGCCTCTGGGA AG A--- A
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ATG CGTCTG GTCTCCGTCG
A- AAGG
GAM1216 TACAGGCAGGC TGFB1 NM_000660.1 3 CTGCCTCCTCCTG TA- CA-- A
ACAGAGGCAGT CCTGTCTGCAC CAGGCAGGCA GAGGCAG
GTCTGTCCGT CTCCGTC
CAC CCTC

GAM1216 TACAGGCAGGC TGFB1 NM_000660.1 3 TCTGCCTCCTCCT TA CA-- T A
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GTCTGTCCGT CTCCGTC
AC CCTC T
GAM1217 TATTACATTCA APPBP2 NM_006380.2 3 GACCAGTGTTGAT - TT TG --- A
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ATAATGTAA GT A T ACCAG
T CT GT GTG
GAM1217 TATTACATTCA APPBP2 NM_006380.2 3 GATAATGCAAAAA TCA ATG- A
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ATAATGTA AAAAC TAG
TTA GTAA
GAM1217 TATTACATTCA IL1A NM_000575.3 3 ATCATTTTCAAAA ACA --- A
TTTTGATGGTT TGGAGGGAATA TATT TTCATTTTGA TGGT
ATAA AGGTAAAACT ACTA
GGG TTT
GAM1221 TTCCAGATGGG BACE NM_138971.1 3 ATAATTTCTACCC - ACC A
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AGGGTT TACCCATCTTTA
G ATA
GAM1234 TGTCTTCATCC BACE2 NM_138992.1 3 TGTGCCTGGATGG GT AAC A
AGGAACCACAT GGGTG T CTTCATCCAGG CACA
G GGGGTAGGTCC GTGT
TG ---
GAM1234 TGTCTTCATCC DHCR24 NM_014762.1 3 TGTGTTCCTGGAG A C A
AGGAACCACAT AAGGCA TGTCTTC TCCAGGAAC ACA
ACGGAAG AGGTCCTTG TGT
- -
GAM1234 GCTGTGGTTCT IAPP NM_000415.1 3 TGTCTTCAATTAA G--- T GCA--- B
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T GACACCA GA ACTTCTGT
TTCA - AAATTA
GAM1234 GCTGTGGTTCT MME NM_007288.1 3 TGTCTTCAAAAGA TG --- GCA B
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CGAC TA AGA ACTTCTGT
GT CGA AA-
GAM1238 TGCACCACTGC CTSB NM_147782.1 5 GGGCTGGTGTGCA T T A
ACTCCAGCCTG GTGGTGCG TGCACCACTGCAC CCAGCC
GCGTGGTGACGTG GGTCGG
T G
GAM1238 TGCACCACTGC FHL2 NM_001450.2 5 CAGGCTGGAGTGC TGCA----- A
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C GGTGACGTGAGGTCGGAC
CTCTAGCAC
GAM1238 TGCACCACTGC IGF1 NM_000618.2 3 CAGGCTGGAGTGC TGCA----- A
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C GGTGACGTGAGGTCGGAC
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GAM1238 TGCACCACTGC PRND NM_012409.1 3 CAGGCTGGAGTGC ACCAC A
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ACG ACGTGAGGTCGGAC
GCA--
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T TG GGTGACGTGAGGTCGGAC
TTCTAG C
GAM1293 GCTGTGTTAAC ADAMTS5 NM_007038.1 3 AGTTTGAATAGTT G---- - A
TGTTCAAACTC AGACATGGAAATT CTGTGTT AACTGTTCAAACT
GGTACAG TTGATAAGTTTGA
TTAAA A
GAM1293 GCTGTGTTAAC APPBP2 NM_006380.2 3 AGTATAGAAAAGT - G AA- A
TGTTCAAACTC TAACACAAGT GCT GTGTTAACT TTC ACT
TGA CACAATTGA AAG TGA
A A ATA
GAM1293 GCTGTGTTAAC DHCR24 NM_014762.1 3 TAGATGAATGGTT - AACT A
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CGA CACAATTGGTAAGT
G AGAT
GAM1293 GCTGTGTTAAC PRNP NM_000311.1 3 TGTTTAGAGCAGT ---- - T A
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TGA TACAATTGACGAG TTTG
AGTC A T
GAM1294 TGGATTAGTAA DHCR24 NM_014762.1 3 CTCATTCTTCTTG ATT A A A
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ACC TCG TTCTTCTTACT
AC- G C
GAM1294 TGGATTAGTAA DHCR24 NM_014762.1 3 TCATTCTTCTTGG ATT A A
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ACC TCG TTCTTCTTACT
AC- G
GAM1294 TGGATTAGTAA DLST NM_001933.2 3 TTCATTCTCCGTT - AAA --- A
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ACTT AGTTA TT TCTTACTT
C CTG GCC
GAM1294 TGGATTAGTAA PSEN1 NM_007318.1 3 TCATTCTTCTCTC ATT TAA A
AGAAGAATGAA CCA TGG AG AGAAGAATGA
ACC TC TCTTCTTACT
C-- ---
GAM1294 TGGATTAGTAA SLC6A4 NM_001045.1 5 TCAGTGTCATTTA A - AGAA A
AGAAGAATGAA CTAACCA TGG TTAGTAAA GA TGA
ACC AATCATTT CT ACT
- A GTG-
GAM1295 GAGAGAGGTAG BACE2 NM_138992.1 3 TCTGCTCCCAGAT G------ G GAG A
AGGGGAGCAGA GCCTTCTAGATTC AGA AGGTA GGGAGCAGA
A TCT TCCGT CCCTCGTCT
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GAM1295 GAGAGAGGTAG DLST NM_001933.2 3 ATGCCTCTTCTAC AG A G A
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C TCTCCATCTTCTC CGT
CT - A

GAM1295 GAGAGAGGTAG GFAP NM_002055.2 3 CTGCTCCCCTCCC G TA- A
AGGGGAGCAGA TCCTCTGTC GA AGAGG GAGGGGAGCAG
CT TCTCC CTCCCCTCGTC
G TCC
GAM1300 TGCTAGGCTTA ADAM10 NM_001110.1 5 GGGCGGCGGCAGG AT T T A
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ACGATCCGGA GG GG GGG
C- C C
GAM1300 TGCTAGGCTTA CHAT NM_020985.1 5 GAGAAAGGAGTAG ATT C- A
TTCTCTTCCTC GAGCCTAGCA TGCTAGGCTT CTCTT CTC
ACGATCCGAG GAGGA GAG
GAT AA
GAM1300 TGCTAGGCTTA NGB NM_021257.2 3 GAGAGAAGAGAAG AG- TA - A
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ACGA CGG AAGAGAAG GAG
CGA -- A
GAM1300 TGCTAGGCTTA PSEN1 NM_000021.2 3 GAGGAAGAGCAGG AG- ATT A
TTCTCTTCCTC CACCAGCA TGCT GCTT CTCTTCCTC
ACGA CGGA GAGAAGGAG
CCA C--
GAM1300 TGCTAGGCTTA S100B NM_006272.1 5 AGGAAGAGGATGT T------ - TT A
TTCTCTTCCTC CTGAGCTGGAGAA GCT AGGC ATTCTCTTCCT
CGA TCTG TAGGAGAAGGA
AAGAGGT G --
GAM1300 TGCTAGGCTTA SNCAIP NM_005460.1 3 AGGAAAGAATAAG AGG C A
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ACGA GAATAAGA AAGGA
CG- -
GAM1310 CACTGCAACCC AVP NM_000490.2 5 TGGGGGTGCGGGG CT A - A
CCGCCTCCCAG GTGTCATG CA GCA CCCCCGC CTCCCA
GT TGT GGGGGCG GGGGGT
AC - T
GAM1310 CACTGCAACCC IAPP NM_000415.1 3 CAGGAGGCGGAGG C CA A
CCGCCTCCCAG TTGCAGTG CACTGCAACC CCGCCTCC
GTGACGTTGG GGCGGAGG
A AC
GAM1310 CACTGCAACCC NGB NM_021257.2 5 CTGGAGGGGGCGG CA-- AA--- -- A
CCGCCTCCCAG GGGCCGTGGCGGC CTGC CCCCCGCCTCC CAG
TTT GGCG GGGGGCGGGGG GTC
TTTC GTGCC AG
GAM1310 CACTGCAACCC TFCP2 NM_005653.2 5 CTGGGAGGGAGGG CA A----- CG A
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A GACG TGGGG GGAGGGTC
AA ACCTCC AG
GAM1332 TGAGGTAGGTG DSCR1 NM_004414.3 3 GCAGTTTCACTGC T A GC A
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TTTCA CCG ACTTTGACG
T A TC
GAM1332 TGAGGTAGGTG FLNB NM_001457.1 3 GCAGTTTCCCACT TGA CT A
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GAM1332 TGAGGTAGGTG FLNB NM_001457.1 3 GCAGTTTCCCACT TGA------ CT A
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CCGTTCAC CTTTGACG
CCCTAGAAA C-
GAM1332 TGAGGTAGGTG IAPP NM_000415.1 3 GTGGCTTTCAGCA AGG - TG A
CTGAAACTGC AACCTCA TGAGGT TGCTGAAA C C
ACTCCA ACGACTTT G G
A-- C GT
GAM1332 TGAGGTAGGTG IGF1 NM_000618.2 3 GCAATATGTCATC C- AAC-- A
CTGAAACTGC TACCTACCTCA TGAGGTAGGTG TGA TGC
ACTCCATCCAT ACT ACG
CT GTATA
GAM1338 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
GCCTGGGCAAC GGAGGGCAAT TGC CTCC AGCCTGGGCAAC
ACG GAGG TCGGACCCGTTG
TA G G
GAM1338 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
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ACGGTA G G
GAM1338 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM1338 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM1338 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCC TG
CC
GAM1338 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM1338 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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CA
GAM1338 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM1338 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM1361 AGAAGTAGTAG APLP2 NM_001642.1 3 TACTACTGTAGAA A A A-- A
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CTTTA CGTCA TGTCATCAT
C A AGA
GAM1361 AGAAGTAGTAG APLP2 NM_001642.1 3 TACTACTGTAGAA A--- A A-- A
TAGCAGTAGTA CTGCAATTTCCAT GAAGT GTAGT GCAGTAGTA
T CTTTA CGTCA TGTCATCAT
TTAC A AGA
GAM1361 AGAAGTAGTAG HTR2A NM_000621.1 3 ACTATTGCTGCTT T------ A A
TAGCAGTAGTA TCTCTTCTACTTC AGAAGTAG AGTAGCAGTAGT
T TCTTCATC TCGTCGTTATCA
TTCTCTT -
GAM1363 AGCTGGTGTGT DSCR1 NM_004414.3 3 CCCTTGTTCTAAT ---------- TAC A
AGCGGGTACCT GCTGCACACCAGT AGCTGGTGTGTAGC GGG
T TTGACCACACGTCG CCC
TAATCTTGTT ---
CT

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GAM1363 AGCTGGTGTGT PRNP NM_000311.1 3 AGTATGGGCTACA G GG C A
AGCGGGTACCT CAGCAGCT AGCTG TGTGTAGC GTAC
TCGAC ACACATCG TATG
G GG A
GAM1363 AGCTGGTGTGT PRNP NM_000311.1 3 CAGTATGGGCTAC G GG CT A
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TCGAC ACACATCG TATG
G GG AC
GAM1372 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A ACA A
AACCTGGACAA GTGCAGTG CACTGCACTCCA CCTGG
GTGACGTGAGGT GGACC
C CGC
GAM1372 CACTGCACTCC IGF1 NM_000618.2 3 TGTCCCCCAGGCT A --- A
AACCTGGACAA GGAGTGCAGTG CACTGCACTCCA CCT GGACA
GTGACGTGAGGT GGA CCTGT
C CCC
GAM1372 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A A A
AACCTGGACAA AGTGCAGTG CACTGCACTCCA CCTGG CAA
GTGACGTGAGGT GGACC GTT
C C
GAM1423 GTCAGCAAGGA HD NM_002111.3 3 TGTCCACCCTCAT CA AG -- A
GGGGTGGACAA TTCTGCCAGC GT GCA GA GGGGTGGACA
CG CGT TT TCCCACCTGT
AC CT AC
GAM1431 CTGGGATGGAG IGF1 NM_000618.2 3 TCTTTATTCTGCC C----- A - T- A
GAGAATTAGAG CCCATCCCAACCC TGGGATGG GG AGAAT AGA

AG ACCCTACC CC TCTTA TCT
GACCCA C G TT
GAM1440 TCCAGTGAAAC BACE NM_012104.2 3 GAAGAGACCAAGC TC T ----- A
AGGTCTCTTTG TTGTTTCCCTGCT CAG GAAACA GGTCTCTTT
GTC CTTTGT CCAGAGAAG
TC C TCGAA
GAM1440 TCCAGTGAAAC TNFRSF5 NM_152854.1 3 ACAGGAGACCTGG AAA TG A
AGGTCTCTTTG CACTGGA TCCAGTG CAGGTCTCTT
AGGTCAC GTCCAGAGGA
G-- CA
GAM1440 TCCAGTGAAAC TNFRSF5 NM_152854.1 3 CAGGAGACCTGGC AAA T A
AGGTCTCTTTG ACTGGA TCCAGTG CAGGTCTCTT
AGGTCAC GTCCAGAGGA
G-- C
GAM1443 GGCATGTGTGA ADAMTS5 NM_007038.1 3 TCTGCAGCTATTT CAT G C- A
GCAGCTGCAGG CAACTTCC GG GT TGAG AGCTGCAGG
CC CA ACTT TCGACGTCT
TT- - TA
GAM1443 GGCATGTGTGA APLP2 NM_001642.1 3 ATTGTATTGTCTG G - C G A
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TCGTACACA TC GTT ATGTT
G T - A
GAM1443 GGCATGTGTGA APLP2 NM_001642.1 3 TTGTATTGTCTGA G - C A
GCAGCTGCAGG CACATGCT GGCATGTGT AG CAG TGCAG
TCGTACACA TC GTT ATGTT
G T -
GAM1443 GGCATGTGTGA APPBP2 NM_006380.2 3 CTGCAGTGAACAC GAGCA A
GCAGCTGCAGG ATGCC GGCATGTGT GCTGCAG
CCGTACACA TGACGTC
AG---
GAM1443 GGCATGTGTGA CNTF NM_000614.2 3 CTGGAAAACAGCT G TG ----- A
GCAGCTGCAGG GCTGTTAGATGTC GGCAT TG AGCAGCTG CAG
CTGTA AT TCGTCGAC GTC
G TG AAAAG
GAM1443 GGCATGTGTGA HD NM_002111.3 3 AGGGAGCTGCTCA GTG GCAG A
GCAGCTGCAGG GAATGCC GGCAT TGAGCAGCT
CCGTA ACTCGTCGA
AG- GGGA
GAM1443 GGCATGTGTGA HD NM_002111.3 3 CCTATGGGCTTCC AGC GC- A
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CCGTACACGC TCGG TCC
CT- GTA
GAM1443 GGCATGTGTGA HD NM_002111.3 3 GTTGCAGCTGCTC ---- T G A
GCAGCTGCAGG TTGCATCTGGGCC GGC ATGTG GAGCAGCTGCAG
CCG TACGT CTCGTCGACGTT
GGTC T G
GAM1443 GGCATGTGTGA HD NM_002111.3 3 TTGCAGCTGCTCT ---- T A
GCAGCTGCAGG TGCATCTGGGCC GGC ATGTG GAGCAGCTGCAG
CCG TACGT CTCGTCGACGTT
GGTC T

GAM1443 GGCATGTGTGA MAPK10 NM_138981.1 5 CCTTTCAGAACCA GAGCAG C- A
GCAGCTGCAGG AACACATGCC GGCATGTGT CTG AGG
CCGTACACA GAC TCC
AACCAA TT
GAM1443 GGCATGTGTGA TRPM2 NM_003307.1 3 ATGCAGGCATCCA T - AG G A
GCAGCTGCAGG CATGCC GGCATGTG GA GC CTGCA
CCGTACAC CT CG GACGT
- A -- A
GAM1443 GGCATGTGTGA TRPM2 NM_003307.1 3 CCTGCAGCCCCTC ATGTG CA A
GCAGCTGCAGG AGCC GGC TGAG GCTGCAGG
CCG ACTC CGACGTCC
----- CC
GAM1447 TGCTGTGCTAA PRND NM_012409.1 3 TAGTTTTTCACTT G--- - A
AGGAAGGATTA TAGCAAAGGGGCA TGCT TGCTAAAG GAAGGATTA
ACGG ACGATTTC CTTTTTGAT
GGAA A
GAM1456 ATACTGAGAGA BACE2 NM_138992.1 3 ACAGGAAGCTTTT T AAAAAG A
AAAAGCTTGTC TGTAT ATAC GAGAG CTTGT
TATG TTTTC GGACA
T GAA---
GAM1456 ATACTGAGAGA IGF1 NM_000618.2 3 ACAAGTATTTTAA T -- A A
AAAAGCTTGTC CTCTCAGTCC A ACTGAGAG AAAA GCTTGT
C TGACTCTC TTTT TGAACA
C AA A
GAM1461 TGGGCTCGCTC BACE2 NM_138992.1 3 CCGCTCAGTCTTT TTC T --- A
TTCAGTCTCGG GAGCGAGCCCA TGGGCTCGCTC AG CT CGG
ACCCGAGCGAG TC GA GCC
TT- T CTC
GAM1469 TTCTATGATTC APBB2 NM_173075.1 3 TGCAGCTAGAGAA TT----- A A A
TCTAAGTAGCA TTATAGTTCACTA CTATGATTCTCTA GT GCA
GATATTAAGAGAT CG CGT
ATCACTT - A
GAM1469 TTCTATGATTC OLR1 NM_002543.1 3 GTTCTTGTTAGAA C- T A
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AGGGTACTAAGA GTTC TTG
TT -
GAM1469 TCTGCTTGGAC BACE2 NM_138992.1 3 TCAATGATGAGTC - T---- G B
TGATCATTGAA CTCTCTGGTCAGA TCTG CT GGACT ATCATTGA
AGAC GG CCTGA TAGTAACT
T TCTCT G
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TCG GA
GAM1479 GAAGGCAGTAG GYPA NM_002099.2 3 GACTATACAGTGT GAA GTAGG A
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CTGT GACATATCAG
TCA -----
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--- TC TTTTTACT
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TATAACCAC TTT CGGT
C - ACAC
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TGTA T CTTTACGAT GTT
GT - -
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GAACGTCACA AGTCG
CCTG GAA
GAM1484 TTTGCAGTGTT ADAMTS5 NM_007038.1 3 AACACTGATGAAT GTG ATT B
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C GC CTTTACGTC GCTGG
GT CT C
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T G T
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AG CC AC
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C TACAC-

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CAAAC ACT AGTATATGT
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TAACG GAGG TCGGACCC TG
G G GT
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T AACGTGAGGTCGGACCC TG
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T AACG AGG GGACCCACTG
TGAGAGA GT A-
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ACTC GTCCACGA CCC
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T GTC TC
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GA CTCC
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G AC A
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A GGGTCCGACCTCAC TCAC
GT A

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TAC C ACC
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TC C
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- GCAC C
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- A C
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ACCGCG - T C
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                                                  C
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GAM1770   TGGAGCAGAAA DLST   NM_001933.2  3  TATTCCTGCCTTT     GC           C         A
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                                            GG     A  G
GAM1770   TGGAGCAGAAA MPO    NM_000250.1  3  GGGCCTGTTGCCC   A       -  G  -         A
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                                       ACC TGTCTTTCC GTT TC GGG
                                         A        C   G  C
GAM1770   TGGAGCAGAAA PRND   NM_012409.1  3  GGTTTTCTGCTCT    G    AAG      T         A
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TA TGTAGG A
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AC TTCAGGAG GGGAAAGGG
AC T
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- GA
GAM1863 TGCTAGGTTTT GYPA NM_002099.2 3 GGAGAAGGAAAAA C -- TC A
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GC ATTCAAG AAAGGAA GG
- AA GA
GAM1864 TCGAGTTGATG IGF1 NM_000618.2 3 ACCCATTCATAGC G A - A
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AG TCGAT ACGAT CTTACCCA
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GAM1887 TTCTCATTGGC BACE NM_012104.2 3 TGTCCCTGTGGTA ATT-- C-- GT A
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AAGAG CC GGTGTCCC T
ACGGT CAT TG
GAM1896 TTCCTCTGCCA DHCR24 NM_014762.1 3 GTGGAAAGTCAGA CCACGT CT A
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T----- TG
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GGAGACGG AGGAGGG GA
CT GAG T
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TG GGAGACGG AGGAGGG GA
GTCCCCT GAG T
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AGGGGACGGTGCGG AAAG
C T AG-
GAM1896 TTCCTCTGCCA MAPK10 NM_002753.2 5 GAGAAATGGCGTG T---------- - A
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CGAGCC AGGGGACGGTGCGG AAAG
CCGAGCGACCC T
CC

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GGGGAGACGG CGGGGA GGA
GT C
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AAGGAGAC CAGAA GG
C--- GT
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C--- GT T
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-- GG T
GAM1937 TGAGTATTCAC ACE NM_152831.1 3 CCCACAAGCACCT TATTCAC --- A
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ACTC GTCCACGA CCC
------- ACA
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GATAAT ACG A
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A CCGAC-
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G CTCGTG GGTCCACG CC
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GAM1942 AGCAAGATGGT BCHE NM_000055.1 5 CTCCTTGCAAACT A- ---- ------ TT A
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TGCAG CGT TCTACCAT CGT CC
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AG
TC

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T CTT --
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GGAGAGG C
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GG C
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GAC T C
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GGAGGAC T C
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T C C
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A A ACG
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TCGCCCCTCTCCGA CCC
TAGGTC - GC
GAM1975 TGGTGGGGAGA DHCR24 NM_014762.1 3 AGAGTAAGCCTCT T GGAA B
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ACC CCCCTCTCCGAAT
T GAGA
GAM1975 TGGTGGGGAGA LRP1 NM_002332.1 3 CTTTGCCAAGGCT T- ---- G - B
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CC CTCT G G
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ACT CTC CTCTCCGA CCC
- A C AG
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GT -- G
GAM1975 TGGTGGGGAGA TGFB1 NM_000660.1 5 GGTCCAAGCCTCC - A AA B
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T C GG
GAM1975 TGGTGGGGAGA TNF NM_000594.2 3 CTTCCCAAACGCC T---- TG A -- B
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T CC CCC CTCCG AACCCTTC
TAACC GT - CA
GAM1976 CTGGCTCCCTC ABCD1 NM_000033.2 3 GGGGGAGCTGTCT CTCTCTT- A
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CGTCTGTC

GAM1976 CTGGCTCCCTC BACE NM_012104.2 3 GGCAGAGAAGAGA CT----- CCC - A
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C TCGA AGAGAAGAGA GG
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GAM1976 CTGGCTCCCTC CRH NM_000756.1 3 GGGAGAGAGGGAG CT C T A
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T C- C
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G CGA GG GGAG AGAGAGGG
GT C C TGTC
GAM1976 CTGGCTCCCTC HD NM_002111.3 3 GGGGGAGCTGAAA CT C TT A
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CC A TC
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- AC T
GAM1976 CTGGCTCCCTC MPO NM_000250.1 5 GGAGAAGAGAGAT T - TC A
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C T GA
GAM1976 CTGGCTCCCTC NGB NM_021257.2 3 GGAGAGAAGAGAA -- - C A
TCTTCTCTCCC GGCAGCAGCAG CTG GCT CC TCTCTTCTCTCC
GAC CGA GG AGAGAAGAGAGG
GA C A
GAM1976 CTGGCTCCCTC NGB NM_021257.2 3 TGGAGAGAAGAGA -- - C C A
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GA C A T
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TCTTCTCTCCC AGGGAGCTGTGTG GGCTCCCTC CTCTCC
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CAGTGTG TGTAGT
GAM1976 CTGGCTCCCTC SLC6A4 NM_001045.1 3 GGAGAGAACAGGG C------ - CTC A
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CG AG T
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GCGGACG AG T
GAM1997 ACTCAGAGCCA LRP1 NM_002332.1 3 CCTGTCTGGAAGA ---- CT A
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CAGA CT
GAM1997 AGCGGAGACCT IGF1 NM_000618.2 3 ACTCATAGCAAAG --- C GA B
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TTGTCT CTG A CGATACTCA
TCA - AA
GAM2010 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA C A A A
ACCCTAGGCAA GTGCAGTG CATTGCACTCCA CCT GGC
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C C C
GAM2010 CATTGCACTCC HD NM_002111.3 3 TGTCTGGTGGGTG CA------ C -- A
ACCCTAGGCAA GAGTCAGGCTTCT TTG ACTCCACCC TAGGCA
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GAM2010 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- C A A
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GTACGGC C C
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GAM2014 GCTTCTCCTGT ABCD1 NM_000033.2 5 CAGGGCACTGACA T CCT----- A A
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- ACAGTCAC C
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- ACAGTCAC CC
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CC C GT
GAM2014 GCTTCTCCTGT BLMH NM_000386.1 3 GAGGGAGGGTGGC -- CT-- - A A
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GT T-- A
GAM2014 GCTTCTCCTGT DHCR24 NM_014762.1 5 TGGCGGCAGTGAC T CC - - A
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C T- C C
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TGAGG GGGACAGGGG AG GGA
TC T A G
GAM2014 GCTTCTCCTGT LRP1 NM_002332.1 5 CCGGGGAGGGGGA T CTG AC A
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C AAA CC
GAM2014 GCTTCTCCTGT LRP1 NM_002332.1 5 CGGGGAGGGGGAA T CTG A A
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C AAA C
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CC T -
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CGG GAC GGGGAGGGGT
TCTC T
GAM2014 GCTTCTCCTGT PIN1 NM_006221.1 5 GAGGGAAGATGGC - - ---- A A
CCCCTCCCTAC GGACGAGGAGAAG GCTTCTCCT GTCC CC TCCCT
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G C TAGA G
GAM2022 GTTGGGTGTGA ABCD1 NM_000033.2 3 TGGGACCCACAGT GG GGG- A
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CGA CACACT CCCAGGGT
GA GACA
GAM2022 GTTGGGTGTGA MAPT NM_173727.1 5 TGGGACCCCAGCC GTT--- T -- A
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GAM2027 CATGGTACTGC BACE NM_012104.2 3 CTTTTCTGTGGTT T ACT- A
CACAGAAGAGT GCAGCCTG CA GGT GCCACAGAAGAG
GT CCG TGGTGTCTTTTC
- ACGT
GAM2027 CATGGTACTGC GSK3B NM_002093.2 5 TTCTTCTGTGGGA -- A G A
CACAGAAGAGT GAACTTAATG CAT GGT CT CCACAGAAGAG
GTA TCA GA GGTGTCTTCTT
AT A G
GAM2027 CATGGTACTGC HD NM_002111.3 3 GCTCTTTGTGGCA CA---- - A A
CACAGAAGAGT GTGGCCAGGCAGG TGGT ACTGCCACAGA GAGT
ACCG TGACGGTGTTT CTCG
GGACGG G -
GAM2027 CATGGTACTGC IGF1 NM_000618.2 3 ACTCTTCTATGCA CA----- - CAC A
CACAGAAGAGT GTTACTACATATC TGGTA CTGC AGAAGAGT
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TCTATAC T TA-
GAM2033 TCAAGCTCATT APLP2 NM_001642.1 5 GAGGAGTCCGAGT TC- TAA-- A
CCTCTAACCTC GTGTGAGCTTGA TCAAGCTCAT CTC CCTC
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TGT CCTGA
GAM2033 TCAAGCTCATT HD NM_002111.3 3 GTCAGAGGGACTG -------- A CTC A
CCTCTAACCTC TCAGCTGAGCTTG TCAAGCTCA TTCCTCT AC
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CGACTGTC C ---

GAM2051 GAACAGCTCCA ACE NM_152831.1 3 AGGCTGGCCAGAC CC A-- C A
GTCTACAGCCC TTCAGCTGTTC GAACAGCT AGTCT CAGCC
CTTGTCGA TCAGA GTCGG
CT CCG A
GAM2051 GAACAGCTCCA ACE NM_152831.1 3 GGCTGGCCAGACT CC A-- A
GTCTACAGCCC TCAGCTGTTC GAACAGCT AGTCT CAGCC
CTTGTCGA TCAGA GTCGG
CT CCG
GAM2051 GAACAGCTCCA DSCR1 NM_004414.3 3 TGTTGTAGGAAAA CCAG C A
GTCTACAGCCC GCTGTTC GAACAGCT TCTACAGC
CTTGTCGA GGATGTTG
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GAM2051 GAACAGCTCCA DSCR1 NM_004414.3 5 GGGCGGCGGCGAC AC TACA-- A
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-- CGGCGG
GAM2051 GAACAGCTCCA HD NM_002111.3 3 GGCCAGGGTAGAC A - A--- A
GTCTACAGCCC TTGGAGCTGTCC G ACAGCTCCA GTCTAC GCC
C TGTCGAGGT CAGATG CGG
C T GGAC
GAM2051 GAACAGCTCCA HD NM_002111.3 3 TGGCCAGGGTAGA A - A--- C A
GTCTACAGCCC CTTGGAGCTGTCC G ACAGCTCCA GTCTAC GCC
C TGTCGAGGT CAGATG CGG
C T GGAC T
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CTTGTCGA CA TCGGG
CGA CA--
GAM2051 GAACAGCTCCA TNFSF5 NM_000074.1 3 GGCTGTGGTGGAG GAA----- GT A
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GGGTCGCA --
GAM2058 TGAAAGAGATG ADAMTS5 NM_007038.1 3 GCACACACCTAAA TG ----- A A
TGGTGTGTGAA GATATCTTTTTAG AAAGAGATGT GGTGTGTG
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GA GAAAT G
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TGGTGTGTGAA CCACAAACCTTTC TGAAAG TGTGGTGT GTG
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CAA ACCAA CA
GAM2058 TGAAAGAGATG MTNR1A NM_005958.2 3 CCACAACCAACAC AGA ----- A A
TGGTGTGTGAA CACAAACCTTTCA TGAAAG TGTGGTGT GTG
ACTTTC ACACCACA CAC
CAA ACCAA C
GAM2062 CCCAGGAGGCG APPBP2 NM_006380.2 3 ACTGCAACCTCCG A A
GAGGTTGCAGT CCTCCCGGG CCC GGAGGCGGAGGTTGCAGT
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GAM2062 CCCAGGAGGCG AVP NM_000490.2 5 TGGCGGCCGTGGG GCGGA AG A
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GGGTG GT
GAM2062 CCCAGGAGGCG HTR2A NM_000621.1 3 ACTGCCATTTCCT GGC T A
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GGGTCCT CCTTTA CGTCA
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GAM2062 CCCAGGAGGCG PRND NM_012409.1 3 ACTACAACCTCCA CA C C A
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AC A A
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AACTCGTGTCG TCCT
TAG GTTC
GAM2098 TTGAGCACAGT ACE NM_152831.1 3 TTGTCCTGATGCT TTG GTG A
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AACTCGTGT TTCTTCA
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GAM2098 TTGAGCACAGT PRND NM_012409.1 3 AGGCTCCACCTTA TGA-- GT A
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TTCCA GA
GAM2098 TTGAGCACAGT PRND NM_012409.1 3 GGCTCCACCTTAA TGA-- G A
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GACTCGTGTCAA CCTCG
TTCCA G
GAM2171 GGCAATATTCC HD NM_002111.3 3 CGGTTCTTCCTGG - A TA A
AGGATAGGCTG AAGTTGACT GG CAAT TTCCAGGA GGCTG
TC GTTG AAGGTCCT TTGGC
A - TC
GAM2171 GGCAATATTCC HD NM_002111.3 3 TAGCTTTTTCCTG AATA T- A
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CCG AAGGTCCT TTCGAT
AA-- TT
GAM2171 GGCAATATTCC HTR2C NM_000868.1 3 CAGCATCCTGGAA G TA AG A
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TGTT AAGGTCCTA CGAC
G TA --

GAM2171 GGCAATATTCC HTR2C NM_000868.1 3 CAGCATCCTGGAA G----- TA AG A
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TGTT AAGGTCCTA CGAC
TTCGTG TA --
GAM2221 TCCAAAGACTC CTSK NM_000396.2 3 TCTATTCATAAGT T----- CAACAGT A
AACAGTTAGAC CTTTGGTACAAG CCAAAGACT TAGA
GGTTTCTGA ATCT
GAACAT ATACTT-
GAM2223 TCTTAGATTGA OGDH NM_002541.1 3 GCCCCTTGCTTCT - A ATGT- A
GAAGATGTGGC CAACTAAAGA TCTT AG TTGAGAAG GGC
AGAA TC AACTCTTC CCG
A - GTTCC
GAM2233 GGACTGCAGTC HD NM_002111.3 3 GGCAGGGAGTGTC T A AAG A
ACACTCTAAGA TGCAGTCC GGACTGCAG CAC CTCT
CCTGACGTC GTG GGGA
T A CGG
GAM2233 GGACTGCAGTC PRND NM_012409.1 3 TCTTAGAGGTAGG C G - A A
ACACTCTAAGA TGTATTCC GGA TGCA TC AC CTCTAAGA
CCT ATGT GG TG GAGATTCT
T - A -
GAM2233 TCTTTCTACAC NGB NM_021257.2 3 GGTGGCAGAGGTG TT A GT B
CTCTGCCAGTG GGATGA TC TCT CACCTCTGCCA
AG AGG GTGGAGACGGT
T- - GG
GAM2233 TCTTTCTACAC OGDH NM_002541.1 3 GCTGGCAGAGGTT T C-- B
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GG GGGAT TGGAGACGGTCG
T CTT
GAM2251 GATTCCTCCTC DSCR1 NM_004414.3 3 ATCATACTCACGG CTTTAAA A
TTTAAAATGGT GAGGAATC GATTCCTCCT ATGGT
CTAAGGAGGG TACTA
CACTCA-
GAM2251 GATTCCTCCTC IGF1 NM_000618.2 3 TTATTTTAAAACA C CTC A
TTTAAAATGGT GAAGAATT GATTC TC TTTAAAATGG
TTAAG AG AAATTTTATT
A ACA
GAM2251 GATTCCTCCTC SNCA NM_000345.2 3 GCCATTTGAAGAA - A A
TTTAAAATGGT GGAGGAATT GATTCCTCCT CTTTAAA TGGT
TTAAGGAGGA GAAGTTT ACCG
A -
GAM2251 GATTCCTCCTC TGFB1 NM_000660.1 3 CCATTTTAAAGGT GA---- C- A
TTTAAAATGGT TGAGGAAACAAGC TTCCTC TCTTTAAAATGG
AAGGAG GGAAATTTTACC
CGAACA TT
GAM2251 ACCCACCCTCT HD NM_002111.3 3 ACCTGCCTACGGA A----- G - A B
GTGAGGAGGAT GGGTGGGCTCTGA CCCACCCTCTGT AGG AGG
GGGTGGGAGGCA TCC TCC
AGTCTC - G A
GAM2251 ACCCACCCTCT MAPK10 NM_138980.1 5 TCACTTTTTATTT T----- - B
GTGAGGAGGAT TTATGGGGGTGGG ACCCACCCTC GTGAGGAG GA

T TGGGTGGGGG TATTTTTC CT
TATTTT A
GAM2260 GGGCATGATGA APPBP2 NM_006380.2 3 GCAGTGCCATAAG A ATG A A
TGGCACTAGCG CAAGTCT GGGC TG ATGGCACT GC
TCTG AC TACCGTGA CG
A GAA -
GAM2260 GGGCATGATGA HTR2C NM_000868.1 5 CGCTAGTGGGTTA G------- A GG A
TGGCACTAGCG TCAGCTAACACCC GGC TGATGAT CACTAGCG
G TCG ACTATTG GTGATCGC
GCCCACAA - G-
GAM2260 GGGCATGATGA PRND NM_012409.1 3 GTGTGTGCCATCA TGA TA A
TGGCACTAGCG TGCCT GGGCATGA TGGCAC GC
TCCGTACT ACCGTG TG
--- TG
GAM2262 TGAGGTAGGAT IGF1 NM_000618.2 3 GGGGCAATATGTC --- ---- AGC A
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A ACTCCATCC TACTG ACGG
ATC TATA GG-
GAM2263 TTATCCTAAAT HTR2C NM_000868.1 5 CTTCAAAAACAAC AAATG - A
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AGTAGGA ACAAAA CTTC
AATCA A
GAM2263 AATTTAGAATC PSEN1 NM_000021.2 3 CTATAGAAAACGA AA----- - A B
GTTTCTGATAG TTTTGAACATACT TTTAGAATCGTTT CTG TAG
T AAGTTTTAGCAAA GAT ATC
TTCATAC A -
GAM2270 ATCACATTGCC ACT NM_020482.3 3 CCTGGTTATATGT CA CC A
AGTGATTACCC AATGTGAT ATCACATTGC GTGATTA
TAGTGTAATG TATTGGT
TA CC
GAM2270 ATCACATTGCC APBA2 NM_005503.2 3 GGGTTTTCCAATG A CCAGT TT A
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AGTGTAAC CT TGGG
C ----- TT
GAM2270 ATCACATTGCC DSCR1 NM_004414.3 3 GGGCCAATCACTG TT - A- A
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TGGTGT TG GTCACTAA GGG
T- A CC
GAM2270 ATCACATTGCC HD NM_002111.3 3 GGGTAGAATTGTT A --- TGA--- A
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A CAC TGTTAA
GAM2270 ATCACATTGCC HD NM_002111.3 3 GGGTAGAATTGTT A-- --- TGA--- A
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AAGC AGT GTAACGGTT GATGGG
CGA CAC TGTTAA
GAM2270 ATCACATTGCC PLAU NM_002658.1 3 AAGTGATCAATAA GCCAG CC A
AGTGATTACCC AATGTGAT ATCACATT TGATTAC
TAGTGTAA ACTAGTG
AATA- AA

GAM2270 ATCACATTGCC PLAU NM_002658.1 3 AGTGATCAATAAA GCCAG C A
AGTGATTACCC ATGTGAT ATCACATT TGATTAC
TAGTGTAA ACTAGTG
AATA- A
GAM2272 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
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GGACGACAC GTGGACG
CG---
GAM2272 TCTGCTGTGAT HTR2C NM_000868.1 3 ACAAGTGTTTCTA TC GA- -- A
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ATGACA ATCT GTGAACA
TT ATG TT
GAM2272 TCTGCTGTGAT HTR2C NM_000868.1 3 ACAAGTGTTTCTA TC-- GA- -- A
GGACACTTGT GTAACAGTATTTC TGCTGT TGGA CACTTGT
ATGACA ATCT GTGAACA
CTTT ATG TT
GAM2272 TCTGCTGTGAT IGF1 NM_000618.2 3 TACTAGTCCATCA -- ACTTG A
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AGA CGATACTACCTG
TC ATCAT
GAM2272 TCTGCTGTGAT PSEN2 NM_012486.1 5 CAAGTGTCCGGGA CT GA A
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AGAC TA GCCTGTGAAC
T- GG
GAM2272 TCTGCTGTGAT TNFRSF6 NM_152877.1 3 ACAATGTCCAAGA A-- C A
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AGACGACAC ACCTGT AACA
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GAM2290 TGTTATTTTGT GLUL NM_002065.3 3 CTCTGCTCTTGGA G G - A
CCAAGAGAGAG GGAGATGGGG T TTATTTT TCCAAGAG AGAG
G GGTAGAG AGGTTCTC TCTC
G G G
GAM2290 TGTTATTTTGT IGF1 NM_000618.2 3 TTCTCTCTTGCCC T TC A
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ATAATAAA C GTTCTCTCTT
- CC
GAM2300 TTAGCAGTTGT APBA2 NM_005503.2 3 TCTAGGGTTTTCC - - TG A
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AATC GT TAAC TTTGGGATCT
A G CT
GAM2300 TTAGCAGTTGT PSEN1 NM_000021.2 3 TCTAGGGTCTTAC TTA---- TT- A
GAGACCCTAGA TCTTTGTATGATG GCAG GTGAGACCCTAGA
A TGTT CATTCTGGGATCT
AGTAGTA TCT
GAM2300 TTTGGGGTCTC APPBP2 NM_006380.2 3 GCTGCTGGGGAGG T---- - T B
CCCAGCATGCA ACCTCAGTTAAC TTGGGGTC TCCCCAGCA GC
GACTCCAG AGGGGTCGT CG
CAATT G -
GAM2300 TTTGGGGTCTC DSCR1 NM_004414.3 3 TGCATGCTTTGGA G C CC B
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AAG TTTA AGG TCGTACGT
G A TT
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TTGAATAGTTT ACTATTCCA TGG TAGTGGTT AAT GTTT
ACC ATCACCAA TTA CGAG
TT A A
GAM2306 TGGGTTAGTGG TNF NM_000594.2 3 TGCTGGCAACCAC --- AA T A
TTGAATAGTTT TAAGAATTCA TGGGT TAGTGGTTG TAGT
ACTTA ATCACCAAC GTCG
AGA G- T
GAM2309 AGTTCCATGGA ACHE NM_015831.1 3 CTTTGTTGTTTGA AG------ GGA A
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A AAGGTA TTTGTTGTTTC
AAAAGGTA AG-
GAM2309 AGTTCCATGGA IAPP NM_000415.1 3 TTTGTTGTGCTTG T TG AA A
AAACAACAAAG CTGGTACT AGT CCA GA ACAACAAA
TCA GGT TT TGTTGTTT
T CG CG
GAM2309 CCCCACCCCAG AVP NM_000490.2 5 TGGGGAGCCACTG A AG AC B
TGGAGCTCACC GGGAGGGG CCCC CCCCAGTGG CTC
GGGG GGGGTCACC GGG
A GA GT
GAM2309 CCCCACCCCAG BACE2 NM_138992.1 5 CTGAGCCCGGCGA CA - A C B
TGGAGCTCACC GGGTGGGG CCCCACCC GT GG GCTCA
GGGGTGGG CG CC CGAGT
AG G - C
GAM2309 CCCCACCCCAG MAPT NM_016835.1 3 GTGAGTGTGACGG ---- GA-- B
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G GGGGTGGGGTT GC TGAGTG
GGGG AGTG
GAM2309 CCCCACCCCAG MPO NM_000250.1 5 GGTGAGCTGTGGA - GTGG B
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GGGGTGG GGT TCGAGTGG
A G---
GAM2350 CCTGCCCATCC AGER NM_172197.1 5 TGGAAGGAAGCAG T -- C A- A
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GG CG GGTAGGACG AGG GGT
C AC A AA
GAM2350 CCTGCCCATCC APBA1 NM_001163.2 5 TGGCGCTGGAGGC T CATC --- A
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GG CGG GACGGAGGT GGT
T CGAC CGC
GAM2350 CCTGCCCATCC MAPT NM_016835.1 3 GGCCGAGGCAGGG C--- -- CA A
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GACGGGT GGGACGGAG GG
GGGA CG CC
GAM2350 CCTGCCCATCC MAPT NM_173727.1 5 TGGTGGCACCAGG GC CCT A
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GGA GGTAGGAC GGTGGT
A- CAC

GAM2350 CCTGCCCATCC PSEN1 NM_000021.2 3 TGGGGAATGGAGA - G -- A A
TGCCTCCACCA GGTGGGCAGG CCTGCCCATC CT CC TCC CCA
GGACGGGTGG GA GG AGG GGT
A - TA -
GAM2350 CCTGCCCATCC PSEN1 NM_007318.1 5 AGTGGAGGCTGGG C--- - - C A
TGCCTCCACCA ATGGGTGAGAGAA CT GCCCATCCT GCCTCCAC
GA TGGGTAGGG CGGAGGTG
AAGA G T A
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GG GGTAGGAC GAGG GG
TCC C AA
GAM2350 CCTGCCCATCC TGFB1 NM_000660.1 3 TTGGGAGGCAGAG G - ACC A
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- A GTT
GAM2350 CCTGGGGGCCA DSCR1 NM_004414.3 3 CCTGTTTCTAAGT G TGC- B
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G TCTT
GAM2350 CCTGGGGGCCA NOTCH1 NM_017617.2 3 GCCTGCACAGTGT C T CAG B
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T C CCG
GAM2350 CCTGGGGGCCA SERPINA NM_001085.2 3 CCTGTGCACCGTA TGGG T--- B
CTTTGCACAGG 3 GTGGCCATGG CC GGCCACT TGCACAGG
GG CCGGTGA ACGTGTCC
TA-- TGCC
GAM2384 AATCTTCACTA APBB2 NM_173075.1 3 TTTTCCATTTTAC C-- CAA A
AAATGGACAAG TTTGAAGATT AATCTTCA TAAAATGGA
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TTC TTT
GAM2384 CGTGTTCAGTA APBB2 NM_173075.1 5 ATCTCCCACCCCA CG----- AGTAT B
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T GCAAG CCACCCTCTA
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GAM2391 TTAGCAGTTGT APBA2 NM_005503.2 3 TCTAGGGTTTTCC - - TG A
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AATC GT TAAC TTTGGGATCT
A G CT
GAM2391 TTAGCAGTTGT PSEN1 NM_000021.2 3 TCTAGGGTCTTAC TTA---- TT- A
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A TGTT CATTCTGGGATCT
AGTAGTA TCT
GAM2391 TTTGGGGTCTC APPBP2 NM_006380.2 3 GCTGCTGGGGAGG T---- - T B
CCCAGCATGCA ACCTCAGTTAAC TTGGGGTC TCCCCAGCA GC
GACTCCAG AGGGGTCGT CG
CAATT G -
GAM2391 TTTGGGGTCTC DSCR1 NM_004414.3 3 TGCATGCTTTGGA G C CC B
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AAG TTTA AGG TCGTACGT
G A TT
GAM2393 AATGAAGCCAC APPBP2 NM_006380.2 3 TCAAATCTCTGTC G C--- C A
AGAGATTTGCT TCTGCTTGGTT AAT AAGC ACAGAGATTTG
TTG TTCG TGTCTCTAAAC
G TCTC T
GAM2393 AATGAAGCCAC HD NM_002111.3 3 GGCGACTGTCATG G GA -- A
AGAGATTTGCT TGGCTTGGTT AAT AAGCCACA GAT TTGCT
TTG TTCGGTGT CTG AGCGG
G A- TC
GAM2398 ATCTAGAGAGG TNFRSF6 NM_152875.1 3 GGCAAGACTGCCC A------- A A G A
CAGTCTGGCCA TTAGAAATTCTAG TCT GAG GGCAGTCT GCC
AGA TTC CCGTCAGA CGG
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GAM2398 CTGCTGCCTTT APLP1 NM_005166.2 3 ACTCCCAGCCTAG TCT CA A B
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GACGACGGGA GA CTC
TCC CC A
GAM2398 CTGCTGCCTTT CHAT NM_020986.1 5 GCTTTGAGAAAGG G TC A B
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GATGA GGAA AGAGTTTC
- -- G
GAM2398 CTGCTGCCTTT FLNB NM_001457.1 3 TGGGGGAGAGAAG AGAGA B
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GAM2424 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
GAM2424 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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CGTG GGACCCGTT
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GAM2424 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM2424 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCCG
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GAM2424 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC

GAM2424 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM2424 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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ACGTGAGGTCGGACCCGTTG
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GAM2424 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM2424 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM2440 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGCTG

GAM2440 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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TGACGTGAGGTCGGACCC CTG
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GAM2440 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- TG A
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T ACGTGAGGTCGGACCC TG
TACGGCA GT
GAM2440 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG TG A
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TGACGTGAGGTCGGACCC TG
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GAM2514 CTGTCCTGTGT CTSG NM_001911.2 3 TCTCGGGGACACA T AG AA A
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GAC GGACACAG GGGCT
C -- CT
GAM2514 GTTTTAGGCAA ADAM10 NM_001110.1 3 TCTTCCTAGTGCC T A A B
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TAA ATCCGT G ATCCTTCT
C - -
GAM2514 GTTTTAGGCAA HD NM_002111.3 3 GTCTTCCTCTTGT T CAT B
CATAGGAAGAC TTACGAC GTT TAGGCAA AGGAAGAC
CAG ATTTGTT TCCTTCTG
C C--
GAM2519 ACTGCAGCTTC ACE NM_152831.1 3 GGGAGCCGGAGGC AG A GT A
AGGGACTTGTG TGCAGT ACTGCAGCTTC GG CTT
TGACGTCGGAG CC GAG
G- - GG
GAM2519 ACTGCAGCTTC ACE NM_152831.1 3 TGGGAGCCGGAGG AG A GTG A
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G- - GGT
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CGAGACCT CTC--
GAM2519 ACTGCAGCTTC CTNND2 NM_001332.1 5 ACAAAAGCGGAAG --- AGGGAC A
AGGGACTTGTG ATGCTGCAGT ACTGCAGC TTC TTGT
TGACGTCG AAG AACA
TAG GCGAA-
GAM2519 ACTGCAGCTTC DHCR24 NM_014762.1 3 CATTGTCCTCTGA T - TT A
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TGACGTCGA GTC CCTG TAC
- T T-
GAM2519 ACTGCAGCTTC IAPP NM_000415.1 5 ATGGGCATCCTGA - A- TG A
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TGA CGTCGAAGTCCT GG A
A AC GT
GAM2519 ACTGCAGCTTC PSEN2 NM_000447.1 3 CACAGGCTGCAAG A----- - GGA A
AGGGACTTGTG CTGCAGGGAATT CTGCAGCTT CAG CTTGTG
GACGTCGAA GTC GGACAC
TTAAGG C ---
GAM2543 TTAATGCTAAT BACE NM_012104.2 3 TCCCTATCAGTTC TTA ATCG A
CGTGATAGGGG TAGCATAGT ATGCTA TGATAGGGG
TACGAT ACTATCCCT
TGA CTTG
GAM2543 TTAATGCTAAT FPRL1 NM_001462.1 5 CCTCTATCACGAA - AA A
CGTGATAGGGG GATATTGA TTAATG CT TCGTGATAGGGG
AGTTAT GA AGCACTATCTCC
A --
GAM2543 TTAATGCTAAT SLC6A4 NM_001045.1 3 ACCCTATCATCAG G C- G A
CGTGATAGGGG TTAGGATTAG TTAAT CTAAT GTGATAGGG
GATTA GATTG TACTATCCC
G AC A
GAM2543 TTAATGCTAAT SLC6A4 NM_001045.1 3 CCCTATCATCAGT G C- A
CGTGATAGGGG TAGGATTAG TTAAT CTAAT GTGATAGGG
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G AC
GAM2565 ATGACACAGTG IGF1 NM_000618.2 3 CATCTGCCAGCTG GG C T A
GGGCCAGTTGG TGTCAT ATGACACAGT GGC AG TG
TACTGTGTCG CCG TC AC
A- - T
GAM2565 ATGACACAGTG MAPT NM_173727.1 3 CCTTGGGGCTCCC A----- T AGTT A
GGGCCAGTTGG TGTGTCAGGGCAC TGACACAG GGGGCC GG
ACTGTGTC CCTCGG CC
CACGGG - GGTT
GAM2591 ACCACAGTGTC NGB NM_021257.2 3 TTTGCTCTGTGCT GT- CCA A
ACAGAGTCCAT GACTGTGGT ACCACAGT CACAGAGT
TGGTGTCA GTGTCTCG
GTC TTT

GAM2608 TAAGGTGCATC BACE NM_138972.1 3 CACTGCACTTGGT - T T A
TAGTGCAGTTA GCTGCTTTG TAAGGT GCATC AGTGCAGT
GTTTCG CGTGG TCACGTCA
T T C
GAM2608 TAAGGTGCATC BACE NM_138973.1 3 CCACTGCACTTGG - T TA A
TAGTGCAGTTA TGCTGCTTTG TAAGGT GCATC AGTGCAGT
GTTTCG CGTGG TCACGTCA
T T CC
GAM2608 TAAGGTGCATC CASP3 NM_032991.1 3 TAACTGCATTTTA TA CA -- A
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TTTAC AGAT TACGTCAAT
TA C- TT
GAM2618 TGGGAAGATGC ADAM17 NM_021832.1 5 AGCCTGGCGGTAG --- G A G A
TGGCAAGGTGC AATCTTCCCA TGGGAAGAT GCTG CA GGT
ACCCTTCTA TGGC GT CCG
AGA G - A
GAM2618 TGGGAAGATGC AGER NM_172197.1 3 CACCTTGCCAAGC TG--- T- - A
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TCTTCT CGA CCGTTCCAC
CAACA TT A
GAM2618 TGGGAAGATGC IGF1 NM_000618.2 3 GCACCTTGCAAAA T AG GCTG A
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TCCT TA CGTTCCACG
G GG AAAA
GAM2618 TGGGAAGATGC PSEN1 NM_000021.2 3 GTGATTGCCATTT TGC GGTG A
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ACCCTTCT ACCGTT
TT- AGTG
GAM2618 TGGGAAGATGC PSEN1 NM_007319.1 3 GCATTGCCAGCTC TG T AG A
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CCTTCT CGACCGT TACG
AA - --
GAM2618 TGGGAAGATGC PSEN1 NM_007319.1 3 GCATTGCCAGCTC TG------ T AG A
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CCTTCT CGACCGT TACG
ACCTCTAA - --
GAM2624 TCTGAGCCCAG ACT NM_020482.3 5 ACTCAAACTTATG CC G G A
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AGACTC GT TTCAAACTC
T- A A
GAM2624 TCTGAGCCCAG CTNND2 NM_001332.1 3 GCCTCCCCCGACT GA- T--- A
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AGG TGGGTCCTCAG CTCCG
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G A G
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GAM2624 TCTGAGCCCAG IGF1 NM_000618.2 3 ACTCAAACTCCTG - CC G A
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T CA A
GAM2624 TCTGAGCCCAG IGF1 NM_000618.2 3 CCTCCACCTCCTG TC----- TTT A
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GAM2624 TCTGAGCCCAG OGDH NM_002541.1 3 CCCACCCTCCTGG A TT A A
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C CC -
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CA GT
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T GG A-
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G GG T
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C TG GTT TCCAATGTCT
- C GCCC
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CGTGAG TCGGACCCG TGTT
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CG- TACT
GAM2628 TCCCTTTGAAG TGFB1 NM_000660.1 3 AGGAACCTGCTTT -- C A A
CCAGGTTCCAG AGTGGGGGA TCCCT TTGAAGC AGGTTCC
AGGGG GATTTCG TCCAAGG
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CATTCTGCAAG CACACG TGTG GT ATTCTGCAAG
GCAC CA TAAGACGTTC
AC-- C-
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GTG AAAC TCCTAATGAT
TTATCC T CG
GAM2732 ATCACTTTGCA APBB1 NM_145689.1 3 ATCTAATCCCTTC --- C CTA A
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TAGTGAA AC TCCCTAAT
GGA T CTA
GAM2762 CACACAGTCGT BLMH NM_000386.1 3 GCCAAAGTTATGC ---- GT - A
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GGAA TG C
GAM2762 CACACAGTCGT CTNND2 NM_001332.1 3 ACAGAATAGTTTA C ---- C A
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- TTGA A
GAM2762 CACACAGTCGT IGF1 NM_000618.2 3 CATGGACTCACCA C T TGC A
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C - TAC
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TCTTGAGTTTT TTAGCCAG CTGGCTAAT TC AGTTT
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TT TTG
GAM2770 CTGGCTAATTT HTR2C NM_000868.1 3 AGGACTGAAGAAA CTA G A
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GACT TAAAAGAA TCAGGA
TCC G
GAM2770 CTGGCTAATTT IDE NM_004969.1 3 AGAGCCTAAGAAA C ----- A A
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C TCTAC C
GAM2770 CTGGCTAATTT IGF1 NM_000618.2 3 AAACTTAGCAAAA CTG----- C A
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TTATATAA C
GAM2780 TGAGTGACAGA SNCAIP NM_005460.1 3 AGAGTGTTTTTTC T---- C- A
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GACGGGTCCGAC CGCG
A- ACC
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GACGGGTCCGAC TTC CG
TAC C ACC
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TC C

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ACT-- C
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CC GGCG TGG AGGTGGAG GACC
CCGG A CTG A
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C GG G
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TACGACGAC AGAATCTT
TTGTTGTA G
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ACTA CATAC TACTCAAA
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CTC GAGTTTACTCT GTAA
T GG
GAM2839 ACATTTCCAAT CHAT NM_020986.1 5 GTCCGACCTCTGG AT- TGG B
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TGTAAAGGT CAG CCTG
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TCCAAGGGACC AATGATG TATTA TT ATTCCAAGGG
GTAGT AA TAAGGTTCCT
- G GC
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GAM2868 TGGAATGGCTG FLNB NM_001457.1 3 TTCACTCTTCAGC TG------ G CT A
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- CC CT
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--- CC A
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G C AG
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- CCC
GAM2908 CCACTGCACTC IGF1 NM_000618.2 3 CCAGGCTGGAGTG A CCA A
CAGCACTCCAG CAGTGG CCACTGCACTCCAGC CT
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C TA AA
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GAM2911 GACACAGGCCC DLST NM_001933.2 3 CTCCCTCTCTGCA C CC C A
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C C AAG
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T AC A
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T C
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CCGACCCG CAC GAGT
AGG A TC
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TATTTCG AATTGTTT CG
AA- T T
GAM2927 ATAAAGCAGGT OLR1 NM_002543.1 3 TTGCTTTTGTTAA AGG - TG A
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AA- T TT
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AGTG AG GTA
GAM2931 TGGAGAGAGCA CTSK NM_000396.2 3 CTTCCTACTTTGC - T CT A
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T C CC

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GAM2931 TGGAGAGAGCA MAPK10 NM_138981.1 3 TCTTGCATCTACC TG------ A --- T A
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ACGAC CG -
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TGGTTC C ACC
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C CC ATTC
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TCAGGATGGTA TAGGA TTCTGGTGAATTC TGGT
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GAM3028 TTCTGGTGAAT BACE2 NM_138992.1 3 GCCAGAATTCACT AGGA A
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GAM3028 TTCTGGTGAAT OLR1 NM_002543.1 3 TACCACTTCCTGA TT--------- GAAT -- A
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GTA
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GAM3057 GGCATGATTCA APBA1 NM_001163.2 3 CTCTCCTCTTCGT TG CAGC A
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GT TGCT

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CC TAC GGTCGTCTCC CTC
TT AC GC
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GAM3057 GGCATGATTCA IGF1 NM_000618.2 3 CTCTCCTCAGAAG CAT AGCA---- A
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TTT AAAGAAGA
GAM3057 GGCATGATTCA THOP1 NM_003249.2 3 TCTCCTCTCTGGG C A-- C A
GCAGAGGAGAG AAACGTCCC GG ATG TTCAG AGAGGAGA
CC TGC GGGTC TCTCCTCT
C AAA -
GAM3057 GGCATGATTCA TRPM2 NM_003307.1 3 TTCTCCTCTGACC A TCAG A
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TCG ACTA GTCTCCTCTT
- CCCA
GAM3061 TTAAAGATCAC DLST NM_001933.2 3 GTCCTCCTCCTGG ACTT CAT A
TTGACATGGAC ATCTTTAG TTAAAGATC GA GGAC
GATTTCTAG CT CCTG
GTC- CCT
GAM3064 TTTAAGCTATA PRND NM_012409.1 3 GGAGTTGTTGAAC C CA- - A
GTTCCAGGCCC TATATTTGGA TTTAAG TATAGTTC GGC CC
AGGTTT ATATCAAG TTG GG
- TTG A
GAM3065 GACATGATGTA ACE NM_152831.1 3 CCATCATCTTCCG A GA A --- A
GCAGATGATGG CGCAGGTGCC G CAT TGT GC AGATGATGG
C GTG ACG CG TCTACTACC
C G- - CCT
GAM3065 GACATGATGTA ADAMTS5 NM_007038.1 3 CAGCAAGTTTTCT TG C GA-- A
GCAGATGATGG ATCATGTC GACATGA TAG AGAT TG
CTGTACT ATC TTTG AC
-- T AACG
GAM3065 GACATGATGTA APCS NM_001639.2 5 TGTTGTCTGCTAC ---- T- TG A
GCAGATGATGG CCTCATCCTGGTC GAC ATGA GTAGCAGA ATG
CTG TACT CATCGTCT TGT
GTCC CC GT
GAM3065 GACATGATGTA MME NM_000902.2 3 TTTTATTTCCATC TAGC TG A
GCAGATGATGG ATGTC GACATGATG AGATGA
CTGTACTAC TTTATT
C--- TT
GAM3065 GACATGATGTA OLR1 NM_002543.1 3 CCATCATCCCTCA GA T CA A
GCAGATGATGG AAGTGTC GACAT TG AG GATGATGG
CTGTG AC TC CTACTACC
AA - C-
GAM3077 TTACCATGTTG ACE NM_152831.1 3 ACCAGCCTGTCCA TTA---- A- C A
GCCAGGCTGGT ACAGAGGGGCAGC CC TGTTGG CAGGCTGGT

C GG ACAACC GTCCGACCA
CCGACGG AG T
GAM3077 TTACCATGTTG ACE NM_152831.1 3 ATCAGCCTGGCCA TTA------ TGT A
GCCAGGCTGGT TCTGGATTTTCAC CCA TGGCCAGGCTGGT
A GGT ACCGGTCCGACTA
ACACTTTTA CT-
GAM3077 TTACCATGTTG ADAM17 NM_003183.3 3 CCAGCCTGGGTGA CA G A
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AGTG ACAGT GGTCCGACC
AG G
GAM3077 TTACCATGTTG IAPP NM_000415.1 3 ACCAGCCTGACCA C A
GCCAGGCTGGT ACGTGGTGA TTACCATGTTGG CAGGCTGGT
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GAM3077 TTACCATGTTG IAPP NM_000415.1 3 CCAGCCTGGGTGG CA G A
GCCAGGCTGGT CAGAGTGA TTAC TGTTG CCAGGCTGG
AGTG ACGGT GGTCCGACC
AG G
GAM3077 TTACCATGTTG IGF1 NM_000618.2 3 AGAGTCTGGCCAA ATG GG A
GCCAGGCTGGT AACGGTAA TTACC TTGGCCAGGCT
AATGG AACCGGTCTGA
CAA GA
GAM3077 TTACCATGTTG TGFB1 NM_000660.1 3 ACCAGCCTGGGTA C G A
GCCAGGCTGGT ACATAGTGA TTAC ATGTTG CCAGGCTGGT
AGTG TACAAT GGTCCGACCA
A G
GAM3081 CTGGGATTACA ADAM17 NM_021832.1 3 TGGCTCATGCCTG A A
GGTGTGAACCA TAATCCCAG CTGGGATTACAGGTGTGA CCA
GACCCTAATGTCCGTACT GGT
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GAM3081 CTGGGATTACA CASP3 NM_004346.2 5 TGGTTGGCGTCGC A - --- G A
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GACCCTAA GT CCG CG TTGGT
A T CTG G
GAM3081 CTGGGATTACA HTR2A NM_000621.1 3 GGCTCGTGCATGT G TG A A
GGTGTGAACCA AATCCTAG CTGGGATTACA G TGA CC
GATCCTAATGT C GCT GG
A GT C
GAM3081 CTGGGATTACA IAPP NM_000415.1 3 TGGTGACATGTGC -- A- A
GGTGTGAACCA CTGTAATCCCAG CTGGGATTACAGGT GTG ACCA
GACCCTAATGTCCG TAC TGGT
TG AG
GAM3081 CTGGGATTACA MTNR1A NM_005958.2 3 CGCTCACACCTGT ACC A
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GACTCTAATGTCCACACT
CGC
GAM3081 CTGGGATTACA MTNR1A NM_005958.2 3 TGGTGCACACGCC A-- A
GGTGTGAACCA TGTAATCCCAG CTGGGATTACAGGTGTG ACCA
GACCCTAATGTCCGCAC TGGT
ACG

GAM3081 CTGGGATTACA TGFB1 NM_000660.1 3 AATGTACACCTGT AACC A
GGTGTGAACCA GGTCCCAG CTGGGATTACAGGTGTG
GACCCTGGTGTCCACAT
GTAA
GAM3081 CTGGGATTACA TGFB1 NM_000660.1 3 GGTGCTCACGCCT -- A
GGTGTGAACCA GTAATCCTAG CTGGGATTACAGGTGTGA ACC
GATCCTAATGTCCGCACT TGG
CG
GAM3081 TGATTCATTTC DSCR1 NM_004414.3 3 GTGGTGGTTTCTA TTCT-- CA- B
TAAACCCAGCT TACATGAATCA TGATTCAT AAACC GC
ACTAAGTA TTTGG TG
CATATC TGG
GAM3081 TGATTCATTTC PRND NM_012409.1 3 AGCTCCATGTTTA G C CC-- B
TAAACCCAGCT GAAATAAATGA T ATT ATTTCTAAAC AGCT
A TAA TAAAGATTTG TCGA
G A TACC
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GAGTCG G GGTCACAAGGGT
ACG GT
GAM3089 TTCAGCATTGC ACE NM_152831.1 3 GGATGTGAATGGC T GTGTT- A
CAGTGTTTCCA ATGCTGAA TTCAGCAT GCCA TCC
AAGTCGTA CGGT AGG
- AAGTGT
GAM3089 TTCAGCATTGC APPBP2 NM_006380.2 3 TGAAACACTGGTC C-- -- C A
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AAGTT TGAC GGTCACAAAG
ACC CT T
GAM3089 TTCAGCATTGC CHAT NM_020549.2 5 GGTGACTGGGAAA G- GTTT A
CAGTGTTTCCA TGCTGAG TTCAGCATT CCAGT CC
GAGTCGTAA GGTCA GG
AG GT--
GAM3089 TTCAGCATTGC HTR2C NM_000868.1 3 TGGAAACATCTGA CATTGC - A
CAGTGTTTCCA TTTCTGAA TTCAG CAG TGTTTCCA
AAGTC GTC ACAAAGGT
TTTA-- T
GAM3091 TGGGAGGCTAC DLST NM_001933.2 3 GGAGGATGCTGTG T C - A
ACGTTTCTCCA CCTCCCA TGGGAGGC ACA GT TTCTCC
ACCCTCCG TGT CG AGGAGG
- - T
GAM3091 TGGGAGGCTAC HD NM_002111.3 3 CCAGAGACATGGG A C CC A
ACGTTTCTCCA CCTCCCA TGGGAGGCT CA GTTTCT
ACCCTCCGG GT CAGAGA
- A CC
GAM3091 TGGGAGGCTAC MAPT NM_173727.1 3 TGGAGGGGCAGCG ACAC- TT A
ACGTTTCTCCA CAGCCTCCCA TGGGAGGCT GT CTCCA
ACCCTCCGA CG GAGGT
CGCGA GG
GAM3123 CTTCAATGCTT PSEN2 NM_012486.1 5 TGGGACTTCTCAG A- CT G A
GAGAAGTCGTA ACGTCAGGAG CTTC ATG TGAGAAGTC TA

GAGG TGC ACTCTTCAG GT
AC AG G
GAM3126 TGAGATCATCG APLP2 NM_001642.1 3 ATGCTTGTACAGT G TCGT G A
TTACAAGCAGC TGATGTCG TGA ATCA TACAAGCA
GCT TAGT ATGTTCGT
G TGAC A
GAM3126 TGAGATCATCG FHL2 NM_001450.2 3 GCTGCTTGTGATC ATCGTT A
TTACAAGCAGC TCA TGAGATC ACAAGCAGC
ACTCTAG TGTTCGTCG

GAM3132 TAAGTGCTGCT NCKAP1 NM_013436.2 3 TTCTAAGAGCAGC TAA----- A A
GATTTTGGAAA AGCATATGTTGTT GTGCTGCTG TTTTGGAA
TACGACGAC AGAATCTT
TTGTTGTA G
GAM3138 TGGTCTCTTGA DSCR1 NM_004414.3 3 GGGAGCCGGTTTG GA A- A
AAGAGGCTCTT GGAGAGACCA TGGTCTCTT AAG GGCTCTT
ACCAGAGAG TTT CCGAGGG
GG GG
GAM3138 TGGTCTCTTGA IL1B NM_000576.2 3 AAGAGCCTAGTTT T C -- A
AAGAGGCTCTT TTAATAGCTA TGG CT TTGAAAG AGGCTCTT
ATC GA AATTTTT TCCGAGAA
- T GA
GAM3140 TGGAGCAGAAA A2M NM_000014.3 5 AGCTCCTTCTTTC GA C C A
GGCAGGAGTCC TGCAACA TG GCAGAAAGG AGGAGT
AC CGTCTTTCT TCCTCG
AA - A
GAM3140 TGGAGCAGAAA APBB1 NM_145689.1 3 GGGTCCCTTCCCC AAA C AG A
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ACCTCGTC CC TCC GGG
CC- T CT
GAM3140 TGGAGCAGAAA CHAT NM_020986.1 3 TGCTCCTGCCACT AGAAA C A
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ACTTTG CCGTCCTCG
GATCA T
GAM3140 TGGAGCAGAAA DLST NM_001933.2 3 ATATTCCTGCCTT GC CC A
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ACCT TCTTTCCGTCCTTA
-- TA
GAM3140 TGGAGCAGAAA DLST NM_001933.2 3 TATTCCTGCCTTT GC C A
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ACCT TCTTTCCGTCCTTA
-- T
GAM3140 TGGAGCAGAAA FPRL1 NM_001462.1 5 CATTCCTGCCTGA AGCAGAA C A
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ACC TCCGTCCTTA
AGGACAG C
GAM3140 TGGAGCAGAAA HTR2C NM_000868.1 5 GATTGCTAGCCTT A- - G A
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ACCTCGTC TTCCG TC TTAG
GG A G

GAM3140 TGGAGCAGAAA MPO NM_000250.1 3 GGGCCTGTTGCCC A - G - A
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ACC TGTCTTTCC GTT TC GGG
A C G C
GAM3140 TGGAGCAGAAA PRND NM_012409.1 3 GGTTTTCTGCTCT G AAG T A
GGCAGGAGTCC GTCCA TGGA CAGA GCAGGAG CC
ACCT GTCT CGTCTTT GG
- --- T
GAM3140 TGGAGCAGAAA SLC6A4 NM_001045.1 3 GGCACGCCTGCCT CA - A - A
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ACCTC CT TTCCGTCC CA GG
CC C G C
GAM3140 TGGAGCAGAAA TGFB1 NM_000660.1 3 CTCCTCCTGCCTG A A TCC A
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ATC CGTCT TCCGTCCTC
A G CTC
GAM3140 TGGAGCAGAAA TGFB1 NM_000660.1 3 TCCTCCTGCCTGT A A TC A
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ATC CGTCT TCCGTCCTC
A G CT
GAM3140 TGGAGCAGAAA TNFRSF5 NM_152854.1 3 GGCTCCAACACTG AAAGGCA A
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ACCTCGTC CCTCGG
GTCACAA
GAM3140 TGGAGCAGAAA TNFRSF5 NM_152854.1 3 TGGCTCCAACACT AAAGGCA C A
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ACCTCGTC CCTCGG
GTCACAA T
GAM3143 CAGAGGATGCG BACE NM_138973.1 5 CCGGATCCCAGCC A TGC A- A
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GTC CCT CCGACCCT GCC
C CT- AG
GAM3143 CAGAGGATGCG HD NM_002111.3 3 CCTTCCCAGCAGA CA---- CG- C A
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CTCCTAC CGACCCTT CC
GGGCTA AGA -
GAM3143 CAGAGGATGCG MPO NM_000250.1 3 AGGGCCCACTTGT C AACG A
GCTGGGAACGG ATCCTCTG CAGAGGATGCGG TGGG
GTCTCCTATGTT ACCC
C GGGA
GAM3157 GTGAAGGTAGG SNCA NM_000345.2 3 CGAACCTGAAGCC GT ------ A
TTTCAGGTTTG TAGAAATATCTTT GAAGGT AGGTTTCAGGTTTG
G TTTCTA TCCGAAGTCCAAGC
G- TAAAGA
GAM3163 CACTGCAATGA FOS NM_005252.2 3 TGTTCTGACATTA C-------- CAA C A
CTGTCAGAACA ACAGTTTTCCATG ACTG TGA TGTCAGAACA
A TGAC ATT ACAGTCTTGT
AGTACCTTT A-- -
GAM3163 CACTGCAATGA HTR2A NM_000621.1 3 TGTTCTGACAGCA T --- A A
CTGTCAGAACA TTTCAGCTGTG CAC GC AATG CTGTCAGAACA

GTG CG TTAC GACAGTCTTGT
T ACT -
GAM3174 TTTGATGCATG GLUL NM_002065.3 3 ATCCAGGTCACGG A A- A A
TGACCTGGGAT GGCACCAAA TTTG TGC TGTGACCTGGG
AAAC ACG GCACTGGACCT
C GG A
GAM3174 TTTGATGCATG TNFSF5 NM_000074.1 3 ATTACAGGTCACA ATG- GG A
TGACCTGGGAT TGAAACCAAA TTTG CATGTGACCTG AT
AAAC GTACACTGGAC TA
CAAA AT
GAM3183 AGTGCAGGTTC CHAT NM_020984.1 5 GCTCAGCCTGTCA A---- A- C A
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G CACG TCGA TGTCCGACTCG
GCGGG AG C
GAM3183 AGTGCAGGTTC CLU NM_001831.1 3 CCCCGCTCTGGAT T A - T A
ACAGGCTGGGC CCTGCACT AGTGCAGG TC CAG GC GGG
TCACGTCC AG GTC CG CCC
T - T C
GAM3183 AGTGCAGGTTC CTSB NM_147782.1 3 CCCAGCCTGTGGT AG-- G- -- A
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ACGT CA GGTGTCCGACCC
ACAG GA TT
GAM3183 AGTGCAGGTTC TRPM2 NM_003307.1 3 TGCAGCCTGTGGA AG-- --- GG A
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ACGTCC AGGTGTCCGAC
CCCG TGT GT
GAM3190 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
AGCCTGGGCAA GAGGGCAATG CATTGC CTCC AGCCTGGGCAA
GTAACG GAGG TCGGACCCGTT
G G
GAM3190 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
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GTAG CGTG GGACCCGTT
GTC TCCTG
GAM3190 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
AGCCTGGGCAA GTGCAGTG CATTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
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GAM3190 CATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM3190 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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TT CACTC
GAM3190 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GTGACGTGAGGTCGGACCC
CC

GAM3190 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM3190 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GTAGCG GGACCCGT
GCGA--- G
GAM3190 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
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GAM3190 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- A
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GAM3190 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM3195 TGAGGGCAGGT ADAM10 NM_001110.1 3 GCATTTTCTTCAC AGG T- A
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AC CGTTCAC CTTTTACG
GGA TT
GAM3195 TGAGGGCAGGT APBB2 NM_173075.1 3 AGCATTTTCCTGC T - TGTG A
GTGAAAATGCT TCCTTC GAGG GCAGG AAAATGCT
TTCC CGTCC TTTTACGA
C T ----
GAM3195 TGAGGGCAGGT APBB2 NM_173075.1 3 AGCATTTTCCTGC T-------- - TGTG A
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G TTCC CGTCC TTTTACG
GATGTATGC T ----

T
A

GAM3195 TGAGGGCAGGT FPRL1 NM_001462.1 3 GCATTTTCTACAT GG G T A
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ATT TGT CAT CTTTTACG
A- A -
GAM3195 TGAGGGCAGGT IGF1 NM_000618.2 5 TCATTTTCAGACT - - G C A
GTGAAAATGCT TTGTACTTCA TGAGG GCAG GT TGAAAATG
ACTTC TGTT CA ACTTTTAC
A T G T
GAM3195 TGAGGGCAGGT MAPK10 NM_138981.1 5 AGCATTTTCTTTA -- A T- A
GTGAAAATGCT CCAGTATCCTTA TGAGG GC GGTG GAAAATGCT
ATTCC TG CCAT CTTTTACGA
TA A TT
GAM3195 TGAGGGCAGGT SNCA NM_007308.1 3 AGTATCTGTACCT A TGAAA A
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AC CCCGTCCAT TATGA
C GTC--
GAM3211 TCTCATATAGC HTR2A NM_000621.1 3 CTGTGGTCCCAGC ATA - TG A
TGGGTTGCAGC TACAGGGGA TCTC TAGCTGGG T CAG
AGGG ATCGACCC G GTC
GAC T GT
GAM3211 TCTCATATAGC NGB NM_021257.2 3 GCTGCAGGAACCC TC----- TA --- A
TGGGTTGCAGC AGCTAGCTGGCCA TCA TAGCTGGGT TGCAGC
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GTGGACC CG AGG
GAM3211 TCACTGTTCCT FLNB NM_001457.1 3 ATTGGCAGAAACA CCTT TG G B
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AGTGACAA AGACG T
---- GT A
GAM3211 TCACTGTTCCT FPRL1 NM_001462.1 3 TCTCTGAAAAGGA CT GTT B
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AGT TAAGGAAAAG CTCT
-- T--
GAM3211 TCACTGTTCCT IGF1 NM_000618.2 3 TCTCAACAAAACT TC- TT ------ B
TTTTGTTGAGA TTATAGGCAGTCT ACTG CCT TTTTGTTGAGA
T TGAC GGA AAAACAACTCT
TTC -- TATTTC
GAM3227 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
GCCTGGGCAAC GGAGGGCAAT TGC CTCC AGCCTGGGCAAC
ACG GAGG TCGGACCCGTTG
TA G G
GAM3227 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
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ACGGTA G G
GAM3227 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM3227 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
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GAM3227 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM3227 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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CC
GAM3227 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -

GAM3227 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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ACGTGAGGTCGGACCCGTTG
CA
GAM3227 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM3227 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGTTG

GAM3236 TTCAAGAAAGC CRYAB NM_001885.1 3 TGCCCTTTCTTGA CCAAGAT T A
CAAGATGGCTG A TTCAAGAAAG GGC
AAGTTCTTTC CCG
------- T
GAM3236 TTCAAGAAAGC GLUL NM_002065.3 3 CAGTTAATCTTGC TTC C - A
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TTCTTTCG TTCTA TTGAC
TGT - A
GAM3236 TTCAAGAAAGC GLUL NM_002065.3 3 CAGTTAATCTTGC TTC----- C - A
CAAGATGGCTG TTTCTTTGTTTGG AAGAAAGC AAGAT GGCTG
C TTCTTTCG TTCTA TTGAC
CGGTTTGT - A
GAM3236 TTCAAGAAAGC NOTCH1 NM_017617.2 3 CGGCCCCCTGCCC AGCCA AT A
CAAGATGGCTG GTTCTTGAA TTCAAGAA AG GGCTG
AAGTTCTT TC CCGGC
GCCCG CC
GAM3263 TTGCCTGGAGA AVP NM_000490.2 5 CTCAGAGATGGTC TG - ACT A
CATTTCTACTG TCCAGGTGA T CCTGGAGAC ATTTCT
A GGACCTCTG TAGAGA
GT G CTC
GAM3263 TTGCCTGGAGA GYPA NM_002099.2 3 CAGTAGAACTATG T----- - GGA -- A
CATTTCTACTG TCGGAGCACTCAC TGC CT GACAT TTCTACTG
T ACG GG CTGTA AAGATGAC
TCACTC A --- TC
GAM3266 AAGCAGCCTTG BACE NM_012104.2 3 TCTTCCTGGTCAT AAGC----- TG A
GACCAGGAGGG AGGCTCACTCTTT AGCCT GACCAGGAGGG
C TCGGA CTGGTCCTTCT
CTTTCTCAC TA
GAM3266 AAGCAGCCTTG BACE NM_138972.1 3 CCTTCAGTATCAA AA----- - CA A
GACCAGGAGGG GGCTGCCTGGAGA GCAGCCTTGG AC GGAGG
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AGAGGTC A A-
GAM3266 AAGCAGCCTTG IL1A NM_000575.3 3 CATTTTGGTCCAA GC- GG A
GACCAGGAGGG GTTGTGCTT AAGCA CTTGGACCAGGA
TTCGT GAACCTGGTTTT
GTT AC
GAM3271 TTCTACTAGTG TNF NM_000594.2 3 AGTGCTGGCAACC AC AT - A
GTTGATGGCCT ACTAAGAA TTCT TAGTGGTTG GGC CT

AAGA ATCACCAAC TCG GA
-- GG T
GAM3293 CTCTTGAAGGA APPBP2 NM_006380.2 3 GCACATGTTTTTC GTATT A
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GAGAACTTTTT ACACG
GT---
GAM3293 AGCAAAAGCCA GAL NM_015973.2 3 CTCCTGGGCATGT AA- - --- B
TGCCCAGGAGA TTGTCTGTGTGCT AGCA AG C CATGCCCAGGAG
TCGT TC G GTACGGGTCCTC
GTG T TTT
GAM3293 AGCAAAAGCCA IGF1 NM_000618.2 5 TCTCTCTGGATTT CCATGC - B
TGCCCAGGAGA CCTTTTGCT AGCAAAAG CCAG GAGA
TCGTTTTC GGTC CTCT
CTTTA- T
GAM3298 AAAGTGCTCAT APP NM_000484.1 3 ATCCCTGTTCATT C -- TAG A
AGTGCAGGTAG GTAAGCACTTT AAAGTGCT ATAGTG CAGG
TTTCACGA TGTTAC GTCC
A TT CTA
GAM3298 AAAGTGCTCAT APP NM_000484.1 3 TCCCTGTTCATTG C -- TA A
AGTGCAGGTAG TAAGCACTTT AAAGTGCT ATAGTG CAGG
TTTCACGA TGTTAC GTCC
A TT CT
GAM3298 AAAGTGCTCAT MTNR1A NM_005958.2 3 ACACCTGTAATCT CATAG AG A
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TTTCACGA ATGTCCA
CTCTA CA
GAM3298 AAAGTGCTCAT MTNR1A NM_005958.2 3 CACCTGTAATCTC CATAG A A
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TTTCACGA ATGTCCA
CTCTA C
GAM3298 AAAGTGCTCAT PRND NM_012409.1 3 CTGCCTCCCAGGC CAT GC--- A
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TTTCACGA TCG TCCGTC
AC- GACCC
GAM3298 AAAGTGCTCAT PSEN1 NM_000021.2 3 CACCTTGCACTAT G C - A A
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TTTCA GG TATCACGT CCA
- T T C
GAM3298 AAAGTGCTCAT PSEN1 NM_000021.2 3 CCACCTTGCACTA G C - AG A
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TTTCA GG TATCACGT CCA
- T T CC
GAM3298 AAAGTGCTCAT TGFB1 NM_000660.1 3 ACGCCTGTAATCC CATAG AG A
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TTTCACGA ATGTCCG
TCCTA CA
GAM3298 AAAGTGCTCAT TGFB1 NM_000660.1 3 CGCCTGTAATCCT CATAG A A
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TTTCACGA ATGTCCG
TCCTA C

GAM3298 AAAGTGCTCAT TRPM2 NM_003307.1 3 CTGCCTGGCCACT AA TA -- A
AGTGCAGGTAG GAGCACTGG AGTGCTCA GTG CAGGTAG
TCACGAGT CAC GTCCGTC
GG -- CG
GAM3298 AAAGTGCTCAT TRPM2 NM_003307.1 3 CTGCCTGGCCACT AA----- TA -- A
AGTGCAGGTAG GAGCACTGGCCGA AGTGCTCA GTG CAGGTAG
G TCACGAGT CAC GTCCGTC
GAGCCGG -- CG
GAM3298 AAAGTGCTCAT UBB NM_018955.2 3 TTACTCTGCACTA A - C - A
AGTGCAGGTAG TAGCCATTTG AAGTG CT ATAGTGCAG GTAG
TTTAC GA TATCACGTC CATT
G C - T
GAM3298 AAAGTGCTCAT UBB NM_018955.2 3 TTACTCTGCACTA A----- - C - A
AGTGCAGGTAG TAGCCATTTGCCC AAGTG CT ATAGTGCAG GTAG
CA TTTAC GA TATCACGTC CATT
ACCCCG C - T
GAM3311 GTGTGTGATAA FOS NM_005252.2 3 TATCTGTGCGTGA GA AGGA A
GGACACAGATA AACACAC GTGTGT TA CACAGATA
CACACA GT GTGTCTAT
AA GC--
GAM3311 GTGTGTGATAA MPO NM_000250.1 3 ATCTGTGTCCTGG G- GATA- A
GGACACAGATA TTAGCAGAGC GT TGT AGGACACAGAT
CG ACG TCCTGTGTCTA
AG ATTGG
GAM3311 GTCTGCTGTCT FLNB NM_001457.1 3 TGTGTAGTGTGGT GT-- B
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CGGACGG GGTGTGATGTGT
GTCT
GAM3330 ATAACTGTGAA BACE2 NM_138991.1 3 TAATTGCCTTTGA GTGA A
GAGGCAATTGT GGTTAT ATAACT AGAGGCAATTG
TATTGG TTTCCGTTAAT
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GAM3350 TGCAGATACAT APPBP2 NM_006380.2 3 TTCAGTTATATTC AGA ----- A
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ACG ATGTACG TATTGACTT
CC- ACTTA
GAM3350 TGCAGATACAT ARHA NM_001664.1 3 TTCGGCCCCATGT C TGTAA A
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AC TCTATGTAC GGCTT
- CCC--
GAM3350 TGCAGATACAT DLST NM_001933.2 3 TTCAGTTAAGTTG AG - TGTG A
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ACG TGT GT ATTGACTT
AA C TGA-
GAM3368 GATTTTCATAG HTR2A NM_000621.1 3 GGTGACTTTCCTA TTT C AA A
GAGCAGAAACC TGACACTC GA TCATAGGAG AG ACC
CT AGTATCCTT TC TGG
CAC - AG
GAM3414 TGGAGAAATTA IL1A NM_000575.3 3 TTGGTAAAATACT G ATTA A
TATTTTACTAA TCTTGA T GAGAA TATTTTACTAA

A TTCTT ATAAAATGGTT
G C---
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ACC CTTTAATA TAAAG TGGT
- AG AGT
GAM3422 TCTTTTTTGGG MME NM_000902.2 3 TGAATCTGTCTCC TTTT G A
AGACGGAGTCG CAGTTATGA TC TTGGGAGACGGA TCG
AG GACCCTCTGTCT AGT
TATT A
GAM3426 TCACCCAGTGT DHCR24 NM_014762.1 3 TCATTAGCTGTGT T AA- -- A
AAACAGCATGA GACTCTGGGTGA TCACCCAG GT ACAGC ATGA
AGTGGGTC CA TGTCG TACT
T GTG AT
GAM3426 TCACCCAGTGT PLAU NM_002658.1 3 TCATCCAATCCTC TAAACAGC A
AAACAGCATGA ACTGGGTGG TCACCCAGTG ATGA
GGTGGGTCAC TACT
TCCTAACC
GAM3431 TAATACTGCCG APPBP2 NM_006380.2 3 CATCATTATTGGC TAAT------ G A
GGTAATGATGG AGTTTCTCCTTAT ACTGCCGG TAATGATG
TGACGGTT ATTACTAC
TATTCCTCTT -
GAM3431 TAATACTGCCG BACE NM_012104.2 3 CCAAGTTCATTAC AT CC---- --- A
GGTAATGATGG CTCCCTATCAGTT TA ACTG GGGTAATGA TGG
CTA AT TGAC TCCATTACT ACC
CT TATCCC TGA
GAM3452 GCCTTTCCTCC GFAP NM_002055.2 3 GGGGCAGTCTGGA T-- A A
AGAACTGCTCC GGGGCATGGC GCC TTCCTCCAGA CTGCTCC
CGG GGGGAGGTCT GACGGGG
TAC -
GAM3452 GCCTTTCCTCC OGDH NM_002541.1 3 GAGCAGTTTTCCA G-- TT --- A
AGAACTGCTCC GGAGGCCGGGGGG CCT CCTCC AGAACTGCTC
GGG GGAGG TTTTGACGAG
GGG CC ACC
GAM3452 GCCTTTCCTCC OGDH NM_002541.1 3 GGAGCAGGAGGAG AGAA A
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GAM3461 TATTACATTCA APPBP2 NM_006380.2 3 GACCAGTGTTGAT - TT TG --- A
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ATAATGTAA GT A T ACCAG
T CT GT GTG
GAM3461 TATTACATTCA APPBP2 NM_006380.2 3 GATAATGCAAAAA TCA ATG- A
TTTTGATGGTT TTATGTAATA TATTACAT TTTTG GTT
ATAATGTA AAAAC TAG
TTA GTAA
GAM3461 TATTACATTCA IL1A NM_000575.3 3 ATCATTTTCAAAA ACA --- A
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ATAA AGGTAAAACT ACTA
GGG TTT

GAM3463 CACAATATAGC SNCA NM_000345.2 3 GCCTTTTATTAAC C----- GCA- A
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TT TGTTATAT TTATTTTCCG
TTTTAT ACAA
GAM3479 TACAGGCAGGC ADAMTS5 NM_007038.1 3 AAACCTTTGACTG GCA CAG A
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ATGTCCGTC GTTTCC
A-- AAA
GAM3479 TACAGGCAGGC APBA2 NM_005503.2 3 GCTGCCTCTGCCA TA G GCA A
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GTC GTC GTCTCCGTCG
AC A ACC
GAM3479 TACAGGCAGGC DLST NM_001933.2 3 CAGCCTCTGTCCT G C AG A
ACAGAGGCAGT GGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - AC
GAM3479 TACAGGCAGGC DLST NM_001933.2 3 GCAGCCTCTGTCC G C AGT A
ACAGAGGCAGT TGGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - ACG
GAM3479 TACAGGCAGGC NGB NM_021257.2 3 TTGCTCTGTGCTG GCA G A
ACAGAGGCAGT ACTGTG TACAG GGCACAGAG CAG
GTGTC TCGTGTCTC GTT
AG- -
GAM3479 TACAGGCAGGC NGB NM_021257.2 3 TTTGCTCTGTGCT GCA G T A
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GTGTC TCGTGTCTC GTT
AG- - T
GAM3479 TACAGGCAGGC SNCG NM_003087.1 5 CTGCGAGCTCCGT TA-------- C A --- A
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GCACA GTCCGTCC TG CTC CG
ACACGACGAC - C GAG

AG
TC

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ATG CGTCTG GTCTCCGTCG
A- AAGG
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GTCTGTCCGT CTCCGTC
CAC CCTC
GAM3479 TACAGGCAGGC TGFB1 NM_000660.1 3 TCTGCCTCCTCCT TA CA-- T A
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AC CCTC T
GAM3486 TTAGTGTTCAG OGDH NM_002541.1 3 TTCATCTTGAGCC T - A
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GATT CGAGTCCGAGTT TACTT
C C
GAM3486 TTAGTGTTCAG SNCA NM_000345.2 3 TTTAATTGAGCCT TTC A A
GCTCAAATGAA TTTATTAA TTAGTG AGGCTCAA TGAA
AATTAT TCCGAGTT ATTT
TT- A
GAM3513 CACTGCAAGCT ADAM17 NM_003183.3 5 CCAGAGAGGTGGA A AA CC- A
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G GATG TGAGGTGGAG CC
C GC AGA
GAM3513 CACTGCAAGCT IAPP NM_000415.1 3 CCAGGAGGCGGAG G A C A
CCACCTCCCGG GTTGCAGTG CACTGCAA CTCC CCTCC GG
GTGACGTT GAGG GGAGG CC
G C A
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ATAATTTGATC ATTTGTGA TCAT GTT AATTTGAT
AGTG TAA TTAAACTA
TT GAAT
GAM3593 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM3595 AGGCTGCAGTG ADAM10 NM_001110.1 3 CATGAGACGCTAC TA GG A
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TTCGACGTCAT CA GTAC
CG GA
GAM3595 AGGCTGCAGTG ADAM17 NM_003183.3 3 TGCGCCACTACAC C ATG A
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TCCGAC TCACATCACCG
C CGT
GAM3595 AGGCTGCAGTG ADAM17 NM_021832.1 3 CAGGCCGCCTGCA TGTA A A
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TCCGACGTC CGCCG AC
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TCCGAC TCACATCACCG
C CGTT
GAM3595 AGGCTGCAGTG FPRL1 NM_001462.1 5 GCACCCACTGCAT - CATG A
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TCCGACGTT ACGTCACC
T CACG
GAM3595 AGGCTGCAGTG FPRL1 NM_001462.1 5 TGCACCCACTGCA - CATGA A
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TCCGACGTT ACGTCACC
T CACGT
GAM3595 AGGCTGCAGTG HADH2 NM_004493.1 3 GGGGCCATTCGTA GTGT ATG A
TAGTGGCATGA TGCAGCCT AGGCTGCA AGTGGC
TCCGACGT TTACCG
ATGC GGG

GAM3595 AGGCTGCAGTG NCKAP1 NM_013436.2 5 CATGTCGCGCTCA A- TG A---- A
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CCGACGTC G CGCTGTAC
AC GT ACTCG
GAM3595 AGGCTGCAGTG PRND NM_012409.1 3 CATGATTTTGGCT T GG---- A
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TCCGACGTCAC TCG GTAC
- GTTTTA
GAM3595 AGGCTGCAGTG PRND NM_012409.1 3 GCATGATTTTGGC T GG---- A A
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TCCGACGTCAC TCG GTAC
- GTTTTA G
GAM3605 TTGTCAGAGGC ACE NM_152831.1 3 ACATAGGCCTGCT T----- TC - --- A
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CAGGA AC TCTCCGAC CGTCC TAC
AGGACC GA T GGA

T
A

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AACAGTCTTTGAC CTTACG
GA-
GAM3605 TTGTCAGAGGC DLST NM_001933.2 3 ACACCCTACAAGT CA -- G A
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GACG CT TTGA CATCCCACA
TA AG A
GAM3605 TTGTCAGAGGC SNCA NM_000345.2 3 ATGCTGTACCTTT CT G A
TGGTAGGGTGT CTGACAA TTGTCAGAGG GGTA GGTGT
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GAM3605 GCAGCTCCCTA APLP2 NM_001642.1 3 TGGGGTGGAATAG C GA B
TTCCATGACAG GGAACTGT GCAG TCCCTATTCCAT CA
TGTC AGGGATAAGGTG GT
A GG
GAM3605 GCAGCTCCCTA HD NM_002111.3 3 CCTCCTGGGAAGG A- AT- CA B
TTCCATGACAG AGGGAGCTGC GCAGCTCCCT TTCC GA
CGTCGAGGGA AAGG CT
GG GTC CC
GAM3630 ACTGGCACAGA MAPK10 NM_138981.1 5 CTTGACAGAAATG AC------ - GACA A
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G ACCG TGT AGACAGTTC
GAAGAATT G AA--
GAM3630 ACTGGCACAGA MTNR1A NM_005958.2 3 CTTGACAGATGTC A-- GCA--- A
CATCTGTCAAG TGGGAAAGCAGAG CTG CAGACATCTGTCAAG
T GAC GTCTGTAGACAGTTC
TGA GAAAGG
GAM3640 GGGGGATCATT ARHA NM_001664.1 3 AGTATTTTGTATA GG-- -- - A
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A TCTTAG TAATAT TTTTATGA
ATAA GT G
GAM3640 GGGGGATCATT BACE NM_012104.2 3 GTATTTTTAAATT ATCATTA A
ATAAAAATACT CTGCTCCT GGGGGG TAAAAATAC
TCCTC ATTTTTATG
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GAM3640 GGGGGATCATT CASP3 NM_032991.1 3 GAATTTTTATGAT TC AC A
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CCCCCT TAGTATTTTTA
TA AG
GAM3640 GGGGGATCATT CAV2 NM_001233.2 3 AGTATACATTTTA GG- --- A
ATAAAAATACT TAATGATGAACTT GGG ATCATTATAAAA ATACT
TTC TAGTAATATTTT TATGA
AAG ACA
GAM3666 AGCTGAGAAAG CNTF NM_000614.2 3 TCTCTCTTCCTTG CT --- TG A
CGAAGAGGTGG CTTTCTCTTCT AG GAGAAAGC GAAGAGG
TC CTCTTTCG CTTCTCT
TT TTC CT
GAM3666 CTACTTGTTCC BACE NM_012104.2 3 TTGAGGGGAGAGG CTA- ---- A B
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A GAAT AAGGAGAG GGAGTT
ATTA TCTA G
GAM3666 CTACTTGTTCC FPRL1 NM_001462.1 5 AGAGGTGGGGAAC C----- T T A B
TCTCACCTCAA AAGTAAAAGCT TACTTGTTCC C CACCTC
ATGAACAAGG G GTGGAG
TCGAAA - - A
GAM3691 CTGGGCTCTGG BACE2 NM_138991.1 3 AGACCTGGAACCA - CTG A
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GAC CCGAGACCA GTCCAGA
A AG-
GAM3691 CTGGGCTCTGG TNF NM_000594.2 3 TTCCTTGAGACAC - GT TT A
TCTGTAGGTTT GGAGCCCAG CTGGGCTCTG GTCT AGG
GACCCGAGGC CAGA TCC
A GT TT
GAM3691 ATGACCTGCAG ABCD1 NM_000033.2 3 CTGGGCCCTGTCC AT --- AGT--- B
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C CTG GACG GTCCCGGGTC
C- AGT GGACCT
GAM3747 TGGCACAGATC A2M NM_000014.3 3 CCTGTTCTCTGAG CAC A C A
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ACC TC AGTC TCTTGTCC
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GAM3747 TGGCACAGATC BACE2 NM_138991.1 3 TCTGTTCTGCTCC T----- CAGATC A
AGCAGAACAGG CAGATGCCTTCTA GGCA AGCAGAACAGG
G CCGT TCGTCTTGTCT
GATCTT AGACCC
GAM3747 TGGCACAGATC DSCR1 NM_004414.3 3 CTTTTCTGGTAGG T ------- C A
AGCAGAACAGG TTCTGTCTGTGCC TGGCACAGA CAG CAGAA AG
A ACCGTGTCT GTC GTCTT TC
- TTGGATG T

GAM3747 TGGCACAGATC OGDH NM_002541.1 3 CCGTCCTCCTCGC ATC C A A A
AGCAGAACAGG TGTGCCA TGGCACAG AG AG AC GG
ACCGTGTC TC TC TG CC
GC- C C -
GAM3747 TGGCACAGATC OGDH NM_002541.1 3 TCGTTTTCTTTGC ATC C AG A
AGCAGAACAGG TGTGCCA TGGCACAG AG AGAAC
ACCGTGTC TC TTTTG
GTT - CT
GAM3768 ATGAGAGTAGG CASP3 NM_004346.2 3 CTCTCATTTTGAC -- TT CT A
AGTTTGGGCTC CTACTCTCAT ATGAGAGTAGG AG TGGG
TACTCTCATCC TT ACTC
AG TT TC
GAM3768 ATGAGAGTAGG IGF1 NM_000618.2 3 GGACTCAAACTCC TG AG - A
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T TC GTCCTCAAACTC GG
GT CA A
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A ACTC TATCC TCA AACCCGAG
- CCCA G CT
GAM3781 TTCTGTGCAGG BCHE NM_000055.1 3 GAGATATTAAAAT AGG-- C A
TTAACATTTCT AAGCACAGAA TTCTGTGC TTAA ATTTC
AAGACACG AATT TAGAG
AATAA A
GAM3781 TTCTGTGCAGG TNF NM_000594.2 3 AGGAATGTGTGGC TT----- - A
TTAACATTTCT CTGCACAGTGAAG CTGTGCAGGTTA ACATTTCT
TG GACACGTCCGGT TGTAAGGA
GTGAAGT G
GAM3788 TCACTTGCCTA DHCR24 NM_014762.1 3 CTGTGTGACTCTG TC----- TG A
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A TGA GGGTCTCAGTGTGTC
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GAM3788 TCACTTGCCTA IGF1 NM_000618.2 3 CTGTGTGACCTTG TC----- A
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A TGAACGGGTTCCAGTGTGTC
ACTTCAC
GAM3788 TCACTTGCCTA PSEN2 NM_012486.1 5 CTGTGTGACCATA GC G A
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AGTGAA GAT CCAGTGTGTC
A- A
GAM3810 TGGAGAGAAAG ADAMTS5 NM_007038.1 3 TATATTTTCACAA T C------ G A
CGAAGATGTAG CTACTTTCTCTCT GGAGAGAAAG GAAGATGTA
C TCTCTCTTTC CTTTTATAT
C ATCAACA -
GAM3810 TGGAGAGAAAG ADAMTS5 NM_007038.1 3 TATATTTTCACAA T----- C------ A
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TA

AT

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CGAAGATGTAG CTCTCCA TGGAGAGAA GCGAAG
ACCTCTCTT CGTTTC
- ATCCT
GAM3810 TGGAGAGAAAG IGF1 NM_000618.2 3 AACATCTTCAGTT T----- GC A A
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CCTCTTTTT CTTCTACA
GGTCAC GA A
GAM3810 TGGAGAGAAAG IGF1 NM_000618.2 3 TAACATCTTCAGT T GC AG A
CGAAGATGTAG TTTTCTCCC GGAGAGAAA GAAGATGT
CCTCTTTTT CTTCTACA
C GA AT
GAM3890 GGTCCACAAGG ACE NM_152831.1 5 CTCTGCTCTCCTG CAAG--- A
GGAGAGCAGGG CGGCCATGGGCC GGTCCA GGGAGAGCAGGG
CCGGGT TCCTCTCGTCTC
ACCGGCG
GAM3890 GGTCCACAAGG ADAMTS5 NM_007038.1 3 ACTGTCTCCCCCT CC A - G A
GGAGAGCAGGG TGTCACC GGT ACAAGGGG GAG CAG
CCA TGTTCCCC CTC GTC
C- - T A
GAM3890 GGTCCACAAGG CLU NM_001831.1 3 CCCAGCCTCTCCC CAA- - A A
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CTAGGT CCCCTCTC G CCC
CTCG C A
GAM3890 GGTCCACAAGG CTSK NM_000396.2 3 TCCTGCTCTTCCA TCCACAAG A
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CC CCTTCTCGTCCT
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GAM3890 GGTCCACAAGG DLST NM_001933.2 3 CCAGGCTCTCCCT C CAA AG A
GGAGAGCAGGG CTCTGCACC GGT CA GGGGAGAGC GG
CCA GT TCCCTCTCG CC
C CTC GA
GAM3890 GGTCCACAAGG GFAP NM_002055.2 3 TTCTCCTCTCCCC CACA C A
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CCGG TCCCCTCTC TCTT
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GAM3890 GGTCCACAAGG MAPT NM_173727.1 3 CCCTACTTCCCCT A G C A
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- - A
GAM3890 GGTCCACAAGG MAPT NM_173727.1 3 CCCTGCTCTTCAG CAAGG-- A
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GAM3890 GGTCCACAAGG MAPT NM_173727.1 3 CTCTGGGATCTCC G A ---- A
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C GGGTGTTCCCC CTC GTCTC
G - TAGG

GAM3890 GGTCCACAAGG MT3 NM_005954.1 5 GCTGCTCTCCTCG CAA- G A
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CCAGGT CTCCTCTCGTC
ACAG G
GAM3890 GGTCCACAAGG SLC17A7 NM_020309.1 3 CCCTGCTCCTCTC CC- AG A A
GGAGAGCAGGG TGTCCTGCC GGT ACA GGG GAGCAGGG
CCG TGT CTC CTCGTCCC
TCC CT -
GAM3890 GGTCCACAAGG TNF NM_000594.2 5 CCCTCTCTCCCCT G--- ACA-- C A
GGAGAGCAGGG GGAAAGGACACCA GTCC AGGGGAGAG AGGG
CAGG TCCCCTCTC TCCC
ACCA AAAGG -
GAM3890 GGTCCACAAGG TRPM2 NM_003307.1 3 CCCTGCCACTCTC ACAA --- A
GGAGAGCAGGG CCCAAGAGGGCC GGTCC GGGGAGA GCAGGG
CCGGG CCCCTCT CGTCCC
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GAM3892 AAGTCACCTGA CNTF NM_000614.2 5 AGTTGAGTTAAGG - GAA A
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TTCGGT GGG TTGAGTTGA
A AA-
GAM3946 TTGCCCAGGCT ACE NM_152831.1 3 CATTGCACTCCAG TTG------ G A
GGAGTGCAGTG CTGGGAGACACAG CCCAG CTGGAGTGCAGTG
C GGGTC GACCTCACGTTAC
CGACACAGA -
GAM3946 TTGCCCAGGCT ADAM17 NM_003183.3 3 CACTACACTCCAG TG C A
GGAGTGCAGTG CCTGGGTGA T CCCAGGCTGGAGTG AGTG
A GGGTCCGACCTCAC TCAC
GT A
GAM3946 TTGCCCAGGCT CHAT NM_020984.1 5 CCAGCGCACAGCC GA AGT A
GGAGTGCAGTG TGGGCAG TTGCCCAGGCTG GTGC
GACGGGTCCGAC CGCG
A- ACC
GAM3946 TTGCCCAGGCT FLNB NM_001457.1 3 CCAGCCCTTCATC --- T AGT A
GGAGTGCAGTG AGCCTGGGCAG TTGCCCAGGCTG GAG GC
GACGGGTCCGAC TTC CG
TAC C ACC
GAM3946 TTGCCCAGGCT HTR2A NM_000621.1 3 CACTGCCATTTCC CT - A
GGAGTGCAGTG TCCTGGGCAA TTGCCCAGG GGAGTG CAGTG
AACGGGTCC CTTTAC GTCAC
TC C
GAM3946 TTGCCCAGGCT IAPP NM_000415.1 3 CACTGCACTCCAG TG A
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G GGGTCCGACCTCACGTCAC
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GAM3946 TTGCCCAGGCT NOTCH1 NM_017617.2 3 CCTGCACTCCTCA AGGCT T A
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GACGGG CCTCACGTC
ACT-- C
GAM3946 TTGCCCAGGCT TGFB1 NM_000660.1 3 CAGGCATTTGAGA ----- AGT A
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AGAGT GAC
GAM3946 CACTGCAACCT ADAM17 NM_003183.3 5 CCAGAGAGGTGGA CA-- A --- - B
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CC GGCG TGG AGGTGGAG GACC
CCGG A CTG A
GAM3946 CACTGCAACCT IAPP NM_000415.1 3 CCAGGAGGCGGAG A B
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GTGACGTTGGAGG GGAGGACC
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GAM3946 CACTGCAACCT OGDH NM_002541.1 3 CCAGGAGGCCGGG CA---- AA A- B
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G GACG GGGGG GGAGGACC
GAGGAG AG CC
GAM3978 TTTACAGATGG GFAP NM_002055.2 3 CCAGGGATGCCAT AAGA A
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GAM3978 TTTACAGATGG IGF1 NM_000618.2 3 TCAGATCTTTCTA C A --- A
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- C ATC
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CAAAGATCTGG GTAAA TTTAC AAAGATCTGG
AAATG TTTCTAGACT
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GAM3990 TTGCCTAGGCT ACE NM_152831.1 3 CATTGCACTCCAG TTG------ G A
GGAGTGCAGTG CTGGGAGACACAG CCTAG CTGGAGTGCAGTG
C GGGTC GACCTCACGTTAC
CGACACAGA -
GAM3990 TTGCCTAGGCT ADAM17 NM_021832.1 3 CACTACACTCCAG TG C A
GGAGTGCAGTG CCTGGGTGA T CCTAGGCTGGAGTG AGTG
A GGGTCCGACCTCAC TCAC
GT A
GAM3990 TTGCCTAGGCT IAPP NM_000415.1 3 CACTGCACTCCAG TG A
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G GGGTCCGACCTCACGTCAC
GT
GAM3990 TTGCCTAGGCT IGF1 NM_000618.2 3 CACAATGATTCCT CT---- G -- A
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A AACGGATCT CCTTA GT CAC
TTTCTT - AA
GAM3990 TTGCCTAGGCT MAPT NM_016835.1 3 AGGGCGCCTGAGC - A AGT A
GGAGTGCAGTG CTAGGCGG TTGCCTAGGCT GG GTGC
GGCGGATCCGA TC CGCG
G - GGA
GAM3990 TTGCCTAGGCT NOTCH1 NM_017617.2 3 CCTGCACTCCTCA A CT T A
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GACGGG CT CCTCACGTC
A -- C

GAM4008 TTAGGGCAGGC IL1A NM_000575.3 5 GTTCTCTTCTCTA CAT--- A
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AATCCCGTCC TTCTCTTG
CATCTC
GAM4008 TTAGGGCAGGC TNFSF5 NM_000074.1 3 AGTTCTCTTCTTT T - CAT----- A
ATGAGAGAACT CCACCCTGTCCCT TAGGG CAGG GAGAGAACT
A ATCCC GTCC TTCTCTTGA
- T CACCTTTC
GAM4011 TGTGTTGGAGC ACHE NM_015831.1 3 CCCCGCCTCTGCC T------- TT A A A
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TAC CC CGTCTCCG CCCC
CTCCCTCC T- - -
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C CACG ACCTCGTC CC TTCCC
CTC GGT C C
GAM4011 TGTGTTGGAGC BACE2 NM_138992.1 3 TCTCTGTTCTGCT T--- -- G A
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CGTAG CCTCGTCTT GTCTCT
CTTC AC -
GAM4011 TGTGTTGGAGC CAV1 NM_001753.3 3 TCCCTGCCTCTCA TGT------ AGC A
AGAGGCAGGGG TCAACTGAATGAG GTTGG AGAGGCAGGGG
G CAACT TCTCCGTCCCT
GGAGTAAGT AC-
GAM4011 TGTGTTGGAGC CRAT NM_004003.2 5 CCCCTGCCACTGC TGT----- GA A A
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G CAAC CGTC CCGTCCCC
GTAGCCCC AC A
GAM4011 TGTGTTGGAGC GFAP NM_002055.2 3 CTCCGCCTCTGCT GG A A
AGAGGCAGGGG GGCACA TGTGTT AGCAGAGGC GGGG
ACACGG TCGTCTCCG CCTC
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GAM4011 TGTGTTGGAGC HTR2C NM_000868.1 3 TTCTTGCTCTGCT TG-- G A
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ACACA CTCGTCTC GTTCTT
TCTA -
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ACA AATCTCGTCTC CGT TTT
A A G
GAM4011 TGTGTTGGAGC OGDH NM_002541.1 3 CCCCTCCCTCTGC TT C A
AGAGGCAGGGG TCTCATA TGTG GGAGCAGAGG AGGGG
ATAC TCTCGTCTCC TCCCC
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TGAAC CTT CGAAATGTT
- G TG
GAM4020 ATTTGAGGAGG PSEN1 NM_007319.1 3 TGGTTGGTAAAGC AT----- AG - A
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AG AAC CTCCGAAATG TTGGT
GACCGAC GA G
GAM4020 AGCTGTGAGCC CTSB NM_147783.1 5 GCTGGGCTGCAGG T CT B
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TCGGC CTCGGACG GGGTCG
T TC
GAM4020 AGCTGTGAGCC PRNP NM_000311.1 3 TTGGGATGCAGGC TG-- C B
TGCCTTCCAGT TCAGCCCGCT AGC TGAGCCTGC TTCCAG
TCG ACTCGGACG AGGGTT
CCCG T
GAM4027 TTCCTGGTGGA ABCD1 NM_000033.2 3 CTCCAGGGTGCCT TTCCT----- - A
GGCATTCGGAG CCACCTGCACAAC GGTGGAGGCATTC GGAG
CG CCACCTCCGTGGG CCTC
GCCAACACGT A
GAM4027 TTCCTGGTGGA BLMH NM_000386.1 3 TTCCAGTCTCCAC ATTC A
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AGGAATGAGGG CCTGGCTTTTATT GG CCAG GG AG GAATGAGG
TC GGTC CT TC CTTACTCC
TTATTT - - G A
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TCG AA -
GAM4064 TGGTCCAGAGG DHCR24 NM_014762.1 3 CCCTACCCATTTG TGG----- AG --- A
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GACGGGGG GG CCA
GAM4064 TGGTCCAGAGG GFAP NM_002055.2 3 CCCTCCCTCCTCT T TC AAT A
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CC GTCTCCTCC CTCCC
T CT ---
GAM4064 TGGTCCAGAGG GFAP NM_002055.2 3 CCCTCCCTCCTCT T----- TC AAT A
AGGAATGAGGG GTCCCTAGGTC GG CAGAGGAGG GAGGG
CC GTCTCCTCC CTCCC
CTGGAT CT ---
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C GGGTC TCTTC CTTACTCCC
CAA G ACGA
GAM4064 TGGTCCAGAGG OGDH NM_002541.1 3 CCCTCATTTATCA T C - G A
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CCAG TCTC CT TTTACTCCC
T - A A
GAM4064 TGGTCCAGAGG OGDH NM_002541.1 3 CCCTCATTTATCA T----- C - G A
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A CCAG TCTC CT TTTACTCCC
ACACTT - A A

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TCAGGT CTCCTCC CTCCC
CCC TCT AC-
GAM4064 TGGTCCAGAGG PSEN1 NM_007318.1 3 TCCTCATTCTTCT TCCA - A
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ACC CTC CTTCTTACTCCT
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GAM4064 TGGTCCAGAGG TRPM2 NM_003307.1 3 CCCAAGTTTCTCC TC GA A
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ACC GTCTCCTCTTTG CCC
CA AA
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GTGAC CG CGCTGTACCA
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GGTCGTGGT GT-
GAM4085 TGTAAACATCC CTNND2 NM_001332.1 3 CTGGGTGTGGGAG AAACA A T A
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GGACG - -
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A T TAA
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CTCGG ACTGTCCCT CTA
- T AGT
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GAM4130 GGGCCATGACA PSEN2 NM_000447.1 5 GCTATGCTCACAT CAGG - G A
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TCCGGTACT CTC TATC
TACA G G
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CCCG CTGTCCCT GTCT
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AGGA- TC
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GGTT CACGA CCTAATGTC
- C C
GAM4136 CCAAAGTGCTA CRAT NM_144782.1 5 GGCTGTAACTCAG A - A GA A
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GGTT CA CGA C AATGTCGG
C G - TC
GAM4136 CCAAAGTGCTA HTR2A NM_000621.1 3 GCATGTAATCCTA - A
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GAM4136 CCAAAGTGCTA IAPP NM_000415.1 3 CCTGTAATCCCAG AA - A C A
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GG TCA CGA CCTAATGTC
AC T C C
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GC C
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AC T C C
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CT C
GAM4136 CCAAAGTGCTA TGFB1 NM_000660.1 3 CCTGTAATCCTAG - C A
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GGTTT CACGATCCTAATGTC
T C
GAM4142 TCTTTGATCTC FHL2 NM_001450.2 5 CGCCCCGGAGGGA AT - T A
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GGGAGC GAGG AGGCCCCG
CG G C
GAM4142 TCTTTGATCTC GYPA NM_002099.2 3 AAGTCAAAGACAG T----- GG----- A
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TGAATG GAGACTAGAGAAGG CTG
GTAAGT ACAGAAA

TT
AA

GAM4142 TCTTTGATCTC SLC6A4 NM_001045.1 5 AAGCACCCAGAGA --- TCC - A
TTCCGGGGCTT TCAATTGGGA TCT TTGATCTCT GGG GCTT
AGG AACTAGAGA CCC CGAA
GTT --- A
GAM4147 AATCTCCATTT CTSK NM_000396.2 3 GTACAGGTACAGG - AA A A
GTAAATGTGAC CTGGAGATT AATCTCCA TTTGTA TGTG
TTAGAGGT GGACAT ACAT
C GG G

GAM4152 ATGACCAGGAA ACT NM_020482.3 3 TAGTGTTTGCATT TG G A
TTGAGAGACTG CCTGGTTAT ATGACCAGGAAT AGA ACTG
TATTGGTCCTTA TTT TGAT
CG G
GAM4152 ATGACCAGGAA ADAM17 NM_003183.3 3 AGTGACTTAGCAG GAA--- AG A
TTGAGAGACTG ATGCTGGTCAT ATGACCAG TTGAG ACT
TACTGGTC GATTC TGA
GTAGAC AG
GAM4152 ATGACCAGGAA PRND NM_012409.1 3 AGTCTCTCATTTC A------- CC T A
TTGAGAGACTG TTTCAAGACAGCC TGA AGGAA TGAGAGACT
ACT TTCTT ACTCTCTGA
CCGACAGA -- T
GAM4188 GGAAGAATGTG CAV2 NM_001233.2 3 AACATAAAAGCAC GGA ---- T A
CTTTTGTTGTT CACTGTTCTGTT AGAAT GTGCTTTTGT GTT
TCTTG CACGAAAATA CAA
TTG TCAC -
GAM4188 GGAAGAATGTG CAV2 NM_001233.2 3 AACATAAAAGCAC GGA- ---- T A
CTTTTGTTGTT CACTGTTCTGTTC AGAAT GTGCTTTTGT GTT
TCTTG CACGAAAATA CAA
CTTG TCAC -
GAM4188 GGAAGAATGTG CNTF NM_000614.2 3 AACAACAAGAAAA AGAA- ---- A
CTTTTGTTGTT TGTACAGTTAGTC GGA TGTGC TTTTGTTGTT
C CCT ACATG AGAACAACAA
GATTG TAAA
GAM4188 GGAAGAATGTG ESR2 NM_001437.1 5 GCGGGAAAAGCAC AGA G A
CTTTTGTTGTT GTGTCC GGA ATGTGCTTTT TTGT
CCT TGCACGAAAA GGCG
G-- G
GAM4188 GGAAGAATGTG IGF1 NM_000618.2 3 AGAATAAAAGATG ---- ------ G A
CTTTTGTTGTT TAGCACATTTTGC GGAA GAATGTGCT TTTGTT
TTTCC CCTT TTTACACGA AAATAA
TCGT TGTAGA G
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GAM4188 GGAAGAATGTG IL1A NM_000575.3 5 AATACAAAACTGA GTGC TGT A
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CCTTCTTA AAAACA
AGTC TAA
GAM4188 GGAAGAATGTG MME NM_007289.1 3 GCTCTAAAAGCAC AGAAT TT A
CTTTTGTTGTT CTCC GGA GTGCTTTTG GT
CCT CACGAAAAT CG
C---- CT
GAM4188 GGAAGAATGTG MTNR1A NM_005958.2 3 ACAAAAGGGGTAA ---- G A
CTTTTGTTGTT TTGCATTCTTCT GGAAGAATGT GCTTTT TTGT
TCTTCTTACG TGGGGA AACA
TTAA A
GAM4188 GGAAGAATGTG SNCAIP NM_005460.1 3 ACAGCATAAAGCA A-- - - A
CTTTTGTTGTT CATTGCTGAGCC GG AG AATGTGCTTT TGTTGT

CC TC TTACACGAAA ACGACA
GAG G T
GAM4188 GGAAGAATGTG SNCAIP NM_005460.1 3 TACAGCATAAAGC A-- - - T A
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CC TC TTACACGAAA ACGACA
GAG G T T
GAM4189 GTCCAGTGCTC ABCD1 NM_000033.2 3 TGTCCAGGGCAGT CC TG --- A
ACTGCCGACAT GAGTCCTCTAC GT AG CTCACTGCC GACA
CA TC GAGTGACGG CTGT
TC CT GAC
GAM4189 GTCCAGTGCTC DHCR24 NM_014762.1 3 TGTCATCTGAGTT T - GCC-- A
ACTGCCGACAT GAGCACTGGTC G CCAGTGCTCA CT GACA
C GGTCACGAGT GA CTGT
T T GTCTA
GAM4189 GTCCAGTGCTC GLUL NM_002065.3 3 TGGAGAAGGTGGG GCCGA A
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CCCCCTAC CGTCGG
CGA C
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C T TAC GTCGTCGGTC
TT GA C
GAM4199 CCTCTCCATGT GFAP NM_002055.2 3 GGGGGATCTGTTG C ----- B
ACCCATTCCCC TGTACGTGGAGAG CCTCTCCATGTAC CA TTCCCC
G GGAGAGGTGCATG GT AGGGGG
T TGTCT
GAM4199 CCTCTCCATGT PSEN1 NM_007318.1 3 CAGAATGGGGAAT GTA CC B
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GGAGAGGTA GGGTAAG
AG- AC
GAM4205 TCAGGTTCCTG MPO NM_000250.1 3 GGAGCACAGCTCA A - GA A
ATTGGAGTTCT GGAACTAGA TC GGTTCCTGA TTG GTTCT
AG TCAAGGACT GAC CGAGG
A C A-
GAM4205 TCAGGTTCCTG OLR1 NM_002543.1 3 AGAACTCCTTTGC A C ATT- A
ATTGGAGTTCT AGAAACTGGG TC GGTT CTG GGAGTTCT
GG TCAA GAC CCTCAAGA
G A GTTT
GAM4238 AGAGATAAAGA APBA1 NM_001163.2 3 AGCCAACCTTAAA AG - ----- A A
GGTTTAGGCAG CCTCTTCTATTGC AG ATA AAGAGGTTTA GGC
T TC TAT TTCTCCAAAT CCG
GT C TCCAA A
GAM4238 AGAGATAAAGA CNTF NM_000614.2 3 CTGCACCTCTTTG AGA----- TTAG A
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CTGTTTCTCCA CGTC
GTGGGACA ----

GAM4243 AAAGGCAGACG DLST NM_001933.2 3 GCTCATTCATATT ACG- CCT A
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TTTCCGTC TACTTAC
CTTA TCG
GAM4243 AAAGGCAGACG GFAP NM_002055.2 3 AGGGCACTGCTGC A GAA A
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- TC-
GAM4243 AAAGGCAGACG GYPA NM_002099.2 3 AGGGCATGGCACT A----- --- A- A
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TCAATG ACA GG

T
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- A ATGTC C
GAM4298 TGGCAAGGTGT AGER NM_172197.1 3 TCTCCTGTATAAC T C ----- A
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ACCGTTCCAC CCC AT CTCT
- A ATGTC
GAM4298 TGGCAAGGTGT MAPT NM_173727.1 3 GTCCTAAGCCCAC T A - - A A
GGGCTAGAGAT AATCATGCCT GGCA GGT GTGGGCT AG GAT
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T A A A -
GAM4298 TGGCAAGGTGT TRPM2 NM_003307.1 3 CTCTCTAGCCACC T TGTG T A
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C CCCA C
GAM4298 TGGCAAGGTGT TRPM2 NM_003307.1 3 TCTCTAGCCACCC T----- TGTG A
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TGACCC CCCA
GAM4315 TAGCACCTTCT ACHE NM_015831.1 3 TATTTATTTCAGG A -- CGT A
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ATCG GG GGGACTTTATT
- TC TAT
GAM4315 TAGCACCTTCT SNCA NM_000345.2 3 CTGTTGTTCAGAA C A T A
GAAATAACGTG GTTGTTA TAGCA CTTCTGAA TAACG
ATTGT GAAGACTT GTTGT
T - C
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ATTGT GAAGACTT GTTGT
T - CG
GAM4364 AGGGTTGTTAG APPBP2 NM_006380.2 3 AAACAAAACACTA T GTT A
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TTCTAACAATCA AAAAC
C AAA
GAM4364 AGGGTTGTTAG IGF1 NM_000618.2 3 CAACCAAAACTTT G T- TT A
TTTTTTGGTTG ACAAGCTT AGG TTGT AGTTT TGGTTG
TTC AACA TCAAA ACCAAC
G TT --
GAM4364 AGGGTTGTTAG IGF1 NM_000618.2 3 CAACCAAAATGTC AG------ TAGTT A
TTTTTTGGTTG ACAACCAAAACTT GGTTGT TTTTGGTTG
T CCAACA AAAACCAAC
TTTCAAAA CTGT-
GAM4376 GAGGTAGAGGT APLP2 NM_001642.1 3 GCTCACTGCTTCT GTT A
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GAM4376 GAGGTAGAGGT APPBP2 NM_006380.2 3 GGCTCACTGCAAC TA A
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CC TTTCCG ACGTCACTCA
A- C GGGTTT
GAM4376 GAGGTAGAGGT CNTF NM_000614.2 3 AATCACTGCACCT GGT T GT A
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GAM4376 GAGGTAGAGGT DLST NM_001933.2 3 GACTTCAAGATGC TT GT--- A
TGCAGTGAGTC CTCTTCTACCTC GAGGTAGAGG GCA GAGTC
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GAM4376 GAGGTAGAGGT FHL2 NM_001450.2 5 GCTCACTGCAAGC G A
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GAM4376 GAGGTAGAGGT GYPA NM_002099.2 3 ACTCACTGAAGCT A G A
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GAM4376 GAGGTAGAGGT HTR2C NM_000868.1 3 GCTTTGCAACCTT - GT A
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CATTGACG TCA
GAM4376 GAGGTAGAGGT IGF1 NM_000618.2 3 GGCTCACTGCAAC A A
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GAM4376 GAGGTAGAGGT MAPK10 NM_002753.2 5 GCCGCTGCTTCCT GA----- TT A A
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TATGTCC TT -
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CTT AT CTA TCACTCAG
G AA TT-
GAM4376 GAGGTAGAGGT PRND NM_012409.1 3 GGCTCACTGCAGC A
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GAM4376 GAGGTAGAGGT TNF NM_000594.2 3 ACTCACTGGGGCC AG- G A
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ACA G
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G ATAA
GAM4377 CCCTGGGCTGG CAV1 NM_001753.3 5 CCTTAAAGCACAG G GACTT A
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- ATTCC
GAM4377 GAGTACAAATG DHCR24 NM_014762.1 3 CCCACGGAAAGCC GAG----- AG--- B
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TGAAAGGT CCGAA
GAM4377 GAGTACAAATG OGDH NM_002541.1 3 CCCACAGAGTCTG AG AAT- AG B
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C ATGT CT AGACACCC
CG GTGT G-
GAM4382 TGACTGGAGGA ACHE NM_015831.1 3 AGTGCTCCCTTCC CT GTAA A
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-- GTGA
GAM4382 TGACTGGAGGA ACHE NM_015831.1 3 TAGTGCTCCCTTC CT GTAAG A
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ACT CCTCCTTCCCTC
-- GTGAT
GAM4382 TGACTGGAGGA BACE NM_138971.1 3 TTACCTCCCTATC A -- - A
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AC GATCTT CT TCCCTCCATT
- GA A
GAM4382 TGACTGGAGGA CASP3 NM_032991.1 3 CTACCTCAAACTT AAGG A A
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ACTGACCTTC CTCCAT
AAA- C
GAM4382 TGACTGGAGGA DHCR24 NM_014762.1 3 CGTCCTGCCCCTT CT -- TAA A
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ACT CCTCCTTCCC TCC
T- CG TGC
GAM4382 TGACTGGAGGA NCSTN NM_015331.1 3 ATTGCCTCCCTTC T C G A
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CT GCCTCCTTCCCTCCGTT
C C A
GAM4382 TGACTGGAGGA NCSTN NM_015331.1 3 TTGCCTCCCTTCC T----- C A
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TTTCCC C
GAM4382 TGACTGGAGGA NGB NM_021257.2 3 CTTACCTCCCCTG T-- CT AA--- A
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G CT CCTCC CCCTCCATTC
GGT TT CGGTC
GAM4382 TGACTGGAGGA SLC6A4 NM_001045.1 3 CAACCTCCTCCTC T----- AG AA A
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TTGACCTCCT CCTCCA
GTAGTC -- AC
GAM4398 ATAGAAGAGCA APBA1 NM_001163.2 3 CCAACCTTAAACC CAG AGA A
GTGGGGTAGAA TCTTCTAT ATAGAAGAG TGGGGT
TATCTTCTC ATTCCA
CAA ACC
GAM4398 ATAGAAGAGCA IGF1 NM_000618.2 3 TTAGCACTCACTG - - AGA A
GTGGGGTAGAA ACTCTTCTAT ATAGAAGAG CAGTGGG GT
TATCTTCTC GTCACTC CG
A A ATT
GAM4408 TTTGGATTCCT SERPINA NM_001085.2 3 AGTAGGAACTTGG G T A A
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GAAC TAAGG TCAAGGATG
G T A
GAM4423 AAAGGAGTTTG CASP3 NM_032991.1 3 TGTCAATGACAGT T GA A
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TTTTCTT GACA GTAACTGT
T --
GAM4423 AAAGGAGTTTG CTSB NM_147782.1 3 TGCAATGTCACAA AA---- - T A A
TGACATTGACA CCTCTCTGATCTT AG GAG TTGTGACATTG CA
TC CTC AACACTGTAAC GT
TTCTAG T C -
GAM4426 GAAGTTTGAAG APBB2 NM_173075.1 3 TGGGTGGGACATA CC -- TT A
CCTGTTGTTCA TTTCAAACTTC GAAGTTTGAAG TGTT G CA
CTTCAAACTTT ACAG T GT
AT GG GG
GAM4426 GAAGTTTGAAG CNTF NM_000614.2 3 AGACAACAGGCAT TTT --- C A
CCTGTTGTTCA TTTCTTTCTTT GAAG GAA GCCTGTTGTT
TTTC CTT CGGACAACAG
TTT TTA A
GAM4426 GAAGTTTGAAG MME NM_007288.1 3 GAACAACAACTAT T- - CC A
CCTGTTGTTCA CCTGACTTC GAAGTT GA AG TGTTGTTC
CTTCAG CT TC ACAACAAG
TC A A-

GAM4429 CGACTCTTGAC FLNB NM_001457.1 3 CCCCAGCCAACTT C----- T CCA A
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T CTGGG ACT ACCGACCCC
TTTTCA T TCA
GAM4429 CGACTCTTGAC MAPT NM_173727.1 3 CCCCAGCCAGGTG CG----- T - A A
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A TG GGAC TGG ACCGACCCC
ATAAGGA C G -
GAM4429 CGACTCTTGAC TRPM2 NM_003307.1 3 CCCAGGCCTGTCA A CAT - A
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GC GAGAACTG CCG ACCC
A T-- G
GAM4432 CAGGTGCAAGT GLUL NM_002065.3 3 TTCCATTTAATGG AG- - T A
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GTCCACGT GTAATTT CCT
GGG A T
GAM4446 GTCGGGAGGAA CNTF NM_000614.2 3 TTTTCTTTCTTTT AG A
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GAM4446 TTTTTATCTTT BACE NM_012104.2 3 ATCTTAAGATTAC TT-- CC B
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GAM4446 TTTTTATCTTT BACE NM_012104.2 3 TGTAGGAGTAAAG TT AGAT B
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T- ATGT
GAM4446 TTTTTATCTTT CAV2 NM_001233.2 3 CTTTGGAAATAAA TC- T B
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GAAAATAGAAAA AGGTTT
TAA C
GAM4448 TCTTTGCTGGA GLUL NM_002065.3 5 GGGAACACCTTCC TT C CC A
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AG AC ACCTTCCAC AGGG
T- C A-
GAM4448 TCTTTGCTGGA PIN1 NM_006221.1 3 GGGGGCCCTTCCA TG- T A
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GGGG GACCTTCC CGGGGG
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GAM4448 TCTTTGCTGGA PSEN2 NM_012486.1 5 GGAGCAGGCATTT T G --- A
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AG GACGACCTTT ACGG AGG
T - ACG
GAM4459 TGACAAGATAC PSEN1 NM_007319.1 3 TCTACTTTGCCAC - -------- TGA A
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CA AC TGTTCTAT GTTTCATC
A TAGACACC T--
GAM4516 GGCATGATGGA ADAMTS5 NM_007038.1 3 TCTCCACCTTTTT GG T A
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GTATT CTTTTTCCACCTCT
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C GTATT CTTTTTCCACCTCT
CACTCTGA -
GAM4516 GGCATGATGGA APLP1 NM_005166.2 3 ATTCACCCTCTCA CAT - G A
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CC TTGT CTCTCCCACTT
CT- A A
GAM4516 GGCATGATGGA APLP2 NM_001642.1 3 CTCCACCCCCTCC A-- - A A
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CCG ACTG CCTC CCCACCTC
GCC T C
GAM4516 GGCATGATGGA BACE NM_012104.2 3 CTTCCTACCCTCT ATGA - A A
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CCG ATCTCTCCCA CCTT
GTA- T C
GAM4516 GGCATGATGGA BACE NM_012104.2 3 TTCCTACCCTCTC ATGA - A
GAGGGTGGAGA TAATGGCC GGC TGGAGAGGGT GGAG
CCG ATCTCTCCCA CCTT
GTA- T
GAM4516 GGCATGATGGA DHCR24 NM_014762.1 3 CTGCCATCGCCTC A AG - A
GAGGGTGGAGA CATCAGCC GGC TGATGGAG GGTGG AG
CCG ACTACCTC CTACC TC
- CG G
GAM4516 GGCATGATGGA DLST NM_001933.2 3 CCCTCACGCTCTC -- G AGA A
GAGGGTGGAGA CATCATAGGCT GGC ATGATGGAGAG GTGG
TCG TACTACCTCTC CACT
GA G CCC
GAM4516 GGCATGATGGA DLST NM_001933.2 3 CCTCACGCTCTCC -- G AG A
GAGGGTGGAGA ATCATAGGCT GGC ATGATGGAGAG GTGG
TCG TACTACCTCTC CACT
GA G CC
GAM4516 GGCATGATGGA GLUL NM_002065.3 3 CTTCCCCCTCTCC TGAT T A A
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CTGT CCTCTCCC CCTT
TGAC - C
GAM4516 GGCATGATGGA GLUL NM_002065.3 3 TTCCCCCTCTCCC TGAT T A
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TGAC -
GAM4516 GGCATGATGGA GLUL NM_002065.3 5 GTCCCCTTCTCCA AT T G A
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CCG CTACCTCTTCC CCT
-- - G
GAM4516 GGCATGATGGA GLUL NM_002065.3 5 TGTCCCCTTCTCC AT T GA A
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CCG CTACCTCTTCC CCT
-- - GT

GAM4516 GGCATGATGGA HD NM_002111.3 3 GTCCACCCTCATT T TGGA G A
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CCGT CT CTCCCACCT
- TTA- G
GAM4516 GGCATGATGGA HTR2C NM_000868.1 3 TTGTACTTTACAA GGAG G A
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CCGTACTA TTTCAT TT
ACA- G
GAM4516 GGCATGATGGA IGF1 NM_000618.2 3 CTTTATTTTTCCA GA- A
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TCGTACTAC TTTTTATTTC
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GAM4516 GGCATGATGGA IGF1 NM_000618.2 3 GCTTTATTTTTCC GA- A A
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TCGTACTAC TTTTTATTTC
ACC G
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ACA-- AA
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CTGTACTACCTTT TTC
ATTTTA A
GAM4516 GGCATGATGGA MME NM_007288.1 3 CTTATTTTATTTC GGGTG- A
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CCG GC CTCCCACCTCT
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CC ACTACCTCT CC TCTC
-- AA T
GAM4516 GGCATGATGGA SLC17A7 NM_020309.1 3 TCTCCACCCGTTC T TGGAGA A
GAGGGTGGAGA TGCC GGCA GA GGGTGGAGA
CCGT CT CCCACCTCT
- TG----
GAM4516 GGCATGATGGA TNFRSF6 NM_152873.1 3 CTTTGCCACCTCT T- -- TG A
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CCGT TTACCTCTCC C TTC
TT AC GT
GAM4516 GGCATGATGGA TNFSF5 NM_000074.1 3 TTTCCACCCTGTC CAT- -- G A
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CC CTA CCT TCCCACCTTT
ATCT TC G
GAM4538 GAAACTAGTGT HTR2C NM_000868.1 3 CCTTTGTCAAATG C G GG A
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TTTT AT GTAA CTGTTTCC
T G A-
GAM4538 GAAACTAGTGT MME NM_007288.1 3 CATTGCCTAACTA - A AG A
TGGGACAAAGG CTAGTTTT GAAACTAGT GTTGGG CAA
TTTTGATCA CAATCC GTT
T - AC
GAM4544 GGTGATGCATT BACE NM_138973.1 3 CTGTATTTTTAAA T T --- G A
TAAAAGGGCAG TTCTGCTCCT GG GA GCA TTTAAAAG GCAG
TC CT CGT AAATTTTT TGTC
- - CTT A
GAM4544 GGTGATGCATT MAPK10 NM_138980.1 3 CTGCCCTTTTAAA G---- G - A
TAAAAGGGCAG TGGCATGACAAGG GT ATGC ATTTAAAAGGGCAG
T CA TACG TAAATTTTCCCGTC
TGGAA G G
GAM4544 GGTGATGCATT PRNP NM_000311.1 3 AGCCCTTTTAGTG T ----- A A
TAAAAGGGCAG GTGGTGTCTCACT GGTGA GCAT TTAAAAGGGC
TCACT TGTG GATTTTCCCG
C GTGGT A
GAM4544 GGTGATGCATT S100B NM_006272.1 3 CTGTTCTTTAAAT T A A
TAAAAGGGCAG GCGTTCC GG GATGCATTTAAA GGGCAG
CC TTGCGTAAATTT CTTGTC
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GAM4544 GGTGATGCATT TNFRSF6 NM_152872.1 3 CTGCCCTTAGAAA GATGC AA A
TAAAAGGGCAG TTCTAGCC GGT ATTT AAGGGCAG
CCG TAAA TTCCCGTC
ATCT- GA
GAM4557 TATTACATTCA APPBP2 NM_006380.2 3 GACCAGTGTTGAT - TT TG --- A
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T CT GT GTG
GAM4557 TATTACATTCA APPBP2 NM_006380.2 3 GATAATGCAAAAA TCA ATG- A
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TTA GTAA
GAM4557 TATTACATTCA IL1A NM_000575.3 3 ATCATTTTCAAAA ACA --- A
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ATAA AGGTAAAACT ACTA
GGG TTT
GAM4561 AGTAGACAGTG IGF1 NM_000618.2 3 GACTCTGAAACCT ---- CAA T A
GCAACATAGTC CAAGCTGTCTACT AGTAGACAGT GG CA AGTC
TCATCTGTCG CC GT TCAG
AACT AAA C
GAM4561 AGTAGACAGTG MME NM_000902.2 3 GACTGTGACAACT AG GGCAA A
GCAACATAGTC GTCTAAC TAGACAGT CATAGTC
ATCTGTCA GTGTCAG
CA ACA--
GAM4571 CCTGGAGTGAC ADAM17 NM_003183.3 3 AGGTTGCGCCACT C----- ACA- A
AGGTGTAGCCT ACACTCCAGCCTG CTGGAGTG GGTGTAGCCT
GG GACCTCAC CCGCGTTGGA
GGGTCC ATCA

GAM4571 CCTGGAGTGAC GLUL NM_002065.3 3 GGGGTGCACCTGT GAGT G A
AGGTGTAGCCT CCAATAGG CCTG GACAGGTGTA CCT
GGAT CTGTCCACGT GGG
AAC- G
GAM4571 CCTGGAGTGAC IAPP NM_000415.1 3 AGATTGCACCACT C----- A -- GC A
AGGTGTAGCCT GCACTCCAGCCTG CTGGAGTG CA GGTGTA CT
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GGGTCC - CA TA
GAM4571 CCTGGAGTGAC PLAU NM_002658.1 3 AGGTTATAGGTCA - AGG A
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GGG CCTCACTG ATATTGGA
T G--
GAM4571 GCTGCTGCCTC MPO NM_000250.1 3 CTGAGTATGTGGA G----- - A - B
AACATTTTAGG AGGCAGCAGAGCG CTGCTGCCT C ACAT TTTAG
GA GACGACGGA G TGTA GAGTC
AGGCGA A G T
GAM4571 GCTGCTGCCTC NCKAP1 NM_013436.2 3 CCCAAAATTCTAA - CAAC A B
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CGACGACG GA TAAAA CC
A ATCT C
GAM4633 TCTTTTTGTTG BACE NM_138973.1 3 TCATGACAGCTAC TT - - A
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AGAGG CAA CATCGACA TACT
TC T G
GAM4633 TCTTTTTGTTG BCHE NM_000055.1 3 TTATGTAGCTGAA TC G A
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GT A
GAM4633 TCTTTTTGTTG BCHE NM_000055.1 3 TTATGTAGCTGAA TC----- G A
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A AAAAACAA GTCGATGTATT
AGACCGT A
GAM4633 TCTTTTTGTTG IL1A NM_000575.3 3 ACTATGGCTACCA TT TG A
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-- CA
GAM4633 TCTTTTTGTTG IL1A NM_000575.3 3 GACTATGGCTACC TT TGG A
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AGAAAAAC CATCGGTAT
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GAM4650 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
GCCTGGGTGAT GAGTGCAGT ACTGCACTCCAGCCTGGGTGAT
TGACGTGAGGTCGGACCCGCTG

GAM4650 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
GCCTGGGTGAT GAGTGCAGT ACTGCACTCCAGCCTGGG GAT
TGACGTGAGGTCGGACCC CTG
C
GAM4650 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC TG A
GCCTGGGTGAT GAGTGCAAC TGCACTCCAGCCTGGG AT

ACGTGAGGTCGGACCC TG
CA GT
GAM4650 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG TG A
GCCTGGGTGAT GAGTGCAGT ACTGCACTCCAGCCTGGG AT
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GAM4656 AAGGCACTTGC CTNND2 NM_001332.1 5 TGCAGTTGGGCAA AA A GA A
CCAGAGCTGCA GGTCAG GGC CTTGCCCA GCTGCA
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GA - --
GAM4656 AAGGCACTTGC DHCR24 NM_014762.1 3 TGTAGTTAATTTC TGCCCAG A
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TTCCGTGA TTGATGT
CTTTAA-
GAM4656 AAGGCACTTGC FLNB NM_001457.1 3 TGTAGTGTGGTCT CA-- ---- A
CCAGAGCTGCA GGGCAGGCAGACC AAGG CTTGCCCAGA GCTGCA
TT TTCC GGACGGGTCT TGATGT
AGAC GGTG
GAM4656 AAGGCACTTGC TGFB1 NM_000660.1 3 GCACCTTGGGCAC ------- G C A
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T TTCCGTGA ACGGGT TC ACG
AGTTGTC - C
GAM4671 ACCAGCTGCAT HD NM_002111.3 3 GGTTGTTGCCAGG AC----- T - -- A
CCTGCAAACTT TTGCAGCTGCTCT CAGCTGCA CCTG CAA ACT
TGC GTCGACGT GGAC GTT TGG
CGTTCTC T C GT
GAM4671 CACTTTCAGAG HTR2C NM_000868.1 3 GCTGCAGCTAATT G GCC - B
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GTGAAAGT TTTA GAC TCG
G ATC G
GAM4671 CACTTTCAGAG MAPT NM_016841.1 3 CTGGGCCACTGGC - ----- G B
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G GTG GAGGTCTCTACGG GG TC
T TCACC G
GAM4685 AGACTGGCCTC ACE NM_152831.1 3 CTGGGAGCCGGAG AG--- -- AA A
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TGAC CGGAG CGAGGGTC
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GAM4685 AGACTGGCCTC HTR2A NM_000621.1 3 ATGGGAGGATCAC --- ----- G A
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TTT TTTGA CCGGAGTTC GAGGGT
GAA ACTAG A
GAM4685 AGACTGGCCTC TGFB1 NM_000660.1 5 CTGGGAGCCGGAG AGA---- - AA A
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GGC CGGAG CGAGGGTC
CTCCAGG G GC
GAM4690 TCTGTCATTTT ACE NM_152831.1 3 TGAGAAAGAGAAT G- TTT - A
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AGA AGTA AGAGAAAG GT
AG --- A

GAM4690 TCTGTCATTTT ADAMTS5 NM_007038.1 3 GTGCAAAGAGAAT G ATTT C A
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AGA AG AAGAGAAA GTG
G GATT C
GAM4690 TCTGTCATTTT DHCR24 NM_014762.1 3 GTGGAAAGTCAGA T--- -- ----- A
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AGGT CT AGACT

AT
TG

GAM4690 TCTGTCATTTT PRND NM_012409.1 3 AAGAAAGAGAAAG TCAT CA A
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AGAC GAAAGAGAAAG
TCAT AA
GAM4690 TCTGTCATTTT PRNP NM_000311.1 3 AGGTTGGAGATGA TTTT TT A A
TCTCTTTCCAT CAGA TCTGTCA TCTCT CC
AGACAGT AGAGG GG
---- TT A
GAM4690 TCTGTCATTTT SNCAIP NM_005460.1 3 TGGAAAGAGAACC TCTG----- TT A
TCTCTTTCCAT ATGAAAACAATGC TCAT TTCTCTTTCCA
AGTA AAGAGAAAGGT
CGTAACAAA CC
GAM4690 TCTGTCATTTT TNFRSF6 NM_152873.1 3 TTGGGTGAAGAGA CA-- -- T A
TCTCTTTCCAT AAGGAAGTACAGA TCTGT TTTTTCTCTTT CCA
AGACA GGAAAGAGAAG GGT
TGAA TG T
GAM4690 TCTGTCATTTT TNFRSF6 NM_152874.1 3 ATGGAAAGAAAGA TC- ---- C A
TCTCTTTCCAT AGCGTATGACACA TGTCAT TTTT TCTTTCCAT
T ACAGTA AAGA AGAAAGGTA
TAC TGCG A
GAM4690 TCTGTCATTTT TNFRSF6 NM_152877.1 3 ATGGAAAGAAAGA TC ---- C A
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ACAGTA AAGA AGAAAGGTA
AC TGCG A
GAM4690 TCTGTCATTTT TNFRSF6 NM_152877.1 3 TGGGTGAAGAGAA CA-- -- A
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C C
GAM4707 CATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG A AA A
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GTGACGTGAGGTCGGA CCG
C CT
GAM4707 CATTGCACTCC HD NM_002111.3 3 TGCCTAGGAGCTG CA--- ACT -- A
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GACG GGTCG GATCCGT
TTGTG GTC AG
GAM4707 CATTGCACTCC IGF1 NM_000618.2 3 CTGTCCCCCAGGC A--- A A
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GTGACGTGAGGTCGGA CTGT
CCCC C
GAM4707 CATTGCACTCC IGF1 NM_000618.2 3 TGTCCCCCAGGCT A--- A
AGCCTAGGCAA GGAGTGCAGTG CATTGCACTCCAGCCT GGCA
GTGACGTGAGGTCGGA CTGT
CCCC
GAM4707 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A A
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GC C
GAM4707 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- A A
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G AACGTGAGGTCGGA CCGTT
GTACGGC C
GAM4707 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A A
AGCCTAGGCAA AGTGCAGTG CATTGCACTCCAGCCT GGCAA
GTGACGTGAGGTCGGA CCGTT
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GAM4709 CAGCAGTGTTG ADAMTS5 NM_007038.1 3 GTGATGATTTTCA TG-- C A
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GTTGTT GAC TTTAGTAGTG
GAAA T
GAM4709 CAGCAGTGTTG TNFRSF5 NM_152854.1 3 TCCTGGCTCCAAC C AT TCA A
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GTCGTCACAAC CT GT
- CG CCT
GAM4733 TCCCCAAGCCT CAV1 NM_001753.3 5 TGCTGCCAGAACC CC GTAC A
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CA ACC-
GAM4733 TCCCCAAGCCT GFAP NM_002055.2 3 ACGCTGGTAGAGA - AGC G A
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AGG GGT GAG ATGGTCGCA
A A-- -
GAM4733 TCCCCAAGCCT TFCP2 NM_005653.2 5 TGCTAGTCGGGCT T T C G A
TGTACCAGCGT TGGGGG TCCCCAAGCCT G AC AGC
GGGGGTTCGGG C TG TCG
- - A T
GAM4738 TTAATGCTAAT BACE NM_012104.2 3 TCCCTATCAGTTC TTA ATCG A
CGTGATAGGGG TAGCATAGT ATGCTA TGATAGGGG
TACGAT ACTATCCCT
TGA CTTG
GAM4738 TTAATGCTAAT FPRL1 NM_001462.1 5 CCTCTATCACGAA - AA A
CGTGATAGGGG GATATTGA TTAATG CT TCGTGATAGGGG
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GAM4738 TTAATGCTAAT SLC6A4 NM_001045.1 3 ACCCTATCATCAG G C- G A
CGTGATAGGGG TTAGGATTAG TTAAT CTAAT GTGATAGGG
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G AC A
GAM4738 TTAATGCTAAT SLC6A4 NM_001045.1 3 CCCTATCATCAGT G C- A
CGTGATAGGGG TAGGATTAG TTAAT CTAAT GTGATAGGG
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G AC
GAM4769 CGCTATGTTGG ACE NM_152831.1 3 GACCAGCCTGTCC G A C A
CCAGGCTGGTC AACAGAGGG C CT TGTTGG CAGGCTGGTC
G GA ACAACC GTCCGACCAG
G G T
GAM4769 CGCTATGTTGG ADAM17 NM_021832.1 3 TCCAGCCTGGGTG A G T A
CCAGGCTGGTC ACAGAGTG CGCT TGTTG CCAGGCTGG
GTGA ACAGT GGTCCGACC
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G G T
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T ACTTT T
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                                TGGCGAGGACGA GGGG GG
                                      C    C  TG
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                          C          CGACGAGGACGA AG       GGAG
                                      A  ACCTTCC    T-
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                                  A    --        A
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TTT C AA
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T TGG GT CCGAC TTTACGTCACC
TAC A T G
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GAM5142 CACCCAGGCTG TGFB1 NM_000660.1 3 CCAGGCATTTGAG C----- ----- AG A
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CC

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C C GT
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T T ACCAC
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                              AC    A-  A
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CC
GG
C
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AG GA- T
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GAM5512 GGCCCAGGAGG APLP2 NM_001642.1 3 CCTCCACCCCCTC ----- AGAA A
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CCGG GTCCTCCCCC TCC
CCACT ACC-
GAM5512 GGCCCAGGAGG BACE2 NM_138992.1 5 GCCTTCTCCCCTC CCA- AG A A
GGGAGAAAGGC CCGCGAGCC GGC GG GGGGAGAA GGC
CCG CC CCCCTCTT CCG
AGCG CT -
GAM5512 GGCCCAGGAGG DHCR24 NM_014762.1 3 CCCTTCCTCCTTC A-- A C A
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CCGGGTCC CTTCCTC TTCC
GTA C C
GAM5512 GGCCCAGGAGG DHCR24 NM_014762.1 3 CCTTCCTCCTTCA A-- A A
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CCGGGTCC CTTCCTC TTCC
GTA C
GAM5512 GGCCCAGGAGG FOS NM_005252.2 3 CTTTTCTCTTTCT CC GG A
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CTG TCCTC TCTCTTTTC
AT TT
GAM5512 GGCCCAGGAGG GFAP NM_002055.2 3 CCTAGGCTGACCT ----- GG AA- A
GGGAGAAAGGC TGAACTCCTGGGC GGCCCAGGAG GG AG AGG
T TCGGGTCCTC CC TC TCC
AAGTT AG GGA
GAM5512 GGCCCAGGAGG IGF1 NM_000618.2 3 AGTTTTTCTCCCA GA GG A
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CTGGGTC CCCTCTTTTT
A- GA
GAM5512 GGCCCAGGAGG IGF1 NM_000618.2 3 CAGTTTTTCTCCC GA GGC A
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CTGGGTC CCCTCTTTTT
A- GAC
GAM5512 GGCCCAGGAGG IGF1 NM_000618.2 3 GCAACCTCCACCT G AAAG A
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TTGGGTCCTCC CCTC CG
A CAA-
GAM5512 GGCCCAGGAGG IL1A NM_000575.3 5 CCTTTCTCCCAAT CCCA -- A
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CC CCTCT CCCTCTTTCC
CTTA AA
GAM5512 GGCCCAGGAGG OGDH NM_002541.1 3 GCCCCACCCACCC - AGAAA A
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CCGGGTCCTCCC CC CCG
A CACC-
GAM5512 GGCCCAGGAGG OGDH NM_002541.1 3 GCTGTCGTCCCCC --- -- - AA A
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T TCGG GT CCTCCCCCT CT TCG
TTC GA G G-
GAM5512 GGCCCAGGAGG PRND NM_012409.1 3 CCTCAGGTGATCC A - GAA---- A
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CCGGGTCC CCC CCT TCC
A A AGTGGAC
GAM5514 TGAGGAGGTGC APLP1 NM_005166.2 3 TCCCCACGTGGCA CAGCGTC A
TACCAGCGTCT CCTCCTCA TGAGGAGGTGCTAC
ACTCCTCCACGGTG
CACCCCT
GAM5526 AATGCTGTGCC MAPK10 NM_002753.2 3 GGTGCAGCAGTGA AA------- GC GA A
AGAGCTGCACC CAGCAGTGAGAGT TGCTGT CA GCTGCACC
C ACGACA GT CGACGTGG
CTGAGAGTG -- GA
GAM5526 AATGCTGTGCC THOP1 NM_003249.2 3 GGGGCAGGCTCTG AAT----- - A A
AGAGCTGCACC GCACAGTGCCTGG GCTGTGCCAGAGC TGC CC
GA TGACACGGTCTCG ACG GG
AGGGTCCG G G

GAM5560 TGAAATGCTTT BACE NM_138973.1 3 TAGTACCTGTAAG T AC A
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ATTTTACGAA GTCC TGAT
T A-
GAM5560 TGAAATGCTTT BCHE NM_000055.1 3 TAGTATTTTACCT TT- C A
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ACTTTACGA ATTTT TGAT
TCC A
GAM5560 TGAAATGCTTT CAV2 NM_001233.2 3 CAGATTGCTTAAA T----- A -- A
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T TTTTACGAAAATTC GT GAC
TATTAT - TA
GAM5560 TGAAATGCTTT CAV2 NM_001233.2 3 TCAGATTGCTTAA T A -- C A
TAGGACACTGC AAGCATTTTT GAAATGCTTTTAGG CA CTG
TTTTACGAAAATTC GT GAC
T - TA T
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TAGGACACTGC AGCATTTGT AAATGCTT ACACTGC
TTTACGAA TGTGACG
TG CCCAA
GAM5560 TGAAATGCTTT CNTF NM_000614.2 3 GCAGTGTAACCCA TG----- TTAGG A
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A TTTACGAA TGTGACG
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GAM5560 TGAAATGCTTT FLNB NM_001457.1 3 CAGTGTCCGTGTT TG-- TTTTA--- A
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TTTATG CCTGTGAC
TCGG TAATTGTG
GAM5560 TGAAATGCTTT HTR2A NM_000621.1 3 AAAATGTTCTGAC T CTGC A
TAGGACACTGC AGCATTTCA TGAAATGCT TTAGGACA
ACTTTACGA AGTCTTGT
C AAAA
GAM5560 TGAAATGCTTT HTR2A NM_000621.1 3 AAATGTTCTGACA T CTG A
TAGGACACTGC GCATTTCA TGAAATGCT TTAGGACA
ACTTTACGA AGTCTTGT
C AAA
GAM5597 TTGTTTTAGAA IGF1 NM_000618.2 3 TTTTGTGCACTCT -- AG - A
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GACAAAATCT TCT CG GTTTT
CG CA T
GAM5597 TTGTTTTAGAA PRND NM_012409.1 3 TCTGTTTTAAATT AG- T A
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AACAAAATTT TTTT GTCT
AAA -
GAM5597 TTGTTTTAGAA PSEN1 NM_000021.2 3 TCAGACCTTCTTC TTA A A
GAAGGTCAGAA CACAGCAA TTGTT GAAGAAGGTC GA
AACGA CTTCTTCCAG CT
CAC A
GAM5615 AAATCCAGAAT ACE NM_152831.1 3 ATCAGCCTGGCCA AT- A A A
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TTTAGGTCT GGTC GACT
ACC C A
GAM5615 ATTTGGGGAAA FOS NM_005252.2 3 GAGAAACACATCT A---- - G B
TGTGTTTCTGG TCCCTAGAGGGTT TTTGGGGAA ATGTGTTTCT
AGATCCCTT TACACAAAGA
TTGGG C G
GAM5615 ATTTGGGGAAA NCKAP1 NM_013436.2 3 TTAGAAGCAGATC A------ -- G B
TGTGTTTCTGG ATTTCCCAAAATT TTTGGGGAA AT TGTTTCTGG
CTAA AAACCCTTT TA ACGAAGATT
AATCTTA AC G
GAM5617 ACCAGCTGTGT MME NM_000902.2 3 TTCTTGTTGCCAC A----- TG TT A
GAACTTAGGAA AGCTGGAGCTCT CCAGCTGTG AAC AGGA
GGTCGACAC TTG TCTT
TCTCGA CG T-
GAM5617 CTTCCTGGGTT MAPT NM_016835.1 5 ACCAGGATGGCTG CT ---- -- B
CATATCCTGGT AGCCCCGCCAGGA TCCT GGGTTCA TATCCTGGT
G AGGA CCCGAGT GTAGGACCA
G- CCGC CG
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CTTTTGTTGTT CACTGTTCTGTT AGAAT GTGCTTTTGT GTT
TCTTG CACGAAAATA CAA
TTG TCAC -
GAM5623 GGAAGAATGTG CAV2 NM_001233.2 3 AACATAAAAGCAC GGA- ---- T A
CTTTTGTTGTT CACTGTTCTGTTC AGAAT GTGCTTTTGT GTT
TCTTG CACGAAAATA CAA
CTTG TCAC -
GAM5623 GGAAGAATGTG CNTF NM_000614.2 3 AACAACAAGAAAA AGAA- ---- A
CTTTTGTTGTT TGTACAGTTAGTC GGA TGTGC TTTTGTTGTT
C CCT ACATG AGAACAACAA
GATTG TAAA
GAM5623 GGAAGAATGTG ESR2 NM_001437.1 5 GCGGGAAAAGCAC AGA G A
CTTTTGTTGTT GTGTCC GGA ATGTGCTTTT TTGT
CCT TGCACGAAAA GGCG
G-- G
GAM5623 GGAAGAATGTG IGF1 NM_000618.2 3 AGAATAAAAGATG ---- ------ G A
CTTTTGTTGTT TAGCACATTTTGC GGAA GAATGTGCT TTTGTT
TTTCC CCTT TTTACACGA AAATAA
TCGT TGTAGA G
T
A
GAM5623 GGAAGAATGTG IL1A NM_000575.3 5 AATACAAAACTGA GTGC TGT A
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AGTC TAA
GAM5623 GGAAGAATGTG MME NM_007289.1 3 GCTCTAAAAGCAC AGAAT TT A
CTTTTGTTGTT CTCC GGA GTGCTTTTG GT
CCT CACGAAAAT CG
C---- CT

GAM5623 GGAAGAATGTG MTNR1A NM_005958.2 3 ACAAAAGGGGTAA ---- G A
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TCTTCTTACG TGGGGA AACA
TTAA A
GAM5623 GGAAGAATGTG SNCAIP NM_005460.1 3 ACAGCATAAAGCA A-- - - A
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CC TC TTACACGAAA ACGACA
GAG G T
GAM5623 GGAAGAATGTG SNCAIP NM_005460.1 3 TACAGCATAAAGC A-- - - T A
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CC TC TTACACGAAA ACGACA
GAG G T T
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GAAAGG GACCCGACG
TGTAA TAAGGT
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TCTGGGCTGTG AGGAAGGG CTTTTCCTGGGT TGG C T
GGGAAGGACCCA ACC G G
C G GT
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A G G
GAM5653 CACTGCACTCC BACE2 NM_138991.1 3 TTGCCCAGGGTCC CACT TCCAG A
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CGTG GGACCCGTT
GGTC TCCTG
GAM5653 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

-
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GTGACGTG GGTCGG C CG
T GT G AC
GAM5653 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - A A
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GTGACGTG GGTCGG C CG
T GT G A
GAM5653 CACTGCACTCC CTSK NM_000396.2 3 CTTCCACGATGGT CT GCC CA A
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GTGACGT GGT ACCT
-- AGC TC
GAM5653 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GAM5653 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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AGCCTGGGCAA ACTGCTTTG CA GCA GCCTGGGCAA
GT CGT TGGACCCGTT
TT CACTC
GAM5653 CACTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM5653 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM5653 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
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GTGACGTG TC TCTGTT
T-- AC-
GAM5653 CACTGCACTCC NGB NM_021257.2 3 TGCTTCTTCAGGT CA----- CA ---- A
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GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM5653 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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GAM5653 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM5654 TACAAATTCCT PIN1 NM_006221.1 3 GAGGCTCCCAGAC AAT ----- G A
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GTGT GGGACCCAGA GGA
GAC CCCTC G
GAM5654 TACAAATTCCT S100B NM_006272.1 5 AAGGAGACCAGGA AAA G G A
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GTG AAGGACC AGAGGA
GGG - A
GAM5657 ACTGCACTCCT FHL2 NM_001450.2 5 GTCGCCCAGGCTG T A A
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TGACGTGAGG CGGA CCGCTG
T C

GAM5657 ACTGCACTCCT IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A T A
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TGACGTGAGG CGGA CC CTG
T C C
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TGACGTGAGG CGGA CC TG
T C GT
GAM5657 ACTGCACTCCT PRNP NM_000311.1 3 GTCACCTAGCAGA AC CTC C A
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ATGT GACG ATCCACTG
TT ATA -
GAM5657 ACTGCACTCCT PRNP NM_000311.1 3 GTCACCTAGCAGA AC------ CTC C A
GCCTAGGTGAC TATGTATTACTTT TGCA CTGC TAGGTGAC
T ATGT GACG ATCCACTG
TTTTCATT ATA -
GAM5673 GGAAAGTTAAA IGF1 NM_000618.2 3 AATATTATCTTTC -- --- T A A
GATGTATGTAT TTAACTTTTTCC GGAA AGTTAA AGATG ATGT
CCTT TCAATT TCTAT TATA
TT CTT - A
GAM5673 GGAAAGTTAAA IGF1 NM_000618.2 3 CAATATTATCTTT -- --- T AT A
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CCTT TCAATT TCTAT TATA
TT CTT - AC
GAM5673 GGAAAGTTAAA IGF1 NM_000618.2 3 GTGCAACCTAATT AA GTA-- A
GATGTATGTAT AGTAACTTTCC GGAAAGTTA GAT TGTAT
CCTTTCAAT TTA ACGTG
GA ATCCA
GAM5673 GGAAAGTTAAA MAPK10 NM_138981.1 3 AATGTATATTTAA A AA A A
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TCTT CAAT TTATATGTA
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GAM5691 GGCCCAGGAGG ACE NM_152830.1 3 GCCCTGTCCCTGT CCCA ---- AA- A
GGGAGAAAGGC CCCCCTCCCCTCC GG GGAGGGGGA GA GGC
C CC CCTCCCCCT CT CCG
CTCC GTCC GTC
GAM5691 GGCCCAGGAGG ADAMTS5 NM_007038.1 3 ACTGTCTCCCCCT CCAG A G A
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CTG TTCCCCCTCT TC
---- G A
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CC GGTCCTCC CTC CCG
A TA CGGA
GAM5691 GGCCCAGGAGG APBB2 NM_173075.1 3 GCTCTATCCCCCT CCA GAAA A
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TCG TCTCCCCCT TCG
TAG ATC-
GAM5691 GGCCCAGGAGG APLP2 NM_001642.1 3 CCTCCACCCCCTC ----- AGAA A
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CCGG GTCCTCCCCC TCC
CCACT ACC-
GAM5691 GGCCCAGGAGG BACE2 NM_138992.1 5 GCCTTCTCCCCTC CCA- AG A A
GGGAGAAAGGC CCGCGAGCC GGC GG GGGGAGAA GGC
CCG CC CCCCTCTT CCG
AGCG CT -
GAM5691 GGCCCAGGAGG DHCR24 NM_014762.1 3 CCCTTCCTCCTTC A-- A C A
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CCGGGTCC CTTCCTC TTCC
GTA C C
GAM5691 GGCCCAGGAGG DHCR24 NM_014762.1 3 CCTTCCTCCTTCA A-- A A
GGGAGAAAGGC TGCCTGGGCC GGCCCAGG GGGGGAG AAGG
CCGGGTCC CTTCCTC TTCC
GTA C
GAM5691 GGCCCAGGAGG FOS NM_005252.2 3 CTTTTCTCTTTCT CC GG A
GGGAGAAAGGC CCTTAGTC GGC AGGAG GGAGAAAGG
CTG TCCTC TCTCTTTTC
AT TT
GAM5691 GGCCCAGGAGG GFAP NM_002055.2 3 CCTAGGCTGACCT ----- GG AA- A
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T TCGGGTCCTC CC TC TCC
AAGTT AG GGA
GAM5691 GGCCCAGGAGG IGF1 NM_000618.2 3 AGTTTTTCTCCCA GA GG A
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A- GA
GAM5691 GGCCCAGGAGG IGF1 NM_000618.2 3 CAGTTTTTCTCCC GA GGC A
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CTGGGTC CCCTCTTTTT
A- GAC
GAM5691 GGCCCAGGAGG IGF1 NM_000618.2 3 GCAACCTCCACCT G AAAG A
GGGAGAAAGGC CCTGGGTT GGCCCAGGAGG GGAG GC
TTGGGTCCTCC CCTC CG
A CAA-
GAM5691 GGCCCAGGAGG IL1A NM_000575.3 5 CCTTTCTCCCAAT CCCA -- A
GGGAGAAAGGC CTCCATTCCC GG GGAGG GGGAGAAAGG
CC CCTCT CCCTCTTTCC
CTTA AA
GAM5691 GGCCCAGGAGG OGDH NM_002541.1 3 GCCCCACCCACCC - AGAAA A
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A CACC-
GAM5691 GGCCCAGGAGG OGDH NM_002541.1 3 GCTGTCGTCCCCC --- -- - AA A
GGGAGAAAGGC TCCAGTGCTTGGC GGCC CA GGAGGGGGA GA GGC
T TCGG GT CCTCCCCCT CT TCG
TTC GA G G-
GAM5691 GGCCCAGGAGG PRND NM_012409.1 3 CCTCAGGTGATCC A - GAA---- A
GGGAGAAAGGC ACCCACCTGGGCC GGCCCAGG GGG GGA AGG
CCGGGTCC CCC CCT TCC
A A AGTGGAC

GAM5697 TATTGATCTGT APPBP2 NM_006380.2 3 CCAGGCTGGGAGG AT G T A
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GTAAC GG AGGGTCGGAC
-- G C
GAM5697 TATTGATCTGT APPBP2 NM_006380.2 3 CCCAGGCTGGGAG AT G TG A
CCCAGCCTGTG GGCAATG TATTG CT TCCCAGCCTG
GTAAC GG AGGGTCGGAC
-- G CC
GAM5703 GTCCAGTGCTC ABCD1 NM_000033.2 3 TGTCCAGGGCAGT CC TG --- A
ACTGCCGACAT GAGTCCTCTAC GT AG CTCACTGCC GACA
CA TC GAGTGACGG CTGT
TC CT GAC
GAM5703 GTCCAGTGCTC DHCR24 NM_014762.1 3 TGTCATCTGAGTT T - GCC-- A
ACTGCCGACAT GAGCACTGGTC G CCAGTGCTCA CT GACA
C GGTCACGAGT GA CTGT
T T GTCTA
GAM5703 GTCCAGTGCTC GLUL NM_002065.3 3 TGGAGAAGGTGGG GCCGA A
ACTGCCGACAT CACTGGAT GTCCAGTGCTCACT CA
TAGGTCACGGGTGG GT
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GAM5728 GGCATGTGTGA ADAMTS5 NM_007038.1 3 TCTGCAGCTATTT CAT G C- A
GCAGCTGCAGG CAACTTCC GG GT TGAG AGCTGCAGG
CC CA ACTT TCGACGTCT
TT- - TA
GAM5728 GGCATGTGTGA APLP2 NM_001642.1 3 ATTGTATTGTCTG G - C G A
GCAGCTGCAGG ACACATGCT GGCATGTGT AG CAG TGCAG
TCGTACACA TC GTT ATGTT
G T - A
GAM5728 GGCATGTGTGA APLP2 NM_001642.1 3 TTGTATTGTCTGA G - C A
GCAGCTGCAGG CACATGCT GGCATGTGT AG CAG TGCAG
TCGTACACA TC GTT ATGTT
G T -
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GCAGCTGCAGG ATGCC GGCATGTGT GCTGCAG
CCGTACACA TGACGTC
AG---
GAM5728 GGCATGTGTGA CNTF NM_000614.2 3 CTGGAAAACAGCT G TG ----- A
GCAGCTGCAGG GCTGTTAGATGTC GGCAT TG AGCAGCTG CAG
CTGTA AT TCGTCGAC GTC
G TG AAAAG
GAM5728 GGCATGTGTGA HD NM_002111.3 3 AGGGAGCTGCTCA GTG GCAG A
GCAGCTGCAGG GAATGCC GGCAT TGAGCAGCT
CCGTA ACTCGTCGA
AG- GGGA
GAM5728 GGCATGTGTGA HD NM_002111.3 3 CCTATGGGCTTCC AGC GC- A
GCAGCTGCAGG GCACATGCC GGCATGTGTG AGCT AGG
CCGTACACGC TCGG TCC
CT- GTA
GAM5728 GGCATGTGTGA HD NM_002111.3 3 GTTGCAGCTGCTC ---- T G A
GCAGCTGCAGG TTGCATCTGGGCC GGC ATGTG GAGCAGCTGCAG

CCG TACGT CTCGTCGACGTT
GGTC T G
GAM5728 GGCATGTGTGA HD NM_002111.3 3 TTGCAGCTGCTCT ---- T A
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CCG TACGT CTCGTCGACGTT
GGTC T
GAM5728 GGCATGTGTGA MAPK10 NM_138981.1 5 CCTTTCAGAACCA GAGCAG C- A
GCAGCTGCAGG AACACATGCC GGCATGTGT CTG AGG
CCGTACACA GAC TCC
AACCAA TT
GAM5728 GGCATGTGTGA TRPM2 NM_003307.1 3 ATGCAGGCATCCA T - AG G A
GCAGCTGCAGG CATGCC GGCATGTG GA GC CTGCA
CCGTACAC CT CG GACGT
- A -- A
GAM5728 GGCATGTGTGA TRPM2 NM_003307.1 3 CCTGCAGCCCCTC ATGTG CA A
GCAGCTGCAGG AGCC GGC TGAG GCTGCAGG
CCG ACTC CGACGTCC
----- CC
GAM5744 TTCACATGTTG ADAMTS5 NM_007038.1 3 GCCTATTGTTAAA TG-- ---- TTT A
CTCAGTTTTGC GATTTGCATGTGA TTCACATGT CT CAGT GC
A AAGTGTACG GA GTTA CG
TTTA AATT TC-
GAM5744 TTCACATGTTG APLP2 NM_001642.1 3 TGAAACTGAGTCT TT - ----- A
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G- C GTGTC
GAM5744 TTCACATGTTG GFAP NM_002055.2 3 GCTTTGACTGAGC ATG- TT- A
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GAGTG GACGAGTCAG CG
GTCA TTT
GAM5744 TTCACATGTTG GFAP NM_002055.2 3 GTAAAACTGAGGC A- --- - A
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A AAGTG ACG ACG AGTCAAAATG
AA AGC G
GAM5744 TTCACATGTTG GYPA NM_002099.2 3 GTGAAAAATTAAC CTCAG TG A
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TAA-- GT
GAM5744 TTCACATGTTG TRPM2 NM_003307.1 5 GCAGCTGGGAACA TT G TT A
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AC - --
GAM5744 TTCACATGTTG TRPM2 NM_003307.1 5 GCAGCTGGGAACA TT----- G TT A
CTCAGTTTTGC TGTGCAGGCTG CACATGTT CTCAGT TGC
GTGTACAA GGGTCG ACG
GTCGGAC - --
GAM5749 CTGCACTAGAA DSCR1 NM_004414.3 3 ACAGGAAGCCGCC AA ACTA A
GGCACTATGTT TAGTGCAG CTGCACTAG GGC TGT
GACGTGATC CCG ACA
CG AAGG

GAM5749 CTGCACTAGAA HTR2C NM_000868.1 3 AACATAGTGGTAT AC--- GG- A
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GACG ATTTT GTGATACAA
ATACA ATG
GAM5749 CTGCACTAGAA PLCD1 NM_006225.1 3 AACATAGTGTCTG CT C A A
GGCACTATGTT CTGCTGCCT GCA TAG AGGCACTATGTT
CGT GTC TCTGTGATACAA
TC C G
GAM5764 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
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CG---
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ATGACA ATCT GTGAACAT
TT ATG TT
GAM5764 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
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C ATGACA ATCT GTGAACAT
CTTT ATG TT
GAM5764 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
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AGA ACACTACCT AACG
ACA TCAAA
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AGAC TA GCCTGTGAAC
T- GG C
GAM5764 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 ACAATGTCCAAGA A-- C A
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AGACGACAC ACCTGT AACA
AGA -
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GAM5798 GAAAGTAGTAA ARHA NM_001664.1 3 GGCTGTAACTACT G----- AAGTTG A
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TTTCATCA ATGTCGG
TCAATA ------
GAM5800 AGTATTACAGC CAV2 NM_001233.2 3 GATTGGGATACTG CAGGTA TG A
AGGTACTGGTT TAATACT AGTATTACAG C GTT
TCATAATGTC G TAG
ATAG-- GT
GAM5806 GCCTGGATGTG ABCD1 NM_000033.2 3 TGAGGGTGGTCAG - ATG A
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CGGA CC ACTGGTGGGAGT
A G--
GAM5806 GCCTGGATGTG DHCR24 NM_014762.1 3 GTGAGGGCTGGGG GA - A
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CGGACCTACG GGT GGGAGTG
GG C
GAM5809 GACAAGAGGCA CAV1 NM_001753.3 3 TCTGCTTGATTTT --- C - - A
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C CTG TTCTCCGT TTT GT CGTCT
ACC T A T
GAM5809 GACAAGAGGCA CRAT NM_004003.2 5 CCCGCTGAATCTT G C -- A A
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CTGTTCTC GT TCT GTCG CC
G - AA C
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CTGTT CT TGTCTGTC TCT
G ACA T
GAM5809 GACAAGAGGCA MAPT NM_173727.1 3 CTTTCTGTCTGTG AGAGG C A
CAGACAGCAGG AATGTC GACA CACAGACAG AGG
CTGT GTGTCTGTC TTC
AA--- T
GAM5809 GACAAGAGGCA PLCD1 NM_006225.1 3 CCTGCTCCCAGCC - ACAGAC A
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CT GTTCTCCG TCGTCC
C ACCC--
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GAM5809 GACAAGAGGCA PSEN1 NM_007318.1 3 CCTGCTGTCAGAC GAC CACA A
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- GC
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- GCG
GAM5809 GACAAGAGGCA TNF NM_000594.2 3 CCTGGCCTCTGTG GA --- CAG A
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GTT TTCCGTGTCT GTCC
TA TTC CCG
GAM5814 TGCAAGTCTGT ADAM17 NM_003183.3 3 CTACAAATCAATC T --- T A
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ATGTTC GACACTAA AACAT
- CTA C
GAM5814 TGCAAGTCTGT FHL2 NM_001450.2 3 AACCAAGATTATG - T A
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ACGTTCAG GTATTAGAAC CAA
T -

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ACG AGA TAAAACACAG
GTG AGGTTA
GAM5814 TGCAAGTCTGT HTR2C NM_000868.1 3 AATATAAATCACA C T A
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AC TTTAGACACTAAA TATAA
C -
GAM5814 TGCAAGTCTGT IGF1 NM_000618.2 3 GACACAAAAGTCC AG T A-- A
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ACGT AG CAC AAAACACAG
-- T CTG
GAM5823 GGAAAGTTAAA IGF1 NM_000618.2 3 AATATTATCTTTC -- --- T A A
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CCTT TCAATT TCTAT TATA
TT CTT - A
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CCTT TCAATT TCTAT TATA
TT CTT - AC
GAM5823 GGAAAGTTAAA IGF1 NM_000618.2 3 GTGCAACCTAATT AA GTA-- A
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CCTTTCAAT TTA ACGTG
GA ATCCA
GAM5823 GGAAAGTTAAA MAPK10 NM_138981.1 3 AATGTATATTTAA A AA A A
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TCTT CAAT TTATATGTA
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ACTCCAGT CG AC TCCAG
CC GA TC
GAM5826 TGAGGTCATGT IGF1 NM_000618.2 3 ACTTTCAAAAACA T----- CTGTC A
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TTCCAGTACAA TTCA
AACACC AAACT
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CCGG AC AAGACAGTCCG
TTTACA C CA
GAM5826 TGAGGTCATGT MME NM_000902.2 3 TCCTGACAGGGTG T------- GT T A
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TTCCAGTG GGACAGTCC
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GAM5826 TGAGGTCATGT MME NM_007289.1 3 CTCCTGACAGGGT T GT TT A
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TTCCAGTG GGACAGTCC
G -- TC
GAM5826 TGAGGTCATGT TRPM2 NM_003307.1 3 AGTCTGCTGCAGA TGT -- GT A
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ACTCCAGT AGACG GTC A
--- TC TG
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ACTCCG TACAAGAC TCC
AC TC T
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GAM5836 CACCCAGGCTG ADAM17 NM_021832.1 3 CCACTACACTCCA C A
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GTGGGTCCGACCTCAC TCACC
A
GAM5836 CACCCAGGCTG FLNB NM_001457.1 3 CAAAGCCCTCCAG C-- T AG A
GAGTGCAGTGG CCTGTTTGTG CAC CAGGCTGGAG GC TG
GTG GTCCGACCTC CG AC
TTT C AA
GAM5836 CACCCAGGCTG FPRL1 NM_001462.1 5 CCACTGCATTTGC C-- - - - A
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T TGG GT CCGAC TTTACGTCACC
TAC A T G
GAM5836 CACCCAGGCTG IAPP NM_000415.1 3 CCACTGCACTCCA A
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GAM5836 CACCCAGGCTG TGFB1 NM_000660.1 3 CCAGGCATTTGAG C----- ----- AG A
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ACATA TGGGTCCGACC TTACG A
ATACAA AGAGT G-

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CC

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AGTGACGT GGAGGC GA GGT
C C G
GAM5836 TCACTGCAACC AGER NM_172197.1 3 GGCAGGCGAGAGT C AAC - B
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GGT ATG GAG GCGGACGG
C AT- A
GAM5836 TCACTGCAACC IAPP NM_000415.1 3 GGAGGCGGAGGTT G B
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AGTGACGTTGGAGGCGGA GG
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GAM5859 TCCCTGAGCCC ACHE NM_015831.1 3 ATACTATTTATTT T------- TG ----- A
TGAAGGGTGTT CAGGGCTGGGCTA CCC AGCCCTGAAG GG
TAACA GGG TCGGGACTTT TC
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TGT
ATA

GAM5859 TCCCTGAGCCC MTNR1A NM_005958.2 3 AATGCGGTTCAGG - G GG A
TGAAGGGTGTT GCTGGGGTGA TC CCT AGCCCTGAA GTGTT
AG GGG TCGGGACTT CGTAA
T G GG
GAM5868 TCAAAGCTGCA ARHA NM_001664.1 3 CTCAGGCAATTAG C CA- TG A
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GGTTTC AC TTAACGGAC
- AGA TC
GAM5868 TCAAAGCTGCA ARHA NM_001664.1 3 TCAGGCAATTAGA C CA- T A
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GGTTTC AC TTAACGGAC
- AGA T
GAM5868 TCAAAGCTGCA DLST NM_001933.2 3 CACAGGCAAAGAG T-- T GA--- A
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T GTTTCG CGT AACGGACAC
TTC T GGAGA
GAM5868 TCAAAGCTGCA TNF NM_000594.2 3 CACTGGGGCCTAC C ATT -- A
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AGTTTCGAC TC CGGG CAC
A --- GT
GAM5868 TCAAAGCTGCA VLDLR NM_003383.1 3 CACATTCTACTTC C ATTGCC A
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T ATCTT-
GAM5872 GTTGTGTGGAA ACE NM_152831.1 3 GCTCTCCATCTTC G CTTT A
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TAA GCACCTTCTAC CG
A CTCT
GAM5872 GTTGTGTGGAA APBA1 NM_001163.2 3 GGCTTAAAGCATC GTGT- A -- A
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CAG CCT CTACGAAA CGG
GTCCT C TT
GAM5874 TCCAAAATTAA BACE NM_012104.2 3 TTCTACAAGTAAT TC-------- AAGG A
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C GTTTTAAT AACATCTT
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CAGACAC G---
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GTTTTAAT AACATCTT
AC G---
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CC AT -
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AGGT AATTTCCGA CATT
--- GTT C
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CG AAATTTTAGTCAA
AA T----
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TCAT AACG
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G AGTAAAAAT TTTAGTCAA
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GAM5886 TATCTCTTGCC BACE2 NM_012105.3 3 TAGGAGGTCATCA TC CCT A
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GTAG AAC ACTGGAGGAT
CC T--
GAM5886 TATCTCTTGCC PSEN1 NM_000021.2 3 TGAGGGACGAGGT -- A- CT A
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AC AG T-
GAM5910 AGCAAGTGTTG ACT NM_020482.3 3 GCCAAAGCATGGG A-- --- A--- -- A
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TGTATT TGTT CACAACTTTG CGA C
TTA TTG GGTA AA

GT
CG

GAM5910 AGCAAGTGTTG DSCR1 NM_004414.3 3 ACTCTTTGCAACA AAA CT A
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TCGTTCACGAC GTT TCA
AAC TC
GAM5916 AAGCAGCCTTG BACE NM_012104.2 3 TCTTCCTGGTCAT AAGC----- TG A
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C TCGGA CTGGTCCTTCT
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GAM5916 AAGCAGCCTTG BACE NM_138972.1 3 CCTTCAGTATCAA AA----- - CA A
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CGTCGGAACT TG CTTCC
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GAM5916 AAGCAGCCTTG IL1A NM_000575.3 3 CATTTTGGTCCAA GC- GG A
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TTCGT GAACCTGGTTTT
GTT AC
GAM5958 AAGCTGGCCTG CASP3 NM_032991.1 3 CTCAGCAGGTGCG AA ----- - A
TACCTGCTGAG GAGCCGTCACTGC GC TGGC CTGTACCTGCTGAG
A CG GCCG GGCGTGGACGACTC
A- TCACT A
GAM5958 AAGCTGGCCTG CTSG NM_001911.2 3 CTCGGGGACACAG A----- AC G A
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TCGACCGGACA GG GGCTC
GACACC CA -
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CCAC CC
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TC-- T
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ACTGT AAACCAACGA GA
A- G A
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C TCTAGACT GACGACAACC
CT-- CTACCCG
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ATTG ACCA ACGACAAT
GTT-- ATAA
GAM5973 TGGCAGATTTG TRPM2 NM_003307.1 3 CCAAGACATTAAA TG GT A
GTTGCTGTTGG TCTGCCA TGGCAGATTTGGT CT TGG
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CA --
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C - G
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ACGAGAATGAGGG GACT
TAGT
GAM5990 TGCTCTTGCTC MME NM_007288.1 3 CCAGAAGAAGAGT TGCT------ T B
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GAM5998 CTTGGCCCTGT CRAT NM_004003.2 5 GGTGAAGCCTCTG CTT------- TGT A
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C TCGGG CTCCGAAGTGG
CCGAAGTCCT T--
GAM5998 CTTGGCCCTGT DHCR24 NM_014762.1 3 AGTGAAGCCTCCA CCC T C A
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GAATC AC CTCCGAAGTG
CCA - A
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GAATC AC CTCCGAAGTG
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A C -
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GGACCGGGACA CGGGG
GGTA CC
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C CA T C
GAM6024 TGGAGAATTAA BACE NM_138971.1 3 CACCATTCCTTTA AA TA- A
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ACCTCTTAA TTTCCT CAC
A- TAC
GAM6024 TGGAGAATTAA MPO NM_000250.1 3 GCTCCCCTTTTTC GA TT T A
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AC CTT TTTTTCCC TCG
TC C- C

GAM6051 CTCCCTCCACT ADAM10 NM_001110.1 5 CGGCCCCTGAAGT C TGA A A
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GAG GAGGTGAAG CC GC
C TCC G
GAM6055 TTCACCCATCT DHCR24 NM_014762.1 3 AGGGGTGGAGATG TT TT AC A
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GTGGGTAG AGGTGGG
TGACGGT -- G
GAM6055 TTCACCCATCT DHCR24 NM_014762.1 3 TGTGTGGAAAGTC ACCCAT C A
TTCCACCCAC AGAGGAA TTC CTTTCCAC CA
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C AAAT G
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TC A-
GAM6055 TTCACCCATCT UBB NM_018955.2 5 GTGGGTGGACGTG T C TT- A
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AGTGG TGG AGGTGGGTG
T T TGC
GAM6055 TTCACCCATCT UBB NM_018955.2 5 GTGGGTGGACGTG T---- C TT- A
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AGTGG TGG AGGTGGGTG
CGGTT T TGC
GAM6083 GGCCTGAGGTC ABCD1 NM_000033.2 5 CCTCTCAAGGCCC -- CA ---- A
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C CCGGG CTCCAGTC CG TCTCC
GA C- GAAC
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A C GGA
GAM6083 GGCCTGAGGTC APBB1 NM_145689.1 3 GGCTATTCCTAGG - C AG A
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A C GG
GAM6083 GGCCTGAGGTC APLP2 NM_001642.1 3 CCTCTACTTTGTC CC- T-- C A
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CC ACTCC GTT TCATCTCC
TCC CCT -
GAM6083 GGCCTGAGGTC BAX NM_004324.2 3 ATCTACCCTGCTG CCT -- G A
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GAM6083  GGCCTGAGGTC PRND   NM_012409.1  3  TCTTGAACTCCTG G          C  A-          A
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                                  TGGACTCCAGTC TCA  TTCT
                                  G           C   AG
GAM6083  GGCCTGAGGTC PRND   NM_012409.1  3  TCTTGAACTCCTG G-----          C  A-       A
      AGCAGTAGAGG                  ACCTCAGGTGATC      GCCTGAGGTCAG AGT  GAGG
                           CA             TGGACTCCAGTC TCA  TTCT
                                  ACCTAG           C   AG
GAM6083  GGCCTGAGGTC SLC17A7 NM_020309.1  3  CCTCTCTGTCCTG         CA-   T           A
      AGCAGTAGAGG                  CCTCAGGCC     GGCCTGAGGT   GCAG AGAGG
                                  CCGGACTCCG   TGTC TCTCC
                                        TCC    -
GAM6083  GGCCTGAGGTC TRPM2   NM_003307.1  3  CACTACTGCTGTG        T--        AG        A
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                                  TCGGACTCC   GTCGTCATC
                                       CGT        AC
GAM6102  CTGAGGTCAGG ABCD1   NM_000033.2  5  CTCTCAAGGCCCT          A  C-   C        A
      AGTTCGAGACC                  GACCTCAG     CTGAGGTCAGG GTT  GAGA
                                  GACTCCAGTCC CGG  CTCT
                                        -  AA   C
GAM6102  CTGAGGTCAGG IGF1    NM_000618.2  3  GGACTCAAACTCC CT-----          C  A      A
      AGTTCGAGACC                  TGACCTTGTGATT       GAGGTCAGGAGTT GAG CC
                           T              TTCCAGTCCTCAA CTC GG
                                  TTTAGTG           A  A
GAM6102  CTGAGGTCAGG PRND   NM_012409.1  3  GGTCTCGAACTCC     G                  A
      AGTTCGAGACC                  TGACATCAG     CTGA GTCAGGAGTTCGAGACC
                                  GACT CAGTCCTCAAGCTCTGG
                                    A
GAM6102  CTGAGGTCAGG PRND   NM_012409.1  3  GGTCTTGAACTCC                        A
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                                  GACTCCAGTCCTCAAGTTCTGG

GAM6102  CTGAGGTCAGG TRPM2   NM_003307.1  3  GTCTGAACTCCTG     -          G          A
      AGTTCGAGACC                  ACTGTCAG     CTGA GGTCAGGAGTTC AGAC
                                  GACT TCAGTCCTCAAG TCTG
                                    G          -
GAM6121  GAGGTAGAGGT APLP2   NM_001642.1  3  GCTCACTGCTTCT         GTT              A
      TGCAGTGAGTC                  GCTTT        GAGGTAGAG   GCAGTGAGT
                                  TTTCGTCTT   CGTCACTCG
                                        ---
GAM6121  GAGGTAGAGGT APPBP2  NM_006380.2  3  GGCTCACTGCAAC     TA                  A
      TGCAGTGAGTC                  CTCCGCCTC     GAGG  GAGGTTGCAGTGAGTC
                                  CTCC  CTCCAACGTCACTCGG
                                    GC
GAM6121  GAGGTAGAGGT BACE    NM_138973.1  3  ACTCACTGCATTT GA  T     ------          A
      TGCAGTGAGTC                  GGGGCCTTTCCCA   GG AGAGGT     TGCAGTGAGT
                                   CC TTTCCG      ACGTCACTCA
                                  A-  C      GGGTTT
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CT TCTCCA CGTCACT
GTT - AA
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TC AGAAC
GAM6121 GAGGTAGAGGT FHL2 NM_001450.2 5 GCTCACTGCAAGC G A
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G A
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CATTGACG TCA
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TATGTCC TT -
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CACTGA AA CGTC

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AA T T
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- AT GC
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TT A A
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                                  G   TA       --
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                                        GCA       CAG
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                                  C   T         CC
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                                  GGACTC   T         CC
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     AAGACTGTGAA                   CTCATTCACTGT      GAAT  GGCTGAAGA   TGA
                                     CTTA  CCGACTTCT   ACT
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                                  ACCTTACCG C  CTG  CATT
                                       - CC   CT
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                                  ACCTCTCT  TC CTGA    CGG
                                       TC  T    CTCA
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C AG- C
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GAM7135 TTGGTTGCTGA IGF1 NM_000618.2 3 TCAGATTTCATAG G------ C A
TGAGCTTTGAG AAAGGAGCAACCA TTGGTTGCT ATGAG TTTGA
A AACCAACGA TACTT AGACT
GGAAAGA T
GAM7135 TTGGTTGCTGA MTNR1A NM_005958.2 3 TCAGTTAATGGCT T----- C ----- A
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AACCA ACTAAC ACTACTCGG GAC
ACCAAC A TAATT

A
T

GAM7140 TACAGGCAGGC ADAMTS5 NM_007038.1 3 AAACCTTTGACTG GCA CAG A
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ATGTCCGTC GTTTCC
A-- AAA
GAM7140 TACAGGCAGGC APBA2 NM_005503.2 3 GCTGCCTCTGCCA TA G GCA A
ACAGAGGCAGT CTGACTGCA CAG CAG CAGAGGCAGT
GTC GTC GTCTCCGTCG
AC A ACC
GAM7140 TACAGGCAGGC DLST NM_001933.2 3 CAGCCTCTGTCCT G C AG A
ACAGAGGCAGT GGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - AC
GAM7140 TACAGGCAGGC DLST NM_001933.2 3 GCAGCCTCTGTCC G C AGT A
ACAGAGGCAGT TGGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - ACG
GAM7140 TACAGGCAGGC NGB NM_021257.2 3 TTGCTCTGTGCTG GCA G A
ACAGAGGCAGT ACTGTG TACAG GGCACAGAG CAG
GTGTC TCGTGTCTC GTT
AG- -
GAM7140 TACAGGCAGGC NGB NM_021257.2 3 TTTGCTCTGTGCT GCA G T A
ACAGAGGCAGT GACTGTG TACAG GGCACAGAG CAG
GTGTC TCGTGTCTC GTT
AG- - T
GAM7140 TACAGGCAGGC SNCG NM_003087.1 5 CTGCGAGCTCCGT TA-------- C A --- A
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GCACA GTCCGTCC TG CTC CG
ACACGACGAC - C GAG

AG
TC

GAM7140 TACAGGCAGGC TFCP2 NM_005653.2 5 GCTGCCTCTGGGA AG A--- A
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ATG CGTCTG GTCTCCGTCG
A- AAGG
GAM7140 TACAGGCAGGC TGFB1 NM_000660.1 3 CTGCCTCCTCCTG TA- CA-- A
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GTCTGTCCGT CTCCGTC
CAC CCTC
GAM7140 TACAGGCAGGC TGFB1 NM_000660.1 3 TCTGCCTCCTCCT TA CA-- T A
ACAGAGGCAGT GCCTGTCTGCA CAGGCAGGCA GAGGCAG
GTCTGTCCGT CTCCGTC
AC CCTC T
GAM7146 TGCTGTAGTAT APLP2 NM_001642.1 3 GACTATATAAAGT T G- A A
GTATATAGTAT ACTACTGTA TGC GTAGTAT TATATAGT
ATG CATCATG ATATATCA
T AA G
GAM7146 TGCTGTAGTAT MME NM_000902.2 3 ATACTATAACATA TGC----- - A A
GTATATAGTAT TGTACATAAATTG TGTA GTATGT TATAGTAT
C ACAT TATACA ATATCATA
CGTTAAAT G -
GAM7146 TGCTGTAGTAT MME NM_007288.1 3 ATACTATAACATA TGC - A A
GTATATAGTAT TGTACATAA TGTA GTATGT TATAGTAT
ACAT TATACA ATATCATA
AAT G -
GAM7162 CTGGGTGGCCT HD NM_002111.3 3 CATGACAACTGAA TG G C-- A
TCAGTCCATGA GGCAACCTGG C GGT GCCTTCAGT CATG
G CCA CGGAAGTCA GTAC
GT A ACA
GAM7162 CTGGGTGGCCT PLAU NM_002658.1 3 TCTGGACTGAAGC GGT C TG A
TCAGTCCATGA CTGCAG CTG GGC TTCAGTCCA
GAC CCG AAGTCAGGT
GT- - CT
GAM7162 CTGGGTGGCCT TNFRSF5 NM_001250.3 3 AGTGGGCTGCACC CCTT G A
TCAGTCCATGA CACCCAG CTGGGTGG CAGTCCAT
GACCCACC GTCGGGTG
CAC- A
GAM7162 TCAGGCTGAGG APBB2 NM_173075.1 5 ATGCAGATCTGGA TCA----- C----- B
TCATCTGCATC AACCTCAGCCAGA GGCTGAGGT ATCTGCA
GAACT CCGACTCCA TAGACGT
TCAAGAGA AAGGTC

T
A

GAM7162 TCAGGCTGAGG BACE2 NM_138991.1 3 GATGGCAGGAGAA GG AT - B
TCATCTGCATC TCAGCCTGG TCAGGCTGA TC CTGC ATC
GGTCCGACT AG GACG TAG
A- AG G
GAM7162 TCAGGCTGAGG TRPM2 NM_003307.1 3 CTGCAGATGACCT GC-- T B
TCATCTGCATC CATGAACTGG TCAG TGAGGTCATCTGCA
GGTC ACTCCAGTAGACGT
AAGT C
GAM7166 AGGGAGTTTAC CAV1 NM_001753.3 3 TTAGAAAACATAA G TTTAC- A
ATGTTTTCTAA TCTTCTGCCT AGG AG ATGTTTTCTAA
TCC TC TACAAAAGATT
G TTCTAA
GAM7166 AGGGAGTTTAC MME NM_007287.1 3 TAGAAAACAATGC A A- - A
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TTTC CAAA GTA CAAAAGAT
- AC A
GAM7169 TAGACTGAGGC ACE NM_152831.1 3 TTCTGCAGGTACT CTT-- A
TTCCTGCAGGG TCCTCAGTCTG TAGACTGAGG CCTGCAGGG
GTCTGACTCC GGACGTCTT
TTCAT
GAM7169 TAGACTGAGGC DHCR24 NM_014762.1 3 CCCACGGAAAGCC C C CA A
TTCCTGCAGGG TCATTTG TAGA TGAGGCTT CTG GGG
GTTT ACTCCGAA GGC CCC
- A A-
GAM7169 TAGACTGAGGC DHCR24 NM_014762.1 3 CCCTGCAGGCCTC T--------- C TTC A
TTCCTGCAGGG ATCTTTCCCAAAA AGA TGAGGC CTGCAGG
C TCT ACTCCG GACGTCC
CAAAACCCTT - ---

G
C

GAM7169 TAGACTGAGGC DLST NM_001933.2 3 CTCTGCAGGACAC - AGGCT A
TTCCTGCAGGG AGATCTG TAGA CTG TCCTGCAGGG
GTCT GAC AGGACGTCTC
A AC---
GAM7169 TAGACTGAGGC DSCR1 NM_004414.3 3 CCTGCAGGGGCCA CTGA T A
TTCCTGCAGGG CTCTCTA TAGA GGCT CCTGCAGG
ATCT CCGG GGACGTCC
CTCA -
GAM7169 TAGACTGAGGC DSCR1 NM_004414.3 3 GCCTGCAGGGGCC CTGA T G A
TTCCTGCAGGG ACTCTCTA TAGA GGCT CCTGCAGG
ATCT CCGG GGACGTCC
CTCA - G
GAM7169 TAGACTGAGGC TGFB1 NM_000660.1 5 CCCTGAGGAGCCT T------ A T G A
TTCCTGCAGGG CAGCTTTCCCTC AG CTGAGGCT CCT CAGGG
TC GACTCCGA GGA GTCCC
CTCCCTT - - -
GAM7199 TGGCAAAGAAG CAV2 NM_001233.2 3 ACTGTAATACTTC GCAG A
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ATTGTTTCTTC ATGTCA
ATA-
GAM7199 TGGCAAAGAAG CAV2 NM_001233.2 3 TACTGTAATACTT GCAG T A
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ATTGTTTCTTC ATGTCA
ATA- T
GAM7201 TGTCCTTTGTT ACE NM_152831.1 3 CTCCATCTTCCAC T---- -- TTT A
TTGAGATGGAG GAAATGGGCCATT GTCC TTTGT GAGATGGAG
C CGGG AAGCA TTCTACCTC
CTTAC TA CC-
GAM7201 TGTCCTTTGTT ADAM17 NM_021832.1 3 CTTCAACTAAAAA TG G A A
TTGAGATGGAG CAAAGGAGA TCCTTTGTTTT AG TGGAG
AGGAAACAAAA TC ACTTC
AG A A
GAM7201 TGTCCTTTGTT TNF NM_000594.2 5 TCCACCCTCTCTC GTTTT--- --- A
TTGAGATGGAG CCCTGGAAAGGAC TGTCCTTT GAGA TGGA
A ACAGGAAA CTCT ACCT
GGTCCCCT CCC
GAM7212 GGCCAGGACTC A2M NM_000014.3 3 AGTGCTTTGCTGG GC T -- A
TTGCAGAACTG AGTCCTGTTC G CAGGACTCT GCAGA ACT
C GTCCTGAGG CGTTT TGA
TT T CG
GAM7212 GGCCAGGACTC IL1B NM_000576.2 3 AGAGCTGTACCCA - ----- AA A
TTGCAGAACTG GAGAGTCCTGTGC GGC CAGGACTCTT GCAG CT
T TCG GTCCTGAGAG TGTC GA
T ACCCA GA
GAM7212 GGCCAGGACTC SERPINA NM_001085.2 3 CAGTCTGGAGGGT G A A
TTGCAGAACTG 3 CCTGGCC GGCCAGGACTCTT CAGA CTG
CCGGTCCTGGGAG GTCT GAC
- -
GAM7212 GGCCAGGACTC SLC6A4 NM_001045.1 3 CAGTTCTGATGAG C AC-- - A
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CCG TCC GGAGT GTCTTGAC
- GCAC A
GAM7212 GGCCAGGACTC TFCP2 NM_005653.2 3 AAGGTCTGCAAGA ---- AC A G A
TTGCAGAACTG ACCTGACTCGTC GGC CAGG TCTTGCAGA CT
CTG GTCC AGAACGTCT GA
CTCA A- G A
GAM7212 GGCCAGGACTC TFCP2 NM_005653.2 3 AGGTCTGCAAGAA ---- AC A A
TTGCAGAACTG CCTGACTCGTC GGC CAGG TCTTGCAGA CT
CTG GTCC AGAACGTCT GA
CTCA A- G
GAM7212 GGCCAGGACTC TFCP2 NM_005653.2 3 CAGTTCTGCAGCT C TC A
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GAM7241 CTCAGTGTGAA MPO NM_000250.1 3 CCTCTGGTTCTTC -- C A
GAACTACGGGT ATTTATTGAG CTCAGT GTGAAGAACTA GGG
GAGTTA TACTTCTTGGT TCC
TT C

GAM7250 GAAGAGCTGTG ADAM17 NM_003183.3 3 TATTTAGTTCTCA TGT T A
TGCTGTGATGT GCTCTTC GAAGAGCTG GCTG GATG
CTTCTCGAC TGAT TTAT
TCT -
GAM7255 TGGTCTCTTGA DSCR1 NM_004414.3 3 GGGAGCCGGTTTG GA A- A
AAGAGGCTCTT GGAGAGACCA TGGTCTCTT AAG GGCTCTT
ACCAGAGAG TTT CCGAGGG
GG GG
GAM7255 TGGTCTCTTGA IL1B NM_000576.2 3 AAGAGCCTAGTTT T C -- A
AAGAGGCTCTT TTAATAGCTA TGG CT TTGAAAG AGGCTCTT
ATC GA AATTTTT TCCGAGAA
- T GA
GAM7257 TGGGGTTTCTC IAPP NM_000415.1 3 TGACCAACGTGGT T----- T A
CATGTTGGTCA GAAACCCTGTCTC GGGGTTTC CCATGTTGGTCA
T TCCCAAAG GGTGCAACCAGT
TCTCTG T
GAM7260 ATGTCAGTGAA MME NM_007289.1 3 GCCACTAGACTCT ATGT----- G --- A
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TT GTCACTTCTC AGA CCG
TTTTCGATT - TCA
GAM7260 ATGTCAGTGAA PSEN1 NM_000021.2 3 GTCACAGGACGAT A----- AG --- A
GAGGTCTGGCA TTCACTGACACTG TGTCAGTGAAG GTCT GGC
CGA ACAGTCACTTT CAGG CTG
AGCGTC AG ACA
GAM7264 ACTGGCACAGA MAPK10 NM_138981.1 5 CTTGACAGAAATG AC------ - GACA A
CATCTGTCAAG TGGCCATTAAGAA TGGC ACA TCTGTCAAG
G ACCG TGT AGACAGTTC
GAAGAATT G AA--
GAM7264 ACTGGCACAGA MTNR1A NM_005958.2 3 CTTGACAGATGTC A-- GCA--- A
CATCTGTCAAG TGGGAAAGCAGAG CTG CAGACATCTGTCAAG
T GAC GTCTGTAGACAGTTC
TGA GAAAGG
GAM7272 CTGGGCAGTAA APP NM_000484.1 3 TCTCTATACTACA GGC T-- A
TGTAGTTGAGA TTATTAATGG CTG AGTAATGTAGT GAGA
GGT TTATTACATCA CTCT
AA- TAT
GAM7302 GAAACTAGTGT HTR2C NM_000868.1 3 CCTTTGTCAAATG C G GG A
TGGGACAAAGG GTATTTTT GAAA TA TGTT GACAAAGG
TTTT AT GTAA CTGTTTCC
T G A-
GAM7302 GAAACTAGTGT MME NM_007288.1 3 CATTGCCTAACTA - A AG A
TGGGACAAAGG CTAGTTTT GAAACTAGT GTTGGG CAA
TTTTGATCA CAATCC GTT
T - AC
GAM7320 GGTTCTCAAAT GYPA NM_002099.2 3 AGTGTCACTCATT --- - G A
GAGGGACATTT TGTAGTAAAACT GGTT CT CAAATGAG GACATT
TCAA GA GTTTACTC CTGTGA
AAT T A
GAM7320 GGTTCTCAAAT NGB NM_021257.2 3 AATGGGTCTCATT TT GA A
GAGGGACATTT TGAGTCTC GG CTCAAATGAGG CATT

CT GAGTTTACTCT GTAA
CT GG
GAM7320 GGTTCTCAAAT PLAU NM_002658.1 3 AGATGTCCCTTTC TCT AT A
GAGGGACATTT TTGGCC GGT CAA GAGGGACATTT
CCG GTT TTCCCTGTAGA
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GAM7320 GGTTCTCAAAT PSEN1 NM_000021.2 3 TGTGTCCCTCGGT ---- - AA T A
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CCA AGA GT GCTCCCTGTG
TCAA C G- T
GAM7320 ACATTTCCAAT CHAT NM_020986.1 5 GTCCGACCTCTGG AT- TGG B
GTTTGGGGACA AAATGT ACATTTCCA GTT GGAC
TGTAAAGGT CAG CCTG
CTC ---
GAM7331 ACTGCACTCCA FHL2 NM_001450.2 5 GCCCAGGCTGGAG AT A A
GCCTATGGGAT TGCAGT ACTGCACTCCAGCCT GGG
TGACGTGAGGTCGGA CCC
-- G
GAM7331 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG AT A
GCCTATGGGAT GAGTGCAGT ACTGCACTCCAGCCT GGGAT
TGACGTGAGGTCGGA CCCTG
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GAM7331 ACTGCACTCCA PRND NM_012409.1 3 GCCCAGGCTGGAG AC----- AT A A
GCCTATGGGAT TGCAACGGCAT TGCACTCCAGCCT GGG
ACGTGAGGTCGGA CCC
TACGGCA -- G
GAM7331 ACTGCACTCCA PRND NM_012409.1 3 GCCCAGGCTGGAG AT A A
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TGACGTGAGGTCGGA CCC
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GAM7345 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
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GGACGACAC GTGGACG
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GAM7345 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC GA- -- A
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TT ATG TT
GAM7345 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
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CTTT ATG TT
GAM7345 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
GGACACTTGTA TCACAACAAGA TCT TGTGATGGA TTGT
AGA ACACTACCT AACG
ACA TCAAA
GAM7345 TCTGCTGTGAT PSEN2 NM_000447.1 5 CCAAGTGTCCGGG CT GA T A
GGACACTTGTA ATTCAGA TCTG GT TGGACACTTG
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T- GG C

GAM7345 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 ACAATGTCCAAGA A-- C A
GGACACTTGTA CACAGCAGA TCTGCTGTG TGGACA TTGT
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AGA -
GAM7345 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 GACAATGTCCAAG A-- C A A
GGACACTTGTA ACACAGCAGA TCTGCTGTG TGGACA TTGT
AGACGACAC ACCTGT AACA
AGA - G
GAM7349 TGGAGTGTCTG ADAM17 NM_021832.1 3 GAGGTTGCGCCAC CT A --- A
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ACCTCACA TC CCGCG GAG
-- A TTG
GAM7349 TGGAGTGTCTG DHCR24 NM_014762.1 3 AGAGAAACCCCTC T G TG-- A
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CCTCA AGACCTCC AGAGA
C - CCAA
GAM7349 TGGAGTGTCTG DHCR24 NM_014762.1 3 AGAGAAACCCCTC T------ G TG-- A
GAGGTGTCTCT CAGAACTCCCACC GGAGT TCTGGAGG TCTCT
CTG CCTCA AGACCTCC AGAGA
GTCCCAC - CCAA
GAM7349 TGGAGTGTCTG HD NM_002111.3 3 GAACCCCCTCCAG A TGTCTC A
GAGGTGTCTCT ACACCCA TGG GTGTCTGGAGG
ACC CACAGACCTCC
- CCCAAG
GAM7349 TGGAGTGTCTG OLR1 NM_002543.1 3 GGTCCATCTCCAG - T TC A
GAGGTGTCTCT ACTCTACCA TGG AG GTCTGGAGGTG TC
ACC TC CAGACCTCTAC GG
A T CT
GAM7349 TGGAGTGTCTG PLAU NM_002658.1 3 AGAGACACTAACG GTC GA A
GAGGTGTCTCT ACTTCA TGGAGT TG GGTGTCTCT
ACTTCA GC TCACAGAGA
--- AA
GAM7349 TGGAGTGTCTG TGFB1 NM_000660.1 5 GAGACACCCCCGG T- T ----- A A
GAGGTGTCTCT TCCAAGCCTCCCC GGAG GT CTGG GGTGTCTC
CCTC CG GGCC CCACAGAG
CC - AACCT C
GAM7349 TGGAGTGTCTG TNFSF5 NM_000074.1 3 GGAGAACTATTTA C - -- A
GAGGTGTCTCT TTATACACTCCA TGGAGTGT TGG AGGTG TCTCT
ACCTCACA ATT TTTAT AGAGG
T A CA
GAM7350 CTAATTGTTCC ADAM17 NM_021832.1 3 ACTTCCTGCAGGT CT--- -- T A
TGCAGGTAGTA AAACAGTTCTTGT AATTGTT CCTGCAGG AGT
TTGACAA GGACGTCC TCA
TGTTC AT T
GAM7363 GTCAGCAAGGA HD NM_002111.3 3 TGTCCACCCTCAT CA AG -- A
GGGGTGGACAA TTCTGCCAGC GT GCA GA GGGGTGGACA
CG CGT TT TCCCACCTGT
AC CT AC
GAM7366 TATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
AGCCTGGGCAA GAGGGCAATG TATTGC CTCC AGCCTGGGCAA

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GAM7366 TATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
AGCCTGGGCAA GTGCAGTG TATTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
C
GAM7366 TATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
AGCCTGGGCAA AGTGCAGTG TATTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
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GAM7366 TATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TAT CTC ----- A
AGCCTGGGCAA ACTGCTTTGCACC TGCA CAG CCTGGGCAA
G ACGT GTC GGACCCGTT
GCC TTC ACTCT
GAM7366 TATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GTGACGTGAGGTCGGACCC
CC
GAM7366 TATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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CCT
GAM7366 TATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG TA A
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GAM7366 TATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG TA----- A
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GTACGGC
GAM7366 TATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
AGCCTGGGCAA AGTGCAGTG TATTGCACTCCAGCCTGGGCAA
GTGACGTGAGGTCGGACCCGTT

GAM7369 TCTTGGTGCTT APBB2 NM_173075.1 5 TCATCCAGCCCAG GCTTTT A
TTGCTGGATGA AAACCAAGA TCTTGGT GCTGGATGA
AGAACCA CGACCTACT
AAGACC
GAM7369 TCTTGGTGCTT APOC1 NM_001645.2 5 CCTCCAGCAAGGA TGC TG A
TTGCTGGATGA TTCAGGA TCTTGG TTTTGCTGGA
AGGACT GGAACGACCT
TA- CC
GAM7369 TCTTGGTGCTT CHAT NM_020986.1 5 CATCCCTGCACCA ---- TT T- A
TTGCTGGATGA GGACTCACCAAGA TCTTGGTG CT TGC GGATG
AGAACCAC GA ACG CCTAC
TCAG CC TC
GAM7369 TCTTGGTGCTT CLU NM_001831.1 3 ACCGCAAAAAGCA - T ATG A
TTGCTGGATGA CCGGGA TCTTGGTGCTTTT GC GG
AGGGCCACGAAAA CG CC
A - A--

GAM7371 AGAAGGTTGGG A2M NM_000014.3 5 CTCCTCCAGCTCC TT TC A
GCTGGAGGTCT TTCTTTCT AGAAGG GGGGCTGGAGG
TCTTTC CCTCGACCTCC
TT TC
GAM7371 AGAAGGTTGGG BACE NM_138971.1 3 AACCAACTGCCTT TGGA C A
GCTGGAGGTCT AACCTTCT AGAAGGTTGGGGC GGT
TCTTCCAATTCCG CCA
TCAA A
GAM7371 AGAAGGTTGGG SLC17A7 NM_020309.1 3 GGACCTCCATTCC A GT C A
GCTGGAGGTCT ACTCATCT AGA G TGGGG TGGAGGTCT
TCT C ACCTT ACCTCCAGG
A TC -
GAM7371 AGAAGGTTGGG SLC6A4 NM_001045.1 3 AGGCCTCCAGCCA A----- GTT - A
GCTGGAGGTCT CTTATTTCCATGG GAAG GG GGCTGGAGGTCT
A CTTT TC CCGACCTCCGGA
AGGTAC AT- A
GAM7374 GCAGCTGTTTA IL1B NM_000576.2 3 TGGTTCTAAGAAA CT- A T A
TTTAGAACCTG CCCTCTGT GCAG GTTT TTTAGAACC
TGTC CAAA GAATCTTGG
TCC - T
GAM7374 GCAGCTGTTTA MME NM_007287.1 3 CAGCTCTAATAAA AT AC A
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TGTCGACAAA AATCT GAC
AT C-
GAM7374 GCAGCTGTTTA TNFSF5 NM_000074.1 3 CAGGTTGAATTCT GCA----- ----- A
TTTAGAACCTG GAGTAAACAGCAG GCTGTTTATTTAGA ACC
ATAACT CGACAAATGAGTCT TGG
TCAATAGA TAAGT

TG
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GAM7374 CAGATCTGGGA ACT NM_020482.3 3 CCACAGCTTGCTA T GATAC B
TACAGCTGTGG GTTCTG CAGA CTGG AGCTGTGG
GTCT GATC TCGACACC
T GT---
GAM7374 CAGATCTGGGA APBB2 NM_173075.1 3 CTACAGCTGTTTG - GGGAT B
TACAGCTGTGG TGGGATGTTG CAG ATCT ACAGCTGTGG
GTT TAGG TGTCGACATC
G GTGTT
GAM7400 TTAATGCTTTT TNFRSF6 NM_152873.1 3 GCGTATGACACAT CTTTT TC A
TGTCATACTCA TGA TTAATG TGTCATAC
AGTTAC ACAGTATG
----- CG
GAM7415 TACAGGCAGGC ADAMTS5 NM_007038.1 3 AAACCTTTGACTG GCA CAG A
ACAGAGGCAGT CCTGTA TACAGGCAG CAGAGG
ATGTCCGTC GTTTCC
A-- AAA
GAM7415 TACAGGCAGGC APBA2 NM_005503.2 3 GCTGCCTCTGCCA TA G GCA A
ACAGAGGCAGT CTGACTGCA CAG CAG CAGAGGCAGT

GTC GTC GTCTCCGTCG
AC A ACC
GAM7415 TACAGGCAGGC DLST NM_001933.2 3 CAGCCTCTGTCCT G C AG A
ACAGAGGCAGT GGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - AC
GAM7415 TACAGGCAGGC DLST NM_001933.2 3 GCAGCCTCTGTCC G C AGT A
ACAGAGGCAGT TGGCTGTG TACAG CAGG ACAGAGGC
GTGTC GTCC TGTCTCCG
G - ACG
GAM7415 TACAGGCAGGC NGB NM_021257.2 3 TTGCTCTGTGCTG GCA G A
ACAGAGGCAGT ACTGTG TACAG GGCACAGAG CAG
GTGTC TCGTGTCTC GTT
AG- -
GAM7415 TACAGGCAGGC NGB NM_021257.2 3 TTTGCTCTGTGCT GCA G T A
ACAGAGGCAGT GACTGTG TACAG GGCACAGAG CAG
GTGTC TCGTGTCTC GTT
AG- - T
GAM7415 TACAGGCAGGC SNCG NM_003087.1 5 CTGCGAGCTCCGT TA-------- C A --- A
ACAGAGGCAGT CCTGCCTGCAGCA CAGGCAGG AC GAG GC
GCACA GTCCGTCC TG CTC CG
ACACGACGAC - C GAG

AG
TC

GAM7415 TACAGGCAGGC TFCP2 NM_005653.2 5 GCTGCCTCTGGGA AG A--- A
ACAGAGGCAGT AGTCTGCAGTA TAC GCAGGC CAGAGGCAGT
ATG CGTCTG GTCTCCGTCG
A- AAGG
GAM7415 TACAGGCAGGC TGFB1 NM_000660.1 3 CTGCCTCCTCCTG TA- CA-- A
ACAGAGGCAGT CCTGTCTGCAC CAGGCAGGCA GAGGCAG
GTCTGTCCGT CTCCGTC
CAC CCTC
GAM7415 TACAGGCAGGC TGFB1 NM_000660.1 3 TCTGCCTCCTCCT TA CA-- T A
ACAGAGGCAGT GCCTGTCTGCA CAGGCAGGCA GAGGCAG
GTCTGTCCGT CTCCGTC
AC CCTC T
GAM7440 TGTGACTGAGG IAPP NM_000415.1 3 CTTTCAGCAAACC GC AT A
TGCGCATAAAG TCAGTCATA TGTGACTGAGGT GC AAAG
ATACTGACTCCA CG TTTC
AA AC
GAM7446 TCACTGCAACC ACE NM_152831.1 3 CTGGGAGCCGGAG A - G TG A
TCTGCTGCCTG GCTGCAGTGA TCACTGCA CCTCTG CT CC
AGTGACGT GGAGGC GA GG
C C G TC
GAM7446 TCACTGCAACC ACE NM_152831.1 3 TGGGAGCCGGAGG A - G T A
TCTGCTGCCTG CTGCAGTGA TCACTGCA CCTCTG CT CC
AGTGACGT GGAGGC GA GG
C C G T

GAM7446 TCACTGCAACC APBA1 NM_001163.2 5 AGGCAGCAGCGGC A G A T A
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A TC A A
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CAAA A T
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A A---
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CT T GT-----
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GAM7446 TCACTGCAACC MTNR1A NM_005958.2 3 CAGAGGCAGAGGT TG GC A
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GATCT T TA
GAM7446 TCACTGCAACC OGDH NM_002541.1 3 TGGCTGGCAGAGG GC--- - T A
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GGTGG TTGGAGACGG CGG
GATCT T T
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TCAT GAA AATTTCTTTG
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CCTCC T -
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AGG TC T
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G G TT
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TG A- C
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A GAGAA
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TTTCTGTCCTCTA CG CTCGA
T - T
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AC GTCCGTCCTGTCTT CG
CC C
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-- GA TTC
GAM7520 TGCCTAGGCAG SLC17A7 NM_020309.1 3 TGCTCCTCTCTGT T---- - AT--- A
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GAATC C CTCCT
GAM7520 TGCCTAGGCAG SNCG NM_003087.1 5 TGCGAGCTCCGTC C- A-- A
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G GT GTCG GT AT CCAAACTT
G - CCAGTC CC
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-- C
GAM7530 TAGCAGCACAT ADAM10 NM_001110.1 5 TCCGGATCGATGT AA AA A
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GTCGTCGTGTA GCTAGGC
-- CT

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GAM7530 TAGCAGCACAT SLC6A4 NM_001045.1 3 TAGAACCTTCTAA AAT------ GAA A
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G TC C
GAM7546 TGATGCTTGAG PSEN1 NM_007318.1 3 GAGGTACTGTGAG A- GAG-- A
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CTC-
GAM7553 TAGGTAGTTTC IL1A NM_000575.3 3 CCCATAGCCAGGA TA T - T A
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TC TCAAAGGAC GATA CCC
CG - C -
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---- GGT
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-- T- GT
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CTGG T T
GAM7559 TCTGCCTCCCT APP NM_000484.1 3 TGGGTGGGGAGAA CCTG T A
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GAM7559 TCTGCCTCCCT LRP1 NM_002332.1 3 GGGAGACAGGCAG TCTG CA A
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TCTG TGT
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CCC C GC
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CCC C G
GAM7592 TAGGTTGTGCG OLR1 NM_002543.1 3 CTGTAAGCTAATC CGCTC- A A
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CTAATC C
GAM7601 TTAAAGTCACC NOTCH1 NM_017617.2 3 AGTTTACAGAAAA ACCA GG A
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T CT GT GTG
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CAAACCGT ACT GTA GTG
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CAAAC ACT AGTATATGT
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GAM7663 TGTGCTGGTTG ABCD1 NM_000033.2 3 CCCTCGGGCCGGG TGT T----- --- A
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TGACC ACGGG GGCTCCC
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C C AAGAGTC
GAM7663 TGTGCTGGTTG CLU NM_001831.1 3 CCTTACGGGGGCA TGT T------- - A
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T-- TGAGTTCT A
GAM7663 TGTGCTGGTTG NPY NM_000905.2 5 CCCCTCGGAGACG TG ---- T- CC-- A
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-- CAGC CT CAGA

GAM7700 TAGAGTTATAT IAPP NM_000415.1 3 TAAGGACAATGTA GA G AG A
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C CC
GAM7729 ACAGGAGCATG CLU NM_001831.1 3 AGCCTCTCCCCGC ACA----- AT B
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GAM7729 ACAGGAGCATG NCSTN NM_015331.1 3 AGCTTCTTGCTCC TGG B
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GAM7776 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GAM7776 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
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GAM7776 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GAM7776 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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CCT
GAM7776 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
AGCCTGGGCAA GCGATG CATTGC CCTGGGCA
GTAGCG GGACCCGT
GCGA--- G
GAM7776 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
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GAM7776 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- A
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G AACGTGAGGTCGGACCCGTT
GTACGGC
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GAM7777 GCCCTGTTGAC FLNB NM_001457.1 3 AGAAATTCTGCAG - TTGAC GT A
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CGG GAC GTCTTAAA
T ----- GA
GAM7784 CTGTGAGCTAT BACE2 NM_138992.1 3 AACCAAAACAGAG C G A------- A
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A ACG TCGG AGACAAAACCAA
- - GTTAGGTG
GAM7784 CTGTGAGCTAT CNTF NM_000614.2 3 GAGAAAACAGGCT ATT GGT A
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GACACTCGG ACAAAA
--- GAG
GAM7784 CTGTGAGCTAT HTR2C NM_000868.1 3 AGTTGAATGATAA TGT- GG A
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GACACTCGATAA AAG GA
TAGT TT

GAM7784 CTGTGAGCTAT PRNP NM_000311.1 3 GGCTAAAACAAAT --- CT A
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GACA CTC TAAACAAAATCGG
AGA --
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TTAAATTG TTTGTCG GTC
AT AC T
GAM7817 TCACCCAGGCT ACE NM_152831.1 3 CATTGCACTCCAG A G A
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AG GGGTC GACCTCACGTTAC
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GGTG GTCCGACCTC CG AC
TTT C AA
GAM7817 TCACCCAGGCT IAPP NM_000415.1 3 CACTGCACTCCAG A
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GAM7817 TCACCCAGGCT NOTCH1 NM_017617.2 3 ACTGTGGCACTTG TC----- TG --- A
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C TGGGTCCG TTCACG TCA
CACACAC -- GTG
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GCAC TTTCACATT TATTCGTATA
CACGTA CACA G
GAM7837 AGAAGTGTAAA FLNB NM_001457.1 3 CATGCTCTGTGGC ------- - TA A
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T TCTTCACATT TGT TCGTAC
CTTCCGG C --
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AC CGTTCAC CTTTTACG
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GAM7845 TGAGGGCAGGT APBB2 NM_173075.1 3 AGCATTTTCCTGC T - TGTG A
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C T ----
GAM7845 TGAGGGCAGGT APBB2 NM_173075.1 3 AGCATTTTCCTGC T-------- - TGTG A
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G TTCC CGTCC TTTTACG
GATGTATGC T ----

T

A

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ACTTC TGTT CA ACTTTTAC
A T G T
GAM7845 TGAGGGCAGGT MAPK10 NM_138981.1 5 AGCATTTTCTTTA -- A T- A
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TA A TT
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C GTC--
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TGTG TCGAGAGA CTTCTG
AT T- C
GAM7854 ATACAGCTCTC IGF1 NM_000618.2 3 GAGTCCAGAGAGG A--- C-- GG A
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GTGTC GGAGAGA CCTGAG
TAAG AAA --
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GACA GGTCGGTCC CAT
GT AGT
GAM7854 CTGTGCCCAGC BACE2 NM_138992.1 5 ACCGGCTAGGCTG CT----- AG T B
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CGCGGGTCGG TCGGC CA
CCCCCCG A- -
GAM7854 CTGTGCCCAGC HD NM_002111.3 3 GCCAGCCCTCCCT GCC ---- T B
CAGGGCTGTGT GGCTGTGAGCAG CTGT CAGCCA GGGCTG GT
GACG GTCGGT CCCGAC CG
AGT CCCT -
GAM7854 CTGTGCCCAGC MPO NM_000250.1 3 GCCCAGCCCTGTT TG C- T B
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GAC GGGTC GTCCCGAC CG
GT TT C
GAM7854 CTGTGCCCAGC MTNR1A NM_005958.2 3 CATAGGCCGGGCA AGCCA G B
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GACACGGG CC GATAC
----- G
GAM7854 CTGTGCCCAGC NOTCH1 NM_017617.2 3 CGCAGCCCTGGCA C----- G A B
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ACG GGG CGGTCCCGACGC
TGGCGT G A

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G ACACGGGTC TTCCGACA
GGAGGT ACA A
GAM7854 CTGTGCCCAGC TNFRSF6 NM_152877.1 5 GCCAGCCCTGGCT G ---- T B
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GA GCGG GTCGGTCCCGAC CG
G ACCC -
GAM7865 TGGAGAGATAA BACE NM_012104.2 3 GATGGGAAGGGCT AG AAG-- A
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ACC TCTATTCGG GTAG
GA GAAGG
GAM7865 TGGAGAGATAA CTSK NM_000396.2 3 CCTACTTTGCTTC TA C TC A
GCCAAGTATCC TCTCCA TGGAGAGA AGC AAGTA
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-- T CC
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CCTTC A C-
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AGACGTGACAT TGG G CCG
-- T T A
GAM7884 TTTGCACTGTA CTSB NM_147783.1 3 GCCTGTGGTTACA AT T - A
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AGACGTGACAT TGG G CCG
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AGAA TC AACTCTTC CCG
A - GTTCC
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AAATATT TC TTATGACC
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T --- G
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CATCTTT - C-
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GAATA GTCGTTTTATGA
AG AG
GAM7898 TTTGTAATAGC GLUL NM_002065.3 3 ATAGTATTTTTAT T GC G A
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- AT A
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AGGG T
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CAGC CC
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A TT A
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C TG CA AGGT GTCTGAGTCA
CGAAAGG T C -
GAM7915 AATGTGTGGGA ADAMTS5 NM_007038.1 3 AAGACTGTTTCCA AAT------- GA B
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G GT GTCG GT AT CCAAACTT
G - CCAGTC CC
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-- C
GAM7933 TAGCAGCACAT ADAM10 NM_001110.1 5 TCCGGATCGATGT AA AA A
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T----- GGT
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GAM7933 TAGCAGCACAT SLC6A4 NM_001045.1 3 TAGAACCTTCTAA AAT------ GAA A
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G GTCGTCGTGTA CCAAG
CCTAATCTT AT-
GAM7954 TTCACCCATCT DHCR24 NM_014762.1 3 AGGGGTGGAGATG TT----- TT AC A
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TGACGGT -- GA
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TC A- A
GAM7954 TTCACCCATCT PSEN1 NM_007318.1 5 GTGGAGGCTGGGA T- AC A
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TC A-
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T T TGC
GAM7954 TTCACCCATCT UBB NM_018955.2 5 TGTGGGTGGACGT T---- C TT- A
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C AGTGG TGG AGGTGGGTGT
CGGTT T TGC
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T TC C
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TT CAA
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TGT C GC
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C GGGTC GACCTCACGTTAC
CGACACAGA -
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GT A
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A- ACC
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GACGGGTCCGAC TTC CG
TAC C ACC
GAM8013 TTGCCCAGGCT HTR2A NM_000621.1 3 CACTGCCATTTCC CT - A
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TC C
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GT ACG GAGACGGT GACT
T ATT C
GAM8013 CACTGCAACCT OGDH NM_002541.1 3 CCATGGCTGGCAG GC--- - - B
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G GTGG TTGGAGACGGT GG ACC
GATCT C T
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TGGGGAGG G --
GAM8026 AACGATGGGCT MAPK10 NM_138980.1 5 GAAATCACCTGTC T ATT B
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CTTC- A
GAM8047 ATCACAGAGGC ADAM17 NM_021832.1 3 CAGCACTTGGAGA A AGG - A
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A GGA G
GAM8047 ATCACAGAGGC GFAP NM_002055.2 3 TCAGCACTTGGGG C GG- A
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TG TGTCT GGGTTCACGACT
T AGG
GAM8047 ATCACAGAGGC MME NM_007288.1 3 TCAGTTATTCATT GCTTAAGT A
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CG GAG GGGT
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TA TGTAGG A
GAM8047 ATCACAGAGGC PSEN1 NM_007318.1 3 GCACTGACACTCA - CTTA------- TGA A
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G ATTACTCACAG ---
GAM8047 ATCACAGAGGC RAGE NM_014226.1 3 CGAGCAGGCATTT -- TAAG GA A
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GA GTCTGGA CCCCAGGT
G - TC
GAM8109 TCCAGTACAGG ADAMTS5 NM_007038.1 3 GAAATGAGGCCTG TCCA------- CT A
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AATAGTCGGAA --
GAM8109 TCCAGTACAGG TFCP2 NM_005653.2 5 GAGAGCGAGACCT AGTA TCA A
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GAGG CG-
GAM8109 TCCAGTACAGG TNFRSF5 NM_152854.1 3 GAGACAGGAGACC A- CA A
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GAM8145 ACATGATCTCC BLMH NM_000386.1 3 TCCTAGAGTAGAG A GA ---- - A
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G GTG AGGG GAG TGAGATCCT
G GG AGGT A
GAM8145 ACATGATCTCC GSK3B NM_002093.2 5 AAGAGAGTGATCA TCTCC AGG A
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TGTACT AGTGAGA
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GAM8145 ACATGATCTCC MAPT NM_173727.1 3 TCTTGGGGCCAGC A C--- CA A
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GAM8145 ACATGATCTCC PSEN2 NM_012486.1 5 TCCAGCAGTGAGG ACA A - A A
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CCG - C -
GAM8164 GCTTCTCCTGT ABCD1 NM_000033.2 5 CAGGGCACTGACA T CCT----- A A
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CGA GAGGACAGG GGGA
- ACAGTCAC C
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- ACAGTCAC CC
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CGGAGA GGGGAGGGA
TCT-- C
GAM8164 GCTTCTCCTGT AVP NM_000490.2 5 TGGGGAGGGGGTG TT C TG A
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CG GG G GGGGGAGGGGT
CC C GT
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C T- C C
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TC T A G

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C AAA CC
GAM8164 GCTTCTCCTGT LRP1 NM_002332.1 5 CGGGGAGGGGGAA T CTG A A
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CGA GAG GGGGGAGGGG
C AAA C
GAM8164 GCTTCTCCTGT NCKAP1 NM_013436.2 5 GCGGGAGGGGAGG CCTG TA A
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CGG AGGGG C GGGGAGGGGTG
CC T -
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CGG GAC GGGGAGGGGT
TCTC T
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CCCCTCCCTAC GGACGAGGAGAAG GCTTCTCCT GTCC CC TCCCT
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G C TAGA G
GAM8206 TTGCACTCCAG APPBP2 NM_006380.2 3 TGTTGCCCAGGCT A - A
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G G
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AGC GGTCGGACC GTTGT
TCT- G
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TGG GTGAGGTGGGGC TTGC
A G C
GAM8285 AGTAGACAGTG IGF1 NM_000618.2 3 GACTCTGAAACCT ---- CAA T A
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TCATCTGTCG CC GT TCAG
AACT AAA C
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CATGGGTG GAGACATTG
T TGA
GAM8311 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - TG A
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A G G GT
GAM8311 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - G A
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GTGACGTG GGTCGG C CG
T GT G A
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GACGT GGTCGGAC CGC
GCTCTCG CG G
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G CT G
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G CT GT
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ACTT CGGAACAA AACA GTG
A ATC -
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CT TGT G
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ACTTAT--
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G GAG GGGT
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                                   G ATTACTCACAG   ---
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                                    TA ----  GC
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                                    --- TG  A
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                                  GAG     -  G
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                                   C-       TGA
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                                  GAG--         C
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                                  C     AA      A
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                                GGGGACCTCAA CCCCGA CC
                                C        -    C
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                         T          GGGGACCTCAA CCCCGA CC
                                TATCCAC       -    C
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                         C          GGAAACCTC  CCCCGAACT
                                CATCCCCTC       ---
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                                GGGTCTCACCA  CT GT CC
                                   CTC  -  C
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                                AGGTTTTACC   AATTCTAG
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ATGTAGGAC
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- T AGT
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TACA G G
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TCCG GTCCCTCT CCG
AGGA- TC
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GG TCCTCCACTTC CAG GTCG
T TTA A
GAM8447 CCCAGGAGGTG IGF1 NM_000618.2 3 ACTGCAACCTCCA A A
GAGGTTACAGT CCTCCTGGG CCCAGGAGGTGGAGGTT CAGT
GGGTCCTCCACCTCCAA GTCA
C
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A TCTCT CAAT
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GG CTTCCACCTCCAA TCA
AC CA
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G ACATTAGGGTCGATGAGCCT
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GAM8447 CGTGTAATCCC FHL2 NM_001450.2 5 CCCAAGTAGCTGG G A B
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GAM8447  CGTGTAATCCC IGF1  NM_000618.2  3  CCCAAATTGCTGG  G        TAC          B
      AGCTACTTGGG              GATTACAGG    C TGTAATCCCAGC   TTGGG
                                  G ACATTAGGGTCG   AACCC
                                   G         TTA
GAM8447  CGTGTAATCCC IGF1  NM_000618.2  3  CCTGAGTAGCTGG  G           TG        B
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                                  G ACATTAGGGTCGATGA  CC
                                   G           GT
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                                   G        -   A
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                                   G       G
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                                   G
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                                  GTACA  AGGGTCGA   ACTC
                                     --       CGC
GAM8452  CCTCCTTTCAT FLNB  NM_001457.1  3  GCCCGGACCTGAT  ----      --  AA   A     A
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                          GG         GG    AGGAAAGT  AGT  AGGC CG
                                   CACC       GT   CC    C
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                                  GGGG    AAGTAGTT    CTCG
                                    TACT       GAA-
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                                    AG        AA     C
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                                  TTG  CGGTAGGAT  AAATGT
                                    AG        AA
GAM8473  GACCAGCCATC DSCR1  NM_004414.3  3  TGTGGAGGTGGCT          CTGG           A
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CT TC TAGGACCAGATG
AA TT G
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---- GT
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T AG TC
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- A TGG
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ACAG T
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TTT AAC-
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GA GGTTC
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-- - C
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A- G C
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TC T CTCA
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- - G A
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A CC- G
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G G TGC

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T G GAAG
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AAA C-
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G AC CCC
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TC A C
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TGCAGTGAGCT CTCTTGCCT AGGCAAGAGG GCAG TGAGCT
TCCGTTCTCT CGTC ACTTGA
T- G
GAM8665 AGGCAAGAGGT APPBP2 NM_006380.2 3 GGCTCACTGCAAC AA A
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TCCG CTCCAACGTCACTCGG
C-
GAM8665 AGGCAAGAGGT APPBP2 NM_006380.2 3 GTGTACTTCACCT G T C A A
TGCAGTGAGCT CTTGGCT AG CAAGAGGT G AGTG GC
TC GTTCTCCA C TCAT TG
G - T G
GAM8665 AGGCAAGAGGT CTSB NM_147783.1 3 AGTTTGCAATGTC - - --- -- TG A
TGCAGTGAGCT ACAACCTCTCTGA AGG CA AGAGGTTG CA G AGCT
TCT TCT GT TCTCCAAC GT C TTGA
A C ACT AA GT
GAM8665 AGGCAAGAGGT DHCR24 NM_014762.1 3 GCTCCAGTAAAAT GG AGT A
TGCAGTGAGCT CTTGCCT AGGCAAGA TTGC GAGC
TCCGTTCT AATG CTCG
AA AC-
GAM8665 AGGCAAGAGGT DHCR24 NM_014762.1 3 TGCTCCAGTAAAA GG AGT T A
TGCAGTGAGCT TCTTGCCT AGGCAAGA TTGC GAGC
TCCGTTCT AATG CTCG
AA AC- T

GAM8665 AGGCAAGAGGT FHL2 NM_001450.2 3 TCTCACCCAGGCA GG A--- C A
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TCCGTTCT AACG CACTC
-- GACC T
GAM8665 AGGCAAGAGGT FHL2 NM_001450.2 5 AGCTCACTGCAAG AGG ------ A
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T GTTCTCCA ACGTCACTCGA
TG- TCTCGA
GAM8665 AGGCAAGAGGT FHL2 NM_001450.2 5 GCTCACTGCAAGC AGG ------ T A
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T GTTCTCCA ACGTCACTCG
TTG TCTCGA -
GAM8665 AGGCAAGAGGT FHL2 NM_001450.2 5 GCTCACTGCAAGC AGG----- ------ A
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GC
CG

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TTC TTCCAACGT TTCGA
ATG --
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TCC CTCCAACGTCACTCGG
AC-
GAM8665 AGGCAAGAGGT PRND NM_012409.1 3 GGCTCACTGCAGC A A
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GAM8678 GTGTTCCAGGA CHAT NM_020984.1 5 CAAGACGCCCATC GTG----- AGT- A
AGTCGTCTTGA CTGGAAAAGGTCC TTCCAGGA CGTCTTG
C AAGGTCCT GCAGAAC
CCCTGGAA ACCC
GAM8678 GTGTTCCAGGA DHCR24 NM_014762.1 3 CAAGACCTCCCTG GT----- A TC A
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CAAGGTCC TC CAGAAC
GTCTTCC C --
GAM8678 GTGTTCCAGGA DSCR1 NM_004414.3 3 GCGGAACTCTTCC TCG TG A
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CGTAAGGTCCTTC AGG
TCA CG
GAM8678 GTGTTCCAGGA DSCR1 NM_004414.3 3 TGCGGAACTCTTC TCG TGA A
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CGTAAGGTCCTTC AGG
TCA CGT
GAM8678 GTGTTCCAGGA MAPK10 NM_138980.1 3 GGAGATGATGTGA GGAA G A
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CACAAGGT TAGTAGAG
AGTG G
GAM8678 GTGTTCCAGGA MAPK10 NM_138982.1 3 AGGAGATGATGTG GGAA GA A
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CACAAGGT TAGTAGAG
AGTG GA
GAM8678 GTGTTCCAGGA TNFRSF5 NM_152854.1 3 CCCGACGATCTTC ---- - TTG A
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CACAA GGTCCTTC AGCAG
CCTC T CCC
GAM8678 GTGTTCCAGGA TNFRSF5 NM_152854.1 3 TCCCGACGATCTT ---- - TTGA A
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C CACAA GGTCCTTC AGCAG
CCTC T CCCT
GAM8693 CAGTGGGAAAA CAV1 NM_001753.3 3 TTCAGCAAACTCT -- CTCA A
GTTTGTCTCAT TTTCCCACTG CAGTGGGAAA AGTTTGT
GTCACCCTTT TCAAACG
TC ACTT
GAM8693 CAGTGGGAAAA CAV1 NM_001753.3 3 TTTCAGCAAACTC -- CTCAT A
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GTCACCCTTT TCAAACG
TC ACTTT
GAM8693 CAGTGGGAAAA GYPA NM_002099.2 3 TGAAGCTTCGATT AGTTT TC A
GTTTGTCTCAT TCCCACTG CAGTGGGAAA G TCA
GTCACCCTTT C AGT
AGCTT GA
GAM8693 CAGTGGGAAAA HD NM_002111.3 3 ATGAGGCTTTTCC CA----- TTGT A
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CACCCTTTTCG GAGTA
CCTCGAC ----
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C AAGGTCCT GCAGAAC
CCCTGGAA ACCC
GAM336121 GTGTTCCAGGA DHCR24 NM_014762.1 3 CAAGACCTCCCTG GT----- A TC A
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CAAGGTCC TC CAGAAC
GTCTTCC C --
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CGTAAGGTCCTTC AGG
TCA CG
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CACAAGGT TAGTAGAG
AGTG G
GAM336121 GTGTTCCAGGA MAPK10 NM_138982.1 3 AGGAGATGATGTG GGAA GA A
AGTCGTCTTGA ATGGAACAC GTGTTCCA GTCGTCTT
CACAAGGT TAGTAGAG
AGTG GA
GAM336121 GTGTTCCAGGA TNFRSF5 NM_152854.1 3 CCCGACGATCTTC ---- - TTG A
AGTCGTCTTGA CTGGCTCCAACAC GTGTT CCAGGAAG TCGTC
CACAA GGTCCTTC AGCAG
CCTC T CCC
GAM336121 GTGTTCCAGGA TNFRSF5 NM_152854.1 3 TCCCGACGATCTT ---- - TTGA A
AGTCGTCTTGA CCTGGCTCCAACA GTGTT CCAGGAAG TCGTC
C CACAA GGTCCTTC AGCAG
CCTC T CCCT
GAM336122 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - A
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GT ACG GAGG TCGGACCCGTT
A G G
GAM336122 CACTGCACTCC BACE2 NM_138991.1 3 TTGCCCAGGGTCC CACT TCCAG A
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CGTG GGACCCGTT
GGTC TCCTG
GAM336122 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

-
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AGCCTGGGCAA GTGTGCAGTG CACTGCAC CCAGCC G GC
GTGACGTG GGTCGG C CG
T GT G AC
GAM336122 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - A A
AGCCTGGGCAA TGTGCAGTG CACTGCAC CCAGCC G GC
GTGACGTG GGTCGG C CG
T GT G A
GAM336122 CACTGCACTCC CTSK NM_000396.2 3 CTTCCACGATGGT CT GCC CA A
AGCCTGGGCAA GCAGTG CACTGCA CCA TGGG
GTGACGT GGT ACCT
-- AGC TC
GAM336122 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
AGCCTGGGCAA GTGCAGTG CACTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
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GAM336122 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336122 CACTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC CT CTCCA A
AGCCTGGGCAA ACTGCTTTG CA GCA GCCTGGGCAA
GT CGT TGGACCCGTT
TT CACTC
GAM336122 CACTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
AGCCTGGGCAA GTGCAGTG CACTGCACTCCAGCCTGGG
GTGACGTGAGGTCGGACCC
CC
GAM336122 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTGACGTGAGGTCGGACCC
CCT
GAM336122 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
AGCCTGGGCAA GCAGTG CACTGCAC AG GGGCAA
GTGACGTG TC TCTGTT
T-- AC-
GAM336122 CACTGCACTCC NGB NM_021257.2 3 TGCTTCTTCAGGT CA----- CA ---- A
AGCCTGGGCAA GAGTGCAGGCCAA CTGCACTC GCCTG GGCA
GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM336122 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
AGCCTGGGCAA AGTGCAACG TGCACTCCAGCCTGGGCAA
ACGTGAGGTCGGACCCGTT
GCA
GAM336122 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC----- A
AGCCTGGGCAA AGTGCAACGGCAT TGCACTCCAGCCTGGGCAA
G ACGTGAGGTCGGACCCGTT
GTACGGCA
GAM336122 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
AGCCTGGGCAA AGTGCAGTG CACTGCACTCCAGCCTGGGCAA
GTGACGTGAGGTCGGACCCGTT

GAM336123 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - A
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GT ACG GAGG TCGGACCCGTT
A G G
GAM336123 CACTGCACTCC BACE2 NM_138991.1 3 TTGCCCAGGGTCC CACT TCCAG A
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CGTG GGACCCGTT
GGTC TCCTG
GAM336123 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
AGCCTGGGCAA GCTGGAGCAGCAG CA CTGC CTCCAGCCT GGGC
CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

-

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GTGACGTG GGTCGG C CG
T GT G AC
GAM336123 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - A A
AGCCTGGGCAA TGTGCAGTG CACTGCAC CCAGCC G GC
GTGACGTG GGTCGG C CG
T GT G A
GAM336123 CACTGCACTCC CTSK NM_000396.2 3 CTTCCACGATGGT CT GCC CA A
AGCCTGGGCAA GCAGTG CACTGCA CCA TGGG
GTGACGT GGT ACCT
-- AGC TC
GAM336123 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
C
GAM336123 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
AGCCTGGGCAA AGTGCAGTG CACTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
CT
GAM336123 CACTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC CT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
GAM336123 CACTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336123 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTGACGTGAGGTCGGACCC
CCT
GAM336123 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
AGCCTGGGCAA GCAGTG CACTGCAC AG GGGCAA
GTGACGTG TC TCTGTT
T-- AC-
GAM336123 CACTGCACTCC NGB NM_021257.2 3 TGCTTCTTCAGGT CA----- CA ---- A
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GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM336123 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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ACGTGAGGTCGGACCCGTT
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GAM336123 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC----- A
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GAM336123 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
AGCCTGGGCAA AGTGCAGTG CACTGCACTCCAGCCTGGGCAA

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GAM336124 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - A
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GT ACG GAGG TCGGACCCGTT
A G G
GAM336124 CACTGCACTCC BACE2 NM_138991.1 3 TTGCCCAGGGTCC CACT TCCAG A
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CGTG GGACCCGTT
GGTC TCCTG
GAM336124 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

-
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GTGACGTG GGTCGG C CG
T GT G AC
GAM336124 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - A A
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GTGACGTG GGTCGG C CG
T GT G A
GAM336124 CACTGCACTCC CTSK NM_000396.2 3 CTTCCACGATGGT CT GCC CA A
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GTGACGT GGT ACCT
-- AGC TC
GAM336124 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
C
GAM336124 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
AGCCTGGGCAA AGTGCAGTG CACTGCACTCCAGCCTGGGC
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CT
GAM336124 CACTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC CT CTCCA A
AGCCTGGGCAA ACTGCTTTG CA GCA GCCTGGGCAA
GT CGT TGGACCCGTT
TT CACTC
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GAM336124 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM336124 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
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GTGACGTG TC TCTGTT
T-- AC-
GAM336124 CACTGCACTCC NGB NM_021257.2 3 TGCTTCTTCAGGT CA----- CA ---- A
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GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM336124 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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GAM336124 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336125 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
GAM336125 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
GAM336125 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM336125 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336125 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336125 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GAM336125 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC

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CA
GAM336125 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM336125 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336126 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GAM336126 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
AGCCTGGGCAA TGTGCCTGGATG CATT GCAC CCTGGGCAA
GTAG CGTG GGACCCGTT
GTC TCCTG
GAM336126 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
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GAM336126 CATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336126 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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TT CACTC
GAM336126 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336126 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM336126 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GCGA--- G
GAM336126 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
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GTACGGC

GAM336126 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
AGCCTGGGCAA AGTGCAGTG CATTGCACTCCAGCCTGGGCAA
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GAM336127 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - A
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A G G
GAM336127 CACTGCACTCC BACE2 NM_138991.1 3 TTGCCCAGGGTCC CACT TCCAG A
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CGTG GGACCCGTT
GGTC TCCTG
GAM336127 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

-
GAM336127 CACTGCACTCC CTSB NM_147780.1 5 CAGCGCTGGGCTG T TG - AA A
AGCCTGGGCAA GTGTGCAGTG CACTGCAC CCAGCC G GC
GTGACGTG GGTCGG C CG
T GT G AC
GAM336127 CACTGCACTCC CTSB NM_147782.1 5 AGCGCTGGGCTGG T TG - A A
AGCCTGGGCAA TGTGCAGTG CACTGCAC CCAGCC G GC
GTGACGTG GGTCGG C CG
T GT G A
GAM336127 CACTGCACTCC CTSK NM_000396.2 3 CTTCCACGATGGT CT GCC CA A
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GTGACGT GGT ACCT
-- AGC TC
GAM336127 CACTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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C
GAM336127 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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CT
GAM336127 CACTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC CT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
GAM336127 CACTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GTGACGTGAGGTCGGACCC
CC
GAM336127 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTGACGTGAGGTCGGACCC
CCT
GAM336127 CACTGCACTCC IL1A NM_000575.3 3 TTGTCTCACTTGT TCC CCT A
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T-- AC-
GAM336127 CACTGCACTCC NGB NM_021257.2 3 TGCTTCTTCAGGT CA----- CA ---- A
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GG GACGTGAG TGGAC TCGT
GGAACCG -- TTCT
GAM336127 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
AGCCTGGGCAA AGTGCAACG TGCACTCCAGCCTGGGCAA
ACGTGAGGTCGGACCCGTT
GCA
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C AC CATTTAA -
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C AC CATTTAA -
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                                A


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                                      T    GT G  AC
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                                      T    GT G  A
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                                   TT   CACTC
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GAM336198 CACTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG C A - A
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GT ACG GAGG TCGGACCCGTT
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GAM336198 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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CTG GT GACG GAGGTCGGA CCTG
C AC CATTTAA -
A

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T GT G AC
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T GT G A
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CCT
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C AC CATTTAA -
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T GT G AC

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T GT G A
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C AC CATTTAA -
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C AC CATTTAA -
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T GT G A
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-- A CTC
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C AC CATTTAA -
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GGTC TCCTG
GAM336214 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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C AC CATTTAA -
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T GT G AC
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T GT G A
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C AC CATTTAA -
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C AC CATTTAA -
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T GT G A
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C AC CATTTAA -
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C AC CATTTAA -
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T GT G A

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C AC CATTTAA -
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GAM336237 CACTGCACTCC BCHE NM_000055.1 5 GTCCAATTTACAG - A- ------- A A
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GAM336245 ATGGGAGACTG BACE2 NM_138992.1 3 TGTCCCCGCTCAG ATG G C A
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TTTCTGACTC CC CCTGT
GAG G -
GAM336245 ATGGGAGACTG HD NM_002111.3 3 CGCCTTCCCCTCA A -- C- A A
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ATCTT TTGACTCCCC CC GC
A TG TT -
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TAAACGTACTC ATCCCA TGGGATGA GTTA CTC
ACCCTACT CAGT GAG
T GGG---
GAM336247 ACCCGAGAGGT APPBP2 NM_006380.2 3 CTGCAACCTCCGC A A
GGAGGTTGCAG CTCCCGGGT ACCCG GAGGTGGAGGTTGCAG
TGGGC CTCCGCCTCCAACGTC
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GAM336247 ACCCGAGAGGT IGF1 NM_000618.2 3 CTGCAACCTCCAC A A
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TGGGT CTCCACCTCCAACGTC
C
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GT ACG GAGG TCGGACCCGTT
A G G
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GTGACGTG GGTCGG C CG
T GT G AC
GAM336251 CACTGCACTCC CTSK NM_000396.2 3 TCTTCCACGATGG CT GCC C A
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GTGACGT GGT ACCT CT
-- AGC T
GAM336251 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG A
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GAM336251 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG C A
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GTGACGTGAGGTCGGACCC CT
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GCA
GAM336251 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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CCAGGTT GTGGCCTCG
C- AAAG
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TAAGTTAAGTGGT TAGAG
G -- A
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T TTA
GAM336256 TTCATTAGGCC APPBP2 NM_006380.2 3 CTATTATTTCTGG - TGC A
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AAGTAATCT GGTCT TTATC
T TTA
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CGGACCTCCGACC GGACCA
CC A

GAM336257 GTCTGGAGGCT OLR1 NM_002543.1 3 AACTGTGGTCCAT C A - G A
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CAGACCTCT ACCT GG GTCA
- - T A
GAM336259 GAGCAGGTTTG ACE NM_152831.1 3 TGGGCCATTCCAG GA T---- T A
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CGTCC GACCTTACCG GGT
GA TTCAT -
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T AGT
GAM336259 GAGCAGGTTTG DSCR1 NM_004414.3 3 AGGACGCATTCCA CA- G - A A
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CTC CTAAACCTTAC G AGG
ATA - C A
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CTTGTCC AAC ACCGAGGT
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GAM336260 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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CTAC GTCGACCT CC CC CGT
A TG - -
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TACCGTCG TCTACCTC
G --- AA
GAM336261 GATGGCAGCTG MT3 NM_005954.1 5 CGTTCACCGCCTC - -- A A
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C AC C
GAM336264 CTGCCCTGAAC DHCR24 NM_014762.1 3 CGGTGGCCAGAGA CCTGAA C A
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GACG GAGACCGGTGG
ACCGTA C
GAM336267 ACTGCACTCCA APPBP2 NM_006380.2 3 TGTTGCCCAGGCT AC A - - A
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ACG GAGG TCGGACC GTTGT
TA G G C
GAM336267 ACTGCACTCCA FHL2 NM_001450.2 5 TGTCGCCCAGGCT - A
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CA C

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AGAGA TTCTGTTTC TCG
C GTAG T
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CCGAAAAG CCTTTT CGAT
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GAM336272 CAGAATCTTTT APBA2 NM_005503.2 5 TTCTTGTGTCTGG TGTCTCT A
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GAM336272 CAGAATCTTTT HTR2A NM_000621.1 3 TTCTCAGAAGTGA CA - GT- - A
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CTT AGAAAA GA GACTCTT
AA C AGT A
GAM336272 CAGAATCTTTT IGF1 NM_000618.2 3 TTTTTAATCTTAA G TCTC A
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GT TTAGAAAAT ATTTTT
G TCTA
GAM336272 CAGAATCTTTT PSEN2 NM_012486.1 5 TTCTCAGACGTCA GAA- TC- A
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CG TG TACTT TTATGGAC
A AAC -
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CATT GTTTTA TATTATGGAT
CCG --
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-- A G
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C A GG
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ATTT TGC

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TCTT TATTTT CACACACTC
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C - AGC A
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TCTT TATTTT CACACACTC
TTG TAGA
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C - AGC A
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GACGGA G
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ATTT TGC
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TA T C
GAM336293 CAGGTGGTGCT HTR2A NM_000621.1 3 TGCTTCTCTAAAA CA A--- A
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GAM336294 GAGATGGAGTT APBA2 NM_005503.2 3 CAACATGAAAACT GAG AC A
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TTTTGTCTCAAAATG ACAA
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GAM336297 ACAACCTCTGC DLST NM_001933.2 3 GGGCTGAGGAGGC CCT G A
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TTT G
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GAM336299 GGTCCAGACTG THOP1 NM_003249.2 3 GCACTGCGACTGC T A ---- A
GAGTATAGTGC CCAGTCTGGCC GG CCAGACTGG GTA TAGTGC
CC GGTCTGACC CGT GTCACG
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GAM336303 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
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C CT
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GTGACGTGAGGTCGGA CTGT
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T AAC T TC
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- - T
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GAC TTCTGTAC GTCTC GGC
- G CT C
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GACCTTCT CCATCTT
--- CTCC
GAM336309 CTGGAAGACAT IGF1 NM_000618.2 3 GGGGTTTTACCAT AA GA A
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GACC TTGTACCATTTTGG
GG GG
GAM336309 CTGGAAGACAT RAGE NM_014226.1 3 GGAGCGCCATCAT - AGA GA A
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GACC TTCTGTACTA CGA
A CCG GG
GAM336311 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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ACGGTA G G
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GAM336311 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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C -- GAGAG A -
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- CG A
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- CG A
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TA G G
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GAM336380 GAGGTGAAGAT CRAT NM_144782.1 3 AGGGGCCAGGGTG ------ AG G A
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GAM336382 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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C -- GAGAG A -

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GAGTCGAC TGGTCACA
CACAG GGG
GAM336399 TAATGCTCAGC APPBP2 NM_006380.2 3 ACACTGGTCCAGT CTCA A
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GTTAC TGACCTGGTCACA
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TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336403 TTGCTTCATTA HTR2C NM_000868.1 5 TTTGGTTGCTTAA -- AG G A
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AACGAAGT GA TCGTT GTTT
CA AT G
GAM336404 TATGAGTGTGA IGF1 NM_000618.2 3 CTCATGTATTTTT --- TT A
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TTT GT
GAM336404 TATGAGTGTGA PSEN1 NM_000021.2 3 CTCAAGCACTGAC T GA A
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GAM336405 TCTCACACTCT MAPK10 NM_138980.1 5 GGCACGGAATGGC -- G T A
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AGAGTGTGA GG TAAGG ACGG
TC - C
GAM336405 TCTCACACTCT PRND NM_012409.1 3 GGCCCAGAAATCA C CTC T- A
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GGA TGT ACTAAAGA CGG
A CAT CC
GAM336406 CAGAGCATTTG APBB2 NM_173075.1 3 AATACTCCTCATC C A ATTT A
TGAGGAGTGTT AGCCTT AG GC GTGAGGAGTGTT
TC CG TACTCCTCATAA
T - AC--
GAM336406 CAGAGCATTTG BACE2 NM_138991.1 3 GATGGTCCTCACA CA-- G A
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GTCTT GAACACTCCT GTAG
CTCC G
GAM336407 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336407 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336407 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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CGTG GGACCCGTT
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GAM336407 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336407 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336408 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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CGTG GGACCCGTT
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C -- GAGAG A -
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TA G G
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ACGGTA G G
GAM336409 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM336409 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TGACGTGAGGTCGGACCC TG
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GAM336409 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TA G G
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ACGGTA G G

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CGTG GGACCCGTT
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TGACGTGAGGTCGGACCC TG
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GAM336413 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
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C TA A
GAM336414 ATTGTAAATTA IAPP NM_000415.1 3 AAGCAAATTAGTA TA AC C A
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TAAC TTAAT TTAAACGA
TG GA A
GAM336420 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336422 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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G G
GAM336422 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
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GTAG CGTG GGACCCGTT
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GAM336422 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GAM336422 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
GAM336422 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336422 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336424 AGGTGGGGTTT GLUL NM_002065.3 3 ATAATAAGGAATA CA- A G A
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TAA A A
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GAM336424 AGGTGGGGTTT PSEN1 NM_007318.1 5 GCAACTGGTGAAA AG T G A
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CG - G

GAM336424 AGGTGGGGTTT TRPM2 NM_003307.1 3 TCAACATGGAGCC TG TCA A
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TCC TCCGA GGTACAACT
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GAM336426 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336428 GCACACACCTC S100B NM_006272.1 3 GCCCTGCAAGGGC G A C T A
CTTGCAGTGGC GTGGTGG CAC CAC TCCTTGCAG GGC
GTG GTG GGGAACGTC CCG
G - C -
GAM336428 GCACACACCTC TGFB1 NM_000660.1 5 GCCACTGCGGGGA GCACACA A
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TTA AGTA
GAM336430 GTGCTTGACCA APPBP2 NM_006380.2 3 CTGCCACCACGCC GTG A -- A
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GGAT GGT GCACCACCGTC
AAA C CC
GAM336430 GTGCTTGACCA PRND NM_012409.1 3 CTGCCTCCCAGGC - A T T A
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CACGAACT GG AC CC CCGTC
C - - T
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GGAT GGT GCACCACCGTC
AAA C CC
GAM336431 GTGCTTGACCA PRND NM_012409.1 3 CTGCCTCCCAGGC - A T T A
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CACGAACT GG AC CC CCGTC
C - - T
GAM336432 GTGCTTGACCA APPBP2 NM_006380.2 3 CTGCCACCACGCC GTG A -- A
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GGAT GGT GCACCACCGTC
AAA C CC
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C - - T
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AAA C CC
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C - - T
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ATCACGTTTT GATGGTT
TT TCT
GAM336434 TAGTGCAAGGT MME NM_000902.2 3 AAGTGGGGCAAAA TAGT A- A
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CGTTCCAAAACGG TGAA
TAAT GG
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ATTCT GTATTTCTGACATAT
TA TTAA
GAM336435 ACTGGGATATG PIN1 NM_006221.1 3 CACACAGTATTTA AC T-- G A
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ACCCT TATTT TGACACAC
AC TGT A
GAM336439 TGCATGATGCT CASP3 NM_032991.1 3 CTCCAGGCCTCAG GA A A
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GCGTG ACGACTCCGGACCT
G- C
GAM336439 TGCATGATGCT GFAP NM_002055.2 3 ACCCACCTCAGCC -- T TT A A
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ATGTG CT CGACTCCA CCC
TC C -- A
GAM336439 TGCATGATGCT NOTCH1 NM_017617.2 3 TCTTGAAATGTAG GAGG- TG A
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ACGTACTACGG AA TCT
ATGTA GT
GAM336439 TGCATGATGCT NPY NM_000905.2 3 GTTTAAATAAAGT GAG A A
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GAM336440 TGCATGATGCT CASP3 NM_032991.1 3 CTCCAGGCCTCAG GA A A
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G- C
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TC C -- A
GAM336440 TGCATGATGCT NOTCH1 NM_017617.2 3 TCTTGAAATGTAG GAGG- TG A
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GAM336440 TGCATGATGCT NPY NM_000905.2 3 GTTTAAATAAAGT GAG A A
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AA- G

GAM336441 TGCACCACTAC CTSB NM_147782.1 5 AGCGCTGGGCTGG -- -- - A A
ACTCCTAGGCA TGTGCAGTGGTGC TGCACCACT ACACT CCTAG GC
G GCGTGGTGA TGTGG GGGTC CG
CG TC G A
GAM336441 TGCACCACTAC LRP1 NM_002332.1 3 CCACTGGGAGAGC CA- GCA A
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ACGTGGTGGT GAGGGTC
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GAM336441 TGCACCACTAC RAGE NM_014226.1 3 TGCCTAGGATGTT T A CT C A
ACTCCTAGGCA CTGGGCT GC CCA ACA TCCTAGGCA
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GAM336442 AAGCAGAACTG APPBP2 NM_006380.2 3 AGAAAACATTGCC G CT TT A
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TT GTTTT CG ACAAAAGA
G AC TT
GAM336442 AAGCAGAACTG CAV1 NM_001753.3 3 AGAAAACATAATC AA CT T A
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CGTCTT TAA ACAAAAGA
TC C- T
GAM336442 AAGCAGAACTG HTR2C NM_000868.1 3 ACACAGTAAGATA - TTCT A
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GAM336445 GTGGCAAGTGA MAPT NM_173727.1 3 TGGACATCTGGTT - -- TG AC A
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CG CCG TTC TGGTCTACAG
T GT GT GT
GAM336447 TACAGTATCTG ADAM17 NM_021832.1 3 GGCAGTTTTTCTG TATCTGT A
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GAM336448 AGGTGGGGTTT GLUL NM_002065.3 3 ATAATAAGGAATA CA- A G A
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TAA A A
GAM336448 AGGTGGGGTTT IAPP NM_000415.1 3 CCAACGTGGTGAA TG A
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TCT CCCAAAGTGGTGCAACC
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CACCATGTTGG CTCCGCGC GTGGGGTTTCACCA GTTG
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CG - G
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AAT A A
GAM336451 TAGCTGCCAGG DSCR1 NM_004414.3 3 TGTACTTGTTCTT TAG C--- A
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GATGGTCT TTGTTCATGT
TTG TTTC
GAM336451 TAGCTGCCAGG MME NM_007288.1 3 CATTCTTGTTGCC CCA TACG A
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GAM336452 TAGCTGCCAGG DSCR1 NM_004414.3 3 TGTACTTGTTCTT TAG C--- A
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TTG TTTC
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GTCGAC CCGTTGTTC
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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GAM336454 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TGACGTGAGGTCGGACCC TG
CC

GAM336454 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336454 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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--- CG CT
GAM336455 TTGCAATAGTG PRND NM_012409.1 3 TTTAGTTTTTCAC AAT A A
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GCGTT TC TTTTGACTT
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GGTT TC CGATCCTTGT TCCA
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A A
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GAM336456 CCAAAGTGCTA TGFB1 NM_000660.1 3 GCCTGTAATCCTA - A A
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GAM336458 GTACTCCAGCC APBA1 NM_001163.2 3 GTGGCCAGGCAGG - A G A A
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CGT GGGG CGGACGGACC GT
C G G G
GAM336458 GTACTCCAGCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG TA AGCCT A
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GG GT---
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GAM336458 GTACTCCAGCC IGF1 NM_000618.2 3 TGTCCCCCAGGCT CCT TAA A
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C TGA GGTCG ACGGACCC
T TC - TTT
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GAM336460 TGTAGTGTGAA DSCR1 NM_004414.3 3 ATGCAGTGCCTTT T T- A A
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AC TTAC CTTTCCGTG CGTA
- CC A
GAM336461 GCAGTGAAGGA CTNND2 NM_001332.1 3 TGTCAACAAAGTG G --- - C A
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CGTCACTTT TTCGT ACA CTG
- GAA A T
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C CG TCACTTCC TTC TACG CTGG
AAC C - GA
GAM336462 TGGCAAGTGGG A2M NM_000014.3 3 GCTGAAAAGTGCT T GTG G A
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TCGTT TCGTGAAAAGTC
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TA G G
GAM336465 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
GAM336465 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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CGTG GGACCCGTT
GGTAGGTC TCCTG

GAM336465 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336465 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCC TG
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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- C G
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ACG GGAA TTTGAGAAA GACC
A- G ATTT
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GTCGGAAC GAGAGAGACC
TA CG
GAM336469 TGCAGCCTTGA HTR2A NM_000621.1 3 CCAGAAGCTCAAG A CTT A
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ATGTC CTTGAGAAGGG
TAGT AT
GAM336469 TGCAGCCTTGA TNFRSF5 NM_152854.1 3 CAGGAGAGACAGT AAC GG A
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GAC AC
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ACG GGAA TTTGAGAAA GACC
A- G ATTT
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T CC -
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T TCAC -
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GAM336474 TGTCTGGAGGC GFAP NM_002055.2 3 AGGAAAACTGAGA G GCG AG A
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- AGA GA

GAM336474 TGTCTGGAGGC HD NM_002111.3 3 CTTGGAGCTGTCC G C TC A
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G AGACCTCC TGTCGAG TC
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336475 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
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GAM336475 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM336475 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336476 TCCCTTTGAAG DHCR24 NM_014762.1 3 TCATACCTGGCTT TTG TCCA A
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AGGGA TTCGGTCCA
CG- TACT
GAM336476 TCCCTTTGAAG TGFB1 NM_000660.1 3 AGGAACCTGCTTT -- C A A
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CGTGTAAG GTCC CACATTC
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GAM336483 CTCTGAGTCTG GLUL NM_002065.3 5 GCCTACTCTGTGA T CT AG A
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C AG G-
GAM336483 CTCTGAGTCTG MAPT NM_173727.1 5 ACCTACTCCATAC G C AGA A
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GGGA TCA AC CTCATCCA
G T ---
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GATTC ACTCTCTCA TTCG
TC TT C
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GAGG CTCAGA CTCTCA CCG
ACC GA -
GAM336484 TAGGGAATGAA CAV2 NM_001233.2 3 ACCACTGTTCTGT - A C A
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ATCCTTTACTTGT TTGTC CC
C A A
GAM336486 TTACAAAATTT BAX NM_138765.1 3 GCATTTTTCTTAC TTT T A
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AATGTTTT TCTTTTTA CG
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AGTGTTTTAAAT CT GACA
T AGAAG

GAM336487 TGGCTAGGTAA CRYAB NM_001885.1 5 ACCCCTCACACTC A------ AAG A
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GCCG TCCATTCCC
- CGT
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GAM336487 TGGCTAGGTAA PSEN1 NM_000021.2 3 CTTCCCTTTGATT T TAGGT---- A
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GAM336487 TGGCTAGGTAA SNCA NM_000345.2 3 CTTCCCTTTCACT G A- -- A
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CTTGACAT GAC GGTGTCGA
TGA ---
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ATTT TGC
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TGACGTGAGGTCGGACCC TG
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GAM336490 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336491 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GT CGT TGGACCCGTT
TT CACTC
GAM336491 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336491 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GCGA--- G
GAM336491 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
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GAM336491 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336492 CTGGCTAATTT CASP3 NM_004346.2 3 AAACTGTTGATTA TT TTG A
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GACCGATTA AG TCAAA
TT TTG
GAM336492 CTGGCTAATTT HTR2C NM_000868.1 3 AGGACTGAAGAAA CTA G A
TCTTGAGTTTT ATCCTTCAG CTGG ATTTTCTT AGTTTT
GACT TAAAAGAA TCAGGA
TCC G
GAM336492 CTGGCTAATTT IDE NM_004969.1 3 AGAGCCTAAGAAA C ----- A A
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C ACCGGT TAAAAGAAT CGAGA
C TCTAC C
GAM336492 CTGGCTAATTT IGF1 NM_000618.2 3 AAACTTAGCAAAA CTG----- C A
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CGATTAAAA GATTCAAA
TTATATAA C
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TC TC ATCTC ACGTCACT
T - C GA
GAM336494 TATCACGTGCA OLR1 NM_002543.1 3 GTCTGGGAAAAAG TA G GCT--- A
GCTTTGCTGAC TGCACGTGAAG TCACGTGCA CTTT GAC
AGTGCACGT GAAA CTG
GA - AAGGGT
GAM336495 CTGGCTAATTT CASP3 NM_004346.2 3 AAACTGTTGATTA TT TTG A
TCTTGAGTTTT TTAGCCAG CTGGCTAAT TC AGTTT
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GACT TAAAAGAA TCAGGA
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C ACCGGT TAAAAGAAT CGAGA
C TCTAC C
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ACACGTGT TGTCCG
ATTT TGC
GAM336497 GTGCATTTGTA ADAM17 NM_003183.3 3 ATAGATTTGACCT C--- - G A
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CAC TAAACATC AGTTTA ATA
TAAC C G
GAM336497 GTGCATTTGTA FPRL1 NM_001462.1 3 TTGCATTTTATCA TAGTT T A
GTTAAATGTGT AATGCAT GTGCATTTG AAATGTG
TACGTAAAC TTTACGT
TAT-- T
GAM336497 GTGCATTTGTA GYPA NM_002099.2 3 ACACATTTATCAT TGTAGT A
GTTAAATGTGT TTAATGCAT GTGCATT TAAATGTGT
TACGTAA ATTTACACA
TTTACT
GAM336498 GTGCATTTGTA ADAM17 NM_003183.3 3 ATAGATTTGACCT C--- - G A
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CAC TAAACATC AGTTTA ATA
TAAC C G
GAM336498 GTGCATTTGTA FPRL1 NM_001462.1 3 TTGCATTTTATCA TAGTT T A
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TACGTAAAC TTTACGT
TAT-- T
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GTTAAATGTGT TTAATGCAT GTGCATT TAAATGTGT
TACGTAA ATTTACACA
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AA TCG
GAM336502 AGCTGGATTGT APBB2 NM_173075.1 3 GCTAGAGGTAAAC T T GG A
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TCG TCT GCAAATGGA TCG
- T GA
GAM336502 AGCTGGATTGT NOTCH1 NM_017617.2 3 GCCCCAGGTAGAA AGC TG----- A
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C ATCTA AGATGGACCCCG
CTT TTTTCAA

GAM336503 TTACTGGGCTC HADH2 NM_004493.1 3 AGCTTGGGAGGAA - T G A
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GATGACCCGA GGAGGGTT CG
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GAM336504 AGTGGCCCTGG ABCD1 NM_000033.2 5 GCCCTGACCTCAG G ------- AT A
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TCAC GGGACCGGGG TCCCG
- ACTCCAG --
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CCCTGGGGCAT GGGCACT AGTG CCC GGCCCTGGGG
TCAC GGG TCGGGACCCC
- - CCT
GAM336505 ATGGGCAGTTT BACE NM_138971.1 3 GGAAAGGGTGAGG A - C T - A
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AC CT TCAG GAG GGGAAAGG
A A - - T
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TCTTGAGTTTT TTAGCCAG CTGGCTAAT TC AGTTT
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TT TTG
GAM336506 CTGGCTAATTT HTR2C NM_000868.1 3 AGGACTGAAGAAA CTA G A
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GACT TAAAAGAA TCAGGA
TCC G
GAM336506 CTGGCTAATTT IDE NM_004969.1 3 AGAGCCTAAGAAA C ----- A A
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C ACCGGT TAAAAGAAT CGAGA
C TCTAC C
GAM336506 CTGGCTAATTT IGF1 NM_000618.2 3 AAACTTAGCAAAA CTG----- C A
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CGATTAAAA GATTCAAA
TTATATAA C
GAM336507 CTATTGGATTT TNFRSF6 NM_000043.3 3 TCCAAGGATGTTT - --- A
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GGT GATCTAAAATTTGTA ACCT
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GAM336508 CTATTGGATTT TNFRSF6 NM_000043.3 3 TCCAAGGATGTTT - --- A
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GGT GATCTAAAATTTGTA ACCT
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TGACGTGAGGTCGGACCC TG
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TT TTG
GAM336510 CTGGCTAATTT HTR2C NM_000868.1 3 AGGACTGAAGAAA CTA G A
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GACT TAAAAGAA TCAGGA
TCC G
GAM336510 CTGGCTAATTT IDE NM_004969.1 3 AGAGCCTAAGAAA C ----- A A
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C ACCGGT TAAAAGAAT CGAGA
C TCTAC C
GAM336510 CTGGCTAATTT IGF1 NM_000618.2 3 AAACTTAGCAAAA CTG----- C A
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CGATTAAAA GATTCAAA
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GAM336511 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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A C T ATC
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TTGACC
GAM336512 GTAAAGAAATC LRP1 NM_002332.1 3 ATAATTTTTGCTG A - CCA A
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A C ATA
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A CCCCT C
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CTTGAT GA --
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GAM336514 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- C A A
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TA GG G
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CA T T
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G---- CT
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T AG GAATTT -
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ACACGTGT TGTCCG
ATTT TGC
GAM336520 TTCTGTGCAGG BCHE NM_000055.1 3 GAGATATTAAAAT AGG-- C A
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AAGACACG AATT TAGAG
AATAA A
GAM336520 TTCTGTGCAGG TNF NM_000594.2 3 AGGAATGTGTGGC TT----- - A
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GTGAAGT G
GAM336522 TTGAGAGCATA APLP2 NM_001642.1 3 TTGTCTGACACAT AGAGC AAG A
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CACA- GTT
GAM336523 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
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ACCAGAGGAT GATCGA
CA TTAG
GAM336526 GACATGGAGAC B2M NM_004048.1 3 CTTTGAGTGCTGT A GC T A
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TTGTACCTCTGT GT GTTT
C GA C

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TTGTACCTCTGT GT GTTT
C GA C
GAM336528 TCACAGTGATG ACE NM_152831.1 3 ATTCCTGAGTCTG A GA GT A
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- AA TG
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GAACGT CA TGAGTCGGAA
CA CC G
GAM336533 TTTGTACGTCA ACT NM_020482.3 5 GAAGGCTGAGTCC C- CA A A
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GAACGT CA TGAGTCGGAA
CA CC G
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TA G G
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ACGGTA G G
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GAM336534 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336534 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
GAM336534 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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GAM336534 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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CCT CCG TCGTCGTCGTCC
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GAM336535 GAGGAGGTGGG FHL2 NM_001450.2 5 CCATTCTCCTGCC A - C CA- A
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- G C TTA
GAM336535 GAGGAGGTGGG GFAP NM_002055.2 3 CCTGCTGCTGCTG ----- TG - A
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CTTCT TC C TCGTCGTCGTC
AA GT G G
GAM336535 GAGGAGGTGGG MT3 NM_005954.1 5 CCAGCTGCTGCTC GAG T A A
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CTCC TCTCGTCGTCG CC
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GAM336535 GAGGAGGTGGG MTNR1A NM_005958.2 3 CCTGGCTGCTGCC G G G - A
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TCTTT AT CCGTCGTCG TCC
G G A G
GAM336535 GAGGAGGTGGG OGDH NM_002541.1 3 CCTGTTAACCCTC CAGC A
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CTCCTCCACCTC TTGTCC
CCAA

GAM336535 GAGGAGGTGGG PSEN1 NM_007318.1 5 TTTGCTGCTGCTT G T A
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CTC TCC CTTCGTCGTCGTTT
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CTCC CCAC TCGTCGT GTCC
AA G -
GAM336536 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336537 CCAGGGTACTC BACE NM_138972.1 3 GCGTGTGTCCCTG CT- - TT A
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GGTCCCATGG CCCTG GTG
TGT T CG
GAM336537 CCAGGGTACTC FLNB NM_001457.1 3 AAGTGATCTCAGA - A- A
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GAM336538 CCAGGGTACTC BACE NM_138972.1 3 GCGTGTGTCCCTG CT- - TT A
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G CAGC C
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C -- GAGAG A -
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GAM336541 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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GAM336541 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336541 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336541 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336545 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GAM336545 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
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GTC TCCTG
GAM336545 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GT CGT TGGACCCGTT
TT CACTC
GAM336545 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336545 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM336545 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GAM336545 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336546 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336548 TCTGGTTTTAA FLNB NM_001457.1 3 TGCCTTCAGAAAT T- ATC A
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AGATC GAAT GACTTCCGT
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GAM336548 TCTGGTTTTAA LRP1 NM_002332.1 3 TGCCTTCAGGGAG G TTAA A
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GGAC GA GGGACTTCCGT
G CAGA
GAM336549 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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GAM336550 TCAGAGCAGTG ACE NM_152831.1 3 CTGGGCTTTGTCA CA C A
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T GT --
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GTCT- G
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TC A- C
GAM336551 GAGTTAAGCAA HTR2C NM_000868.1 3 CCTTTCTCTCTTT AGTT- C A A
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CGTCT TCA CCTGACTTC
-- - GT
GAM336553 GCAGGATGGTT SERPINA NM_001085.2 3 CTCTTCAGTCTGG G GG- TG A
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GTCCTG G CTGACTTCTC
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GAM336556 GGGAGAAAAGG NGB NM_021257.2 5 CTGGCCGCGCGCC AGGGGATA A
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CTCTCTTTTCC GTC
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GAM336557 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ATTT TGC
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TA G G
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ACGGTA G G
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C CTCCACTTTGG TG GGGAC
- AG T
GAM336560 AAGTGCTGGTA ADAM17 NM_021832.1 3 CATGCCTGTAATC T A A
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C C
GAM336560 AAGTGCTGGTA GLUL NM_002065.3 3 AACACTTGTAATT - TGGT G A
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TTC ATG TAATGTTCACA
T TTT- A
GAM336560 AAGTGCTGGTA MTNR1A NM_005958.2 3 CACACCTGTAATC GT A A
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GAM336561 TGTAGCAGAAC APCS NM_001639.2 5 CTGGTCACTGCTT - C GT A
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C C --
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GTAG CGTG GGACCCGTT
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C C T
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T C
GAM336565 TTCTGCCACTG IGF1 NM_000618.2 3 AGGCTGGAGTGCA T - A
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T T
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T T CA
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A TCT CACAGGGAACCGACC
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- TC C
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CA TG GA
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T- TT T
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T G
GAM336571 GGCCTGGTGGC BACE2 NM_138991.1 3 CCAAAACAGAGTG TG G- G A
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TCGG TA TGA GACAAAACC
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GAM336571 GGCCTGGTGGC PRND NM_012409.1 3 TTGGAACAACAGC --- - TG A
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TCG GATC ATCGACAACAAG T
ATA T GT
GAM336572 AAGTTTTTTTA ADAMTS5 NM_007038.1 3 CCTTGCAATATAG A A T A
AATTAGCTAGG AAAAACTT AAGTTTTTTTA ATT GC AGG
TTCAAAAAGAT TAA CG TCC
A - T
GAM336572 AAGTTTTTTTA S100B NM_006272.1 3 TGTAGCTAATTAG TA GG A
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GAM336573 ATTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG A - TG A
GCCTGGGTGAC GGAGGGCAAT ATTGC CTCC AGCCTGGG AC
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G G GT
GAM336573 ATTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
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GAM336573 ATTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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GAM336573 ATTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A----- TG A
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TACGGC GT
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TGAGAGA GT A-
GAM336574 GCAGCGCTGAG APBB2 NM_173075.1 3 CAACAAATTACAT G G GA A
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GTTG GATT ATTAAACAAC
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G G GT
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GAM336575 ATTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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TACGGC GT
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GAM336578 ACTGCACTCCA APPBP2 NM_006380.2 3 TGTTGCCCAGGCT AC A - - A
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TA G G C
GAM336578 ACTGCACTCCA FHL2 NM_001450.2 5 TGTCGCCCAGGCT - A
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GAM336579 ACTGCACTCCA FHL2 NM_001450.2 5 TGTCGCCCAGGCT - A
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GAM336579 ACTGCACTCCA IGF1 NM_000618.2 3 TGTCCCCCAGGCT C- A
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GAM336580 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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G G GT
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GAM336582 ATTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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T AACGTGAGGTCGGACCC TG
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GAM336583 GAGGTAGAGGT APLP2 NM_001642.1 3 TGCTCACTGCTTC GTT A
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A- C GGGTTT
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GAM336583 GAGGTAGAGGT GYPA NM_002099.2 3 CACTCACTGAAGC A G A
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CTTTA CTTCGA GTCACTCAC
G A
GAM336583 GAGGTAGAGGT IGF1 NM_000618.2 3 CACTCACTGACTC GAG TTG A
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TATCTTC GTCACTCAC
ACG TCA

GAM336583 GAGGTAGAGGT IGF1 NM_000618.2 3 GGCTCACTGCAAC A G A
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GAM336583 GAGGTAGAGGT PRND NM_012409.1 3 GGCTCACTGCAGC G A
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CTCC CTCCAACGTCACTCG
GC G
GAM336584 GAGGTAGAGGT BACE NM_012104.2 3 CACTCACTGCATT GA T ------ A
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A CC TTTCCG ACGTCACTCAC
A- C GGGTTT
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G A
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G A
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ACG TCA
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C G
GAM336584 GAGGTAGAGGT PRND NM_012409.1 3 GGCTCACTGCAGC G A
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CA TGTC AGG TTCTTCTGT
C C TCGG
GAM336585 GTTACAGCTCT GAL NM_015973.2 3 TGTTTGTCTGTGT TCT A - A
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CAATGTCG GT TCT TTTGT
T-- G G
GAM336585 GTTACAGCTCT PSEN1 NM_000021.2 3 TTTCTTCTTTGAC C CTC CA A
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CAAT TC AGTTTCTTCT
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G GA GTGA GTC GGCCGTTG
C G A CCC
GAM336586 CACTGCACTCC FHL2 NM_001450.2 5 TTTGTCGCCCAGG ---- C A
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GTGACGTGAGGTCGG GCTGTT
ACCC T
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GTGACGTGAGGTCGG CC
A CCCT
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GCA AC
GAM336586 CACTGCACTCC PRND NM_012409.1 3 GTTGCCCAGGCTG C- A
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TTTTGTAA CGT AAGTCGTG
C - CTT
GAM336588 TAAGATGTTTG NPY NM_000905.2 3 GTGCTGAATTCTG T T T-- A
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TTTTGTAA CGT AAGTCGTG
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G CGAC -
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GT CGAACT ACCGTCTC
GGT ACA
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A- - T CC
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TTCACGAACT CCGTCTC
T CGGACCCT
GAM336591 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC

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ACTT CTCCTTCC CGTCCT
C C- G
GAM336592 TGAGAGAGGAA IL1A NM_000575.3 5 TCCATGCCTTCCT T CGTAG A
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CTCTTTCCTTCCG CCT
C TA---
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CTCTCTCCTTCCGG ATTCC
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AGGG A-
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ACT- T
GAM336593 TTTGCACACTT IGF1 NM_000618.2 3 GGCAATATAAGGA CA- AA-- A
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CT AAAAAA -
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CTA AATA
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CT AAAAAA -
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G G TCACGTC TACTTCTCTTG
T ACCCT GG
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GT - - C
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C T -
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T ACCCT GG
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GAACA GT
GAM336597 CTGAATGTAAT LRP1 NM_002332.1 3 TTACAACTAAATA AA A C A
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GAC ACA TA AATCAACATT
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ACACGTGT TGTCCG
ATTT TGC

GAM336599 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GTAG CGTG GGACCCGTT
GTC TCCTG
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GAM336602 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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GAM336602 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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C -- GAGAG A -
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TCC CA AACTAATCGG AGG
-- T AT C
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TA G G
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ACGGTA G G
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GAM336606 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
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ACGGTA G G
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C -- GAGAG A -
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TGACGTGAGGTCGGACCC TG
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GAM336608 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336608 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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GAM336609 AACACGTTGCA BACE NM_012104.2 3 GGAGACACAGATG AA T- - A
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CG CC G
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336610 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336610 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GGTAGGTC TCCTG
GAM336610 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336610 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCCG
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GAM336610 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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TGACGTGAGGTCGGACCC TG
CC
GAM336610 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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ACGTGAGGTCGGACCCGTTG
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GAM336610 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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G G C A
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ACACGTGT TGTCCG
ATTT TGC
GAM336615 GTGTTATTAAT ADAMTS5 NM_007038.1 3 AAAAAGTGGTTAA G -- - A
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G AA T
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CA AGTAAT TGAGAAAA
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ACG GAGG TCGGACC GTTGT
TA G G C
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TCT C C
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TGACGTGAGGTCGGACC TGT
CCC
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ACGTGAGGTCGGACC GTTGT
CA C
GAM336617 ACTGCACTCCA PRND NM_012409.1 3 TGTTGCCCAGGCT - A
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TGACGTGAGGTCGGACC GTTGT
C
GAM336618 TTTGTGTCCTG DLST NM_001933.2 3 TTCCTCTGCAGGA ACC C A
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AGACACAGGAC GTCTCCT
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AGACACAGGAC GTCTCCT
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TCGTCGTC TCGTCCA GT
- G CC C
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G CC C
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G CCGT-
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A AGT - T
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ACACGTGT TGTCCG
ATTT TGC
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C TCC ACACAAAAAGTTT
T TTAGTA
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C TCC ACACAAAAAGTTT
T TTAGTA
GAM336630 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336630 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
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GAM336630 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336630 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCCG
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TGACGTGAGGTCGGACCC TG
CC
GAM336630 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TA G G
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ACGGTA G G
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CGTG GGACCCGTT
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TGACGTGAGGTCGGACCCG
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TGACGTGAGGTCGGACCCG
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TGACGTGAGGTCGGACCC TG
CC
GAM336631 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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ATTAAAGG T ACTGT
GT TGTG--
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GT ACG GAGG TCGGACCCGTT
A G G
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T GT G AC
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GTGACGT GGT ACCT CT
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TA C GA T
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ATTT TGC
GAM336639 ATTCAAGATAA ADAMTS5 NM_007038.1 3 TTTCCATTGTTGC AAGGGTC A
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TT A -- G
GAM336640 TGGAATGAGGA BACE NM_138973.1 3 GACCACACCTCCG TG GA- AG A
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CA GTG --
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ACCT CTCCTTCC CCAG
CT GGATT
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CAC TTC TCTTTGGGGTT CGG
CTT - CC
GAM336642 GTGAGGCAGGA PSEN2 NM_012486.1 3 CGCTTTGGGGAGC - AA-- C A
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CAC TTC TCTTTGGGGTT CGG
CTT - CC
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GAM336646 AGGCCTTTTTG GFAP NM_002055.2 3 ATGACTTTGTCCC T---- - A G A
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T TCCGGAAA ACCCT TTTC GT
TCTTT G A A
GAM336646 AGGCCTTTTTG HD NM_002111.3 3 GTGTTTCTTTCCC CT- - G A
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TGT T G
GAM336646 AGGCCTTTTTG MME NM_007288.1 3 CTGTCTCTTGAAA A CTTTT -------- A
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- TTT-- GTAAAAAG
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G CTT AC
GAM336651 AGGCAGGTGGG APBA2 NM_005503.2 3 TGACTAATGACCA - G G T A
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GAM336651 AGGCAGGTGGG DHCR24 NM_014762.1 3 AGACCCATGTGCT A TG TG A
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TCGTTC TC GTACCCAGA
C CT GT
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GAM336651 AGGCAGGTGGG HD NM_002111.3 3 TGTCCCCCACCCC ------ TAT TCT A
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GAAACC C-- TGT
GAM336652 GAGGTTTGAGC ACE NM_152831.1 3 GGCAGGAGAATCA G G CC- A
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G G ACT
GAM336652 GAGGTTTGAGC CASP3 NM_032991.1 3 GGCATGGTCAAAG CT- - A
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ACT T
GAM336652 GAGGTTTGAGC CRAT NM_144782.1 3 AGCAGGAGACTGG G GA T- A
CTTCTCCTGCT CAAGAGCTC GAG TTT GCC TCTCCTGCT
CTC AGA CGG AGAGGACGA
G A- TC

GAM336652 GAGGTTTGAGC IAPP NM_000415.1 3 GGCAGGAGAATCG A TG C- A
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C CCAA TCG AAGAGGACGG
- GT CT
GAM336652 GAGGTTTGAGC NGB NM_021257.2 3 CGCAGGAGAGAGT TT G C T A
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CTCCA CT G GAGAGGACG
TT - A C
GAM336653 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
GAM336653 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
GAM336653 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM336653 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336653 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TACGGCA
GAM336653 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGTTG

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G GATCGTGT TGA TCGT GTGT
ACC - TTTTA
GAM336657 CTAGCACAGTG NGB NM_021257.2 3 TGTGTGCCAGTAC AC---- T A
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GGTCG TCATGA CCGTGTGT
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GAM336657 CTAGCACAGTG PLAU NM_002658.1 3 CCTGTGACCAGCA - C T - CA A
CTTGGCACACA CTGTCTCAG CT AG ACAGTGCT GG CACA
GA TC TGTCACGA CC GTGT
C - - A CC
GAM336658 AGGGCACACGT ADAMTS5 NM_007038.1 3 AATTCAGAGAAAT A A- C A
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CTTGTG GTA AGAGACTTAA
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GAM336658 AGGGCACACGT IGF1 NM_000618.2 5 AATTCAGAGCAGA A ACAC - A
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TCCG TAGA GAGACTTAA
G AGAT C
GAM336659 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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GAM336659 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -

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GAM336659 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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ACACGTGT TGTCCG
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TT CACTC
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GGT CC C
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- C
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T C T
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A T---- G
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G GTG A
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TT G T
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- CTT C
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ATTT TGC
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GAM336704 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TCT- G
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G AC G
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AC- AT
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TAA TGTCG
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GAM336739 TAGCAGATCTG IGF1 NM_000618.2 3 CATAAAGTCCAGA G T CC A
TGACTCCTATG TCTGGTA TA CAGATCTG GACT TATG
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G - A-
GAM336740 GTTTTGTTGTC BACE2 NM_012105.3 3 ACCAACATAAAAC GTCTC TA A
TCTGTGTTGTA AAAAC GTTTTGTT TGTGTTG
CAAAACAA ATACAAC
A---- CA
GAM336743 TATGAATGTAA GYPA NM_002099.2 3 TCCTATCATTCAT TAT------ T ----- A
GGAATGTGGGA TCCTTCATTCTGA GAATG AAGGAATG TG
ACAGGC CTTAC TTCCTTAC AT
CGGACAAGT - TTACT

GGA
CCT

GAM336743 TATGAATGTAA IGF1 NM_000618.2 3 TTCTATAAATAAC TAAGGAA A
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ATACTTAC ATATCTT
CCAATAA

GAM336743 TATGAATGTAA IGF1 NM_000618.2 3 TTCTATATTTTAC TAT----- AG A
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CTTACAT TTTATATCTT
GAAAGGTT --
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GT TTACATTCC AC CTCT
GT G- T
GAM336743 TATGAATGTAA VLDLR NM_003383.1 3 TCCACATTCTACT TA-------- T AA A
GGAATGTGGGA TCAGCTTTGGATG TGAA GT GGAATGTGGG
ACTT CA TCTTACACCT
GTAGGTTTCG - --
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ACAGGC CTTAC TTCCTTAC AT
CGGACAAGT - TTACT

GGA
CCT

GAM336744 TATGAATGTAA IGF1 NM_000618.2 3 TTCTATAAATAAC TAAGGAA A
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ATACTTAC ATATCTT
CCAATAA
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CTTACAT TTTATATCTT
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GAM336744 TATGAATGTAA MME NM_007287.1 3 TCTCTCAGCCTTA TG AA T A
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GT TTACATTCC AC CTCT
GT G- T
GAM336744 TATGAATGTAA VLDLR NM_003383.1 3 TCCACATTCTACT TA-------- T AA A
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ACAGGC CTTAC TTCCTTAC AT
CGGACAAGT - TTACT

GGA
CCT

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ATACTTAC ATATCTT
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CTTACAT TTTATATCTT
GAAAGGTT --
GAM336745 TATGAATGTAA MME NM_007287.1 3 TCTCTCAGCCTTA TG AA T A
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GT TTACATTCC AC CTCT
GT G- T
GAM336745 TATGAATGTAA VLDLR NM_003383.1 3 TCCACATTCTACT TA-------- T AA A
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ACTT CA TCTTACACCT
GTAGGTTTCG - --
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM336746 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336746 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336746 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TA G G
GAM336747 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
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GGTAGGTC TCCTG
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GAM336747 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336747 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TC CA TG
GAM336749 CATAAAATCAG CNTF NM_000614.2 3 AGTAATACAGCCT CAT AAA A
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AAC CGA
GAM336749 CATAAAATCAG NCKAP1 NM_013436.2 3 GGTTGTATTTTCT TAAA T A
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GT TAGTCTTTTATG TGG
TAC- T
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TA G G
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ACGGTA G G
GAM336750 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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CGTG GGACCCGTT
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GAM336750 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TGACGTGAGGTCGGACCC TG
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GAM336750 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336750 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336751 ACTGCACTCCA DLST NM_001933.2 3 GTTAGCCTGGTGA A A CCA A
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GACG GA TGGTCCGATTG
A - CAG
GAM336751 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A A- T A
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TGACGTGAGGT GG CCG CTG
C AC -

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TGACGTGAGGT GG CC CTG
C A CC
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AAGACCCAG GACA CTA GATG
T A T
GAM336752 TTCTGGGTTTT PIN1 NM_006221.1 3 TCACCCCCAATTA TTG TT C A
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AAGACCCAAA ACCC AC
TTA CC T
GAM336755 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GAM336755 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336756 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GTAG CGTG GGACCCGTT
GTC TCCTG
GAM336756 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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TT CACTC
GAM336756 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336756 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336757 GAGGTCTGTTG ACT NM_020482.3 3 ATTTTTCTAAACG AG --- C A
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C TAGACA GCAA TCTTTTTA
CT TTC A
GAM336760 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336760 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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ACGGTA G G
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GAM336760 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TGACGTGAGGTCGGACCCG
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GAM336760 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336760 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GAM336760 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336760 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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GAM336760 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM336760 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336761 CAGAGAATGGC GLUL NM_002065.3 3 AGGCCAGCTGTGG C GG T A
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TCTTTTG GTGTCGAC GGA
T -- C
GAM336761 CAGAGAATGGC TNFSF5 NM_000074.1 3 CGGACAGTTATTC C CAC T A
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TCTCTTACT TTGACAGG
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GAM336762 GTCTTGATCTC IAPP NM_000415.1 3 CACAAGGTCAGGA T A
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CAGAGCT GAGGACTGGAACAC
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GAM336762 GTCTTGATCTC IL1A NM_000575.3 5 CAGAAGAGTAAGA TC G - G A
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CAGAACTAG GA TG GAA AC
GA A A G
GAM336763 AGGGCTGTGGG ACE NM_000789.2 3 ACACACCCCACAC A T C- C A
TGTGGCTGTGC CCCAGCCCA GGGCTG GGGTGTGG TGTG
CCCGAC CCCACACC ACAC
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GAM336763 AGGGCTGTGGG APBB2 NM_173075.1 5 AAAGAGCCCCACC --- T GTGC A
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TAG C GAAA
GAM336763 AGGGCTGTGGG APBB2 NM_173075.1 5 GCACAGCCCCTGC -------- TG TGT A
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TTGGCGT CCGACACG
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GAM336763 AGGGCTGTGGG CHAT NM_020984.1 5 GCACAGCCTGGGC A T G --- A
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TCCGAC TC ACG CCGACACG
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GAM336763 AGGGCTGTGGG FOS NM_005252.2 3 AGGCAGCCGGCAC - --- - GC A
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T TC CCG ACACCCACG CCGACG
A TGA G GA
GAM336763 AGGGCTGTGGG LRP1 NM_002332.1 3 GCTTGCCCGCTCC -- T - TGT A
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TCC CGACACCC CGCC G CG
TT T C TT-
GAM336763 AGGGCTGTGGG SLC17A7 NM_020309.1 3 GCACCCACACCCC A CTGT CT A
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GAM336764 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
GCCTGGGTGAT GAGTGCAGT ACTGCACTCCAGCCTGGGTGAT
TGACGTGAGGTCGGACCCGCTG

GAM336764 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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GAM336764 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC TG A
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ACGTGAGGTCGGACCC TG
CA GT
GAM336764 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG TG A
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TGACGTGAGGTCGGACCC TG
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GAM336765 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
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GAM336765 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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ACGTGAGGTCGGACCC TG
CA GT
GAM336765 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG TG A
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GAM336768 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
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GAM336768 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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TACGGCA GT
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TGACGTGAGGTCGGACCC TG
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T TATG-
GAM336770 TGTGGCTAGTT PLAU NM_002658.1 3 GTCTCAGTTTCAC CT TT A
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ACACT TCA TTTGACTCTG
T- C-
GAM336771 TGTGGCTAGTT ADAMTS5 NM_007038.1 3 ATCTCAGTGTATC T TTTGA A
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T TATG-
GAM336771 TGTGGCTAGTT PLAU NM_002658.1 3 GTCTCAGTTTCAC CT TT A
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ACACT TCA TTTGACTCTG
T- C-
GAM336772 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336772 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336772 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM336772 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336772 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCCG
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TGACGTGAGGTCGGACCC TG
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GAM336772 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336772 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TC CTGTGTCT TACTCTC
C --- C
GAM336775 AGAGACACAGA FOS NM_005252.2 3 CAGGCCTGGGTCT A T GAGA A
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TCTCTGTGTCTG GT CC
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GAM336775 AGAGACACAGA HD NM_002111.3 3 TCCCCCATGTGCC AC-- A A A
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TCTC TGTC GTGTACCC CT
GCAC C C
GAM336775 AGAGACACAGA IGF1 NM_000618.2 3 TCTTTTATCTGTG A G -- A
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CT TGTGTCTGTGT ATTTTCT
- A CT
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CT TGTGTCTGTGT ATTTTCT
A A CT
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CTTT GTCT TACCCTCT
C AG CTC
GAM336775 AGAGACACAGA MAPK10 NM_138981.1 3 CATCCAGCATGTG AG -- GA A
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TCTCTGTG TGTGTAC CCT
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GAM336776 GCAAGTGCTGT ADAM17 NM_003183.3 3 TCTTTTATATTGA GCA --- - A
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TCACGAC AGT ATATTTTCT
CAG AAT T
GAM336776 GCAAGTGCTGT APPBP2 NM_006380.2 3 TCTTCCATGTGGA GCA GT A
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TTATGG GTGTACCTTCT
AAC AG
GAM336776 GCAAGTGCTGT IGF1 NM_000618.2 3 TTTTCCATATAGA - GTC A
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TGT TCACGA TATACCTTTT
A GA-
GAM336777 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336778 ACAGGGCTAAG CAV1 NM_001753.3 3 CAGCAAACTCTTT - CT T A
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TGTC CC TTTCT CAAACGAC
A CT -
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CAC TTT
GAM336781 TACCAGTGTCA PRND NM_012409.1 3 ACTCAGAGGCTGA TAC C T A
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GTCACAGTCGGAG AC CA
ACA - T
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GTCACAGTCGGAG AC CA
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TCGATGTAG AG CCCAGA
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CTGCTGGGTTT TGTAGCT AGCTACATT TC GGGTTT
TCGATGTAG AG CCCAGA
A TT--
GAM336785 CCGTAAAATGT CAV2 NM_001233.2 3 AAGATGTTTCATT CC----- TTC A
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CATTTTAC TTTGTAGAA
TATATGT ---
GAM336785 AAAGCTTTGTT PRND NM_012409.1 3 CAGATACACAAGT TTG --- B
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TTTCGG GAGTG ACATAGAC
--- AAC
GAM336786 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336787 TCACTGTAAAC IGF1 NM_000618.2 3 CGGGCTGTTTGTT T CT T- A
TCAAACTCCTG TTACAGTGT CACTGTAAA CAAAC CCTG
GTGACATTT GTTTG GGGC
T T- TC
GAM336788 AAAGTGTGTTA DHCR24 NM_014762.1 3 TGCTTTCCTAGAT TT T- C A
TCTAGGTAGTC CCACACTTT AAAGTGTG ATCTAGG AGT
TTTCACAC TAGATCC TCG
C- TT T
GAM336789 ATGCCCTTCCT FLNB NM_001457.1 3 AATGGTTGGGGGA A - - G A
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G A T A

GAM336789 ATGCCCTTCCT GYPA NM_002099.2 3 GGAGGCTGGGAAG C -- ATG A
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TACGGGAAG GGAAGG CGG
C GT AGG
GAM336790 TATGGCAAAGT PRND NM_012409.1 3 AGAGACAGTGTTT T A C A
CACTGATTTCC TGCCATG TATGGCAAAG CACTG TTTC
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TCAGATG T AG
GAM336792 TGAGGGGGAAG GYPA NM_002099.2 3 ACACACACATTTA GG A A
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A TC
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AC TCTTCTTCCACACACGT
A T
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GAM336793 TGAGGGGGAAG GYPA NM_002099.2 3 ACACACACATTTA GG A A
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GAM336794 AACCTGTCATT APBA2 NM_005503.2 5 ACTGTCCTGTGGA AA AT - A
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GGGCAG AGGT TCCTGTCA
TG AC G
GAM336794 AACCTGTCATT FLNB NM_001457.1 3 GCTGGCTTTGGAA TG A A
CCAAGGACAGT TGAGGTT AACC TCATTCCAAGG CAGT
TTGG AGTAAGGTTTC GTCG
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GAM336795 TGGCTCTGTGC BCHE NM_000055.1 3 AGATATTAAAATA TGGC C--- A
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AGACACGAA ATTATAGA
TAAA TAAA
GAM336795 TGGCTCTGTGC PSEN2 NM_000447.1 5 AGAAACTGAGGCC - T A A
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C - A
GAM336796 GTTCACAGTTC BACE NM_012104.2 3 TGTTATTCTCGGA AGCCT A
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CCC C
GAM336797 TGAGGGAGGAA FLNB NM_001457.1 3 TCATCCCAAGGTC TGA - AG A
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GTA G G-
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GAM336799 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM336800 GTTAGGAAATG HTR2C NM_000868.1 3 CTCACAGCACATT G TAC A
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TAATT TTTACACGA ACTC
G C--
GAM336801 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336804 GAGTAACAGCA IGF1 NM_000618.2 3 GCTCCAGGGTTTC G CAC A A
CTCACTGGAGT TGTTACTA AGTAACAG TC CTGGAGT
TCATTGTC GG GACCTCG
A TTT -
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ACACGTGT TGTCCG
ATTT TGC
GAM336807 GAAACCTACAC BACE NM_138973.1 3 GTTAGTGGGAAGA CACA- A
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GAM336809 TAAGGCATTTT APOC1 NM_001645.2 3 ACCAATAAAAATC TA C - A
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TCC TAAAAATA CCA
CA - A
GAM336809 TAAGGCATTTT BACE NM_138973.1 3 ACCATGAAGTGAA TAA ----- A
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TTAGA T C

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C TGT
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GAM336809 TAAGGCATTTT MAPK10 NM_138981.1 5 ACCATAAAAACTT GCA- A
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GAM336809 TAAGGCATTTT SNCAIP NM_005460.1 3 AATATCAGGATGC T GT A
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GAM336810 GTCTTGTTCCA APLP2 NM_001642.1 3 TGCTGAGAAATGG G ---- C A
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A GGGG T
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A GGGG T
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AGAGACCCAGA ACTGAGATA TGTCTCAGTGT GA CAG
ATAGAGTCACA CT GTC
GAA CA A
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TGT TGA GTC TTTCGTGAA
CC G G
GAM336815 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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ACGGTA G G
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GAM336815 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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TGACGTGAGGTCGGACCC TG
CC
GAM336815 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336815 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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GAM336815 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM336815 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336816 CTGTGCATGTT BACE NM_138972.1 3 GTCAGTAGGAGAG G GATATC A
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GAM336816 CTGTGCATGTT TRPM2 NM_003307.1 3 GCCAGGATGCAGG C C GA A
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T C AC
GAM336817 CTGTGCATGTT BACE NM_138972.1 3 GTCAGTAGGAGAG G GATATC A
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GACACGTA GA GACTG
G GAGGAT
GAM336817 CTGTGCATGTT TRPM2 NM_003307.1 3 GCCAGGATGCAGG C C GA A
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ACAC TACGG GTAGGACCG
T C AC
GAM336818 TGAGGTGGGAT ADAM10 NM_001110.1 3 GGCTAGGAGGCTC -- - - GA A
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ACTCCACC CT GG GG TCGG
AG C A A-
GAM336818 TGAGGTGGGAT APP NM_000484.1 5 GGCGGATCCCACT T G CGAG A
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CTC ACCCTAGG CGG
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CTCC ACCCTAGG CTC GG
T G C G

GAM336818 TGAGGTGGGAT TGFB1 NM_000660.1 5 GGCCTCGGCCCGG TGAGG ATC A
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GCCC GGCTCCGG
GCGAG ---
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CCATTTAGGGT GTGGGCCAGT ACTGGCCCAC TCC TTT GGT
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C C GA
GAM336820 TGAGTTTAAGC APBA1 NM_001163.2 3 CAGACTTCTTAAA T AAGC A
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GAM336820 TGAGTTTAAGC CNTF NM_000614.2 3 CAGACTCTTTAGT T ---- GA A
TAAGAAGTCTG TGATTTAAACTCT GAGTTTAA GCTAA AGTCTG
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T TAGT TC
GAM336820 TGAGTTTAAGC PSEN1 NM_000021.2 3 CGGAACTCTTCAT - CT- AG A
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A TAC CA
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TA G G
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ACGGTA G G
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GAM336821 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336821 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336821 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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T C TA
GAM336823 TGGACAATGAA IAPP NM_000415.1 3 AAGGTCAGGAGTT ACAA AC A
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ACC GCTT GGACTGGAA
AGA- GA
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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GAM336824 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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C -- GAGAG A -
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TA G G
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TGACGTGAGGTCGGACCC TG
CC
GAM336825 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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TA G G
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ACGGTA G G
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CGTG GGACCCGTT
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TGACGTGAGGTCGGACCC TG
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GAM336826 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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- GGG T
GAM336829 GTACAGTGGGT AVP NM_000490.2 5 TTGGTCCCTTATC - TG TGT A
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CA TGTT TC TCCCTGGTT
C GT TAT

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CGT GTCACCCACGTTT GGT
TTAC A- A
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GGGG G A
GAM336830 ATCTTTCTTAA IGF1 NM_000618.2 3 TGGTCCTGGAGTT TTC C A
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TAGCCCC AA GTCACCGTC
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TCGT C
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TA G G
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ACGGTA G G
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GAM336835 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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CGA CACACT CCCAGGGT
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GAM336837 GTTGGGTGTGA MAPT NM_173727.1 5 TGGGACCCCAGCC GTT--- T -- A
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T CTCAC CTCC CCCCAGGGT
TTGACT T GA
GAM336838 ATGGCCTTTTC ADAM10 NM_001110.1 3 TCAGGATAACAGA G - C A
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TG TGG AAGAGA AATAGGACT
G T C
GAM336838 ATGGCCTTTTC ADAM17 NM_021832.1 3 CCAGAAGTGAAAA AT T ATC A
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TCGGAAAAG GAA GACC
CG T ---

GAM336838 ATGGCCTTTTC APBA1 NM_001163.2 3 CCAGGATAAAAGG AT CT--- --- A
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T CCG AAAGGGG ATAGGACC
T- TCAAT AAA
GAM336838 ATGGCCTTTTC FHL2 NM_001450.2 3 CCAGGGAAAGAGA AT C-- A A
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CCG AAAAGAGAA GGGACC
TC CTC A
GAM336838 ATGGCCTTTTC TNFSF5 NM_000074.1 3 CTATGAAAAGACA TTC A C A
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GAM336840 GGAGGCAGTGG BACE NM_138972.1 3 ACTCACTGCATTT AGTGGT C A
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TCTCC TC TCGA CGTCACTCG
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GAM336840 GGAGGCAGTGG IGF1 NM_000618.2 3 GCTCACTGCAACC CAGT A
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CCTCC CCAACGTCACTCG
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GAM336840 GGAGGCAGTGG PRND NM_012409.1 3 GCTCACTGCAGCC T A
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GAM336841 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
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GAM336842 CTCAGATACTT IGF1 NM_000618.2 3 CTCAGCCTCCCAA ATAC A
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GAM336842 CTCAGATACTT PRND NM_012409.1 3 CTCGGCCTCCCAA A - A
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GGGTC GTGAA CCCTCCGGCTC
- A
GAM336844 AGATGGAGTTT ACT NM_020482.3 5 TATTCTACTCAAA - AG A
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GAM336846 CATTGGGTATC HD NM_002111.3 3 TCTATGTAGGTGA CA -- C A
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GACCT GTAGTGGATGT TCT
TC TT A
GAM336847 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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GAM336848 GTATGTGTGGG FLNB NM_001457.1 3 GGGCTGAGAAGAT GTGT - A
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CATG CCTAGA GAGTCGGG
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GAM336849 GTATGTGTGGG FLNB NM_001457.1 3 GGGCTGAGAAGAT GTGT - A
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CATG CCTAGA GAGTCGGG
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TA G G
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GAM336852 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336852 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GAM336854 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TTTTCACAGA AAAATTA
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A G GTTC
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TA G G
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TCGA CGTCACT GA CTAGCA
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A C CT
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C

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G T GA
GAM336892 GGCAGCTGTGC ARHA NM_001664.1 3 GCCCTCCTCTGCA CAGCT T A
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CTGTC CACGTCTC CCCTC
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CTGT GACACGTC CG CTCCA
- - A
GAM336892 GGCAGCTGTGC OLR1 NM_002543.1 3 TCCACCCACTCTT AG C - T A
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TCG GACAC TCTCACCC CC
-- T A T
GAM336892 GGCAGCTGTGC SNCA NM_000345.2 3 GCCCCCACTCAGC G --- A A
AGAGTGGGGGT ATTTCGGTGCT GGCA CTG TGC GAGTGGGGGT
TCGT GGC ACG CTCACCCCCG
- TTT A
GAM336892 GGCAGCTGTGC UBB NM_018955.2 3 GCATTACTCTGCA AGCT GG A
AGAGTGGGGGT CTATAGCC GGC GTGCAGAGTGG GT
CCG CACGTCTCATT CG
ATAT A-
GAM336893 GGCAGCTGTGC ACE NM_152831.1 3 GCCCCCACTAGGC A T AG A
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TCG TG CACG TCACCCCCG
G T GA
GAM336893 GGCAGCTGTGC ARHA NM_001664.1 3 GCCCTCCTCTGCA CAGCT T A
AGAGTGGGGGT CTCCCACC GG GTGCAGAG GGGGGT
CC CACGTCTC CTCCCG
ACCCT -
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AGAGTGGGGGT ACCTGTC GGCAG GTGCAGAG GGGGG
CTGTC CACGTCTC CCCTC
-- T T
GAM336893 GGCAGCTGTGC NOTCH1 NM_017617.2 3 ACCTCAGCCTGCA G A G A
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CTGT GACACGTC CG CTCCA
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GAM336893 GGCAGCTGTGC OLR1 NM_002543.1 3 TCCACCCACTCTT AG C - T A
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TCG GACAC TCTCACCC CC
-- T A T
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TCGT GGC ACG CTCACCCCCG
- TTT A
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CCG CACGTCTCATT CG
ATAT A-
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- CAA
GAM336894 AGTATTTCTTG GYPA NM_002099.2 3 TATTAATAAAACT - T-- GA A
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TCGT AAAGG CAAAATAATT
T TTT AT
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TC TGAA GAACAAAA GA TCT
T C - G
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TCATAA GAACAAAATAAC
- CAA
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TCGT AAAGG CAAAATAATT
T TTT AT
GAM336895 AGTATTTCTTG NOTCH1 NM_017617.2 3 TCTGAGAAAACAA T - A G A
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T C - G
GAM336896 GAAGCATTGTG CAV1 NM_001753.3 3 AACCTGTTACCTA - TT AGA A
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TTTC GT CAT TTGTCCAA
A TT CCA
GAM336896 GAAGCATTGTG HD NM_002111.3 3 CTCCTGTTTCTCA ATT- TT A
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TTTCG TACTCTTTGTCC
ATCC TC
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GTCCGTCAG TC AATTCA
TT CAA
GAM336897 TAGGCAGTCTC CAV1 NM_001753.3 3 AACCAACAACCTC CTCA GT A
AGTTGTTGGGT AACTGCCTA TAGGCAGT GTTGTTGG

ATCCGTCA CAACAACC
ACTC AA
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AGTTGTTGGGT ACTGCCTG TAGGCAGTCT AGTT TTGGGT
GTCCGTCAGA TCAA GACTCG
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GAM336898 AACCCTGGAGG APPBP2 NM_006380.2 3 TGCAACCTCCGCC T A A
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TTGGG CCTCCG CTCCAACGT
C C
GAM336898 AACCCTGGAGG IGF1 NM_000618.2 3 TGCAACCTCCACC T CA A
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TTGGG CCTCC CTCCAACGT
T AC
GAM336898 AACCCTGGAGG IGF1 NM_000618.2 3 TGCTCTGTGGCTC G G TT A
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TTGGGACCTC GT TCT CGT
G G --
GAM336898 AACCCTGGAGG MAPK10 NM_002753.2 3 AGCCTGCTTCTTC A C T- G A
CAGAGGTTGCG CCCAGGGTT AACCCTGG GG AGAGGT GC
TTGGGACC CC TCTTCG CG
- T TC A
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TTG GGG TTCCGTCTCCGGCGT
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GGACC TCCGTCTCCGACGT
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ACACGTGT TGTCCG
ATTT TGC
GAM336903 TAGTGCAATGG ACE NM_152831.1 3 CCAAGATCGCACC T C C A
CGCGATCTCGG ATTGCACTC AGTGCAATGG GCGATCT GG
TCACGTTACC CGCTAGA CC
C A A
GAM336903 TAGTGCAATGG MTNR1A NM_005958.2 3 CCGAGATCGCGCC TA AA A
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CATG ACCGCGCTAGAGCC
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GTAACG GAGG TCGGACCCGTT
G G
GAM336906 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
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GTAG CGTG GGACCCGTT
GTC TCCTG

GAM336906 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
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GTGACGTGAGGTCGGACCCG
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GT CGT TGGACCCGTT
TT CACTC
GAM336906 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
AGCCTGGGCAA GTGCAGTG CATTGCACTCCAGCCTGGG
GTGACGTGAGGTCGGACCC
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GAM336906 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTAGCG GGACCCGT
GCGA--- G
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GTAG CGTG GGACCCGTT
GTC TCCTG
GAM336907 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
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GTGACGTGAGGTCGGACCCG
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GAM336907 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
GAM336907 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GTGACGTGAGGTCGGACCC
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GAM336907 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTGACGTGAGGTCGGACCC
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GAM336907 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GTAGCG GGACCCGT
GCGA--- G
GAM336907 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
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GAM336907 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- A
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G AACGTGAGGTCGGACCCGTT
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GAM336907 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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GAM336908 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336909 CTGCTAAACAT IGF1 NM_000618.2 3 GCAGAAGGCTAGG CA CA--- A
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GACGATTT AGGAT GACG
TA CGGAA
GAM336911 AAGACACTTTC GYPA NM_002099.2 3 ACTTCTATATATG C C A A
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TTCTGT AAG AT TATCTTCA
- T A
GAM336913 ACAAAAAATAC IGF1 NM_000618.2 3 GGCTAATTTTTTG ACA AC- A
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TTTTTA TTTTTAATCGG
TAA GGT
GAM336913 ACAAAAAATAC PRND NM_012409.1 3 GACTAATTTTGTA A G CT A
GAAAATTAGCT TTTTTAGT AC AAAAATAC AAAATTAG
TG TTTTTATG TTTTAATC
A - AG

GAM336914 ACAAAAAATAC IGF1 NM_000618.2 3 GGCTAATTTTTTG ACA AC- A
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TTTTTA TTTTTAATCGG
TAA GGT
GAM336914 ACAAAAAATAC PRND NM_012409.1 3 GACTAATTTTGTA A G CT A
GAAAATTAGCT TTTTTAGT AC AAAAATAC AAAATTAG
TG TTTTTATG TTTTAATC
A - AG
GAM336916 CTTCTTTGGGG FLNB NM_001457.1 3 GGGTAAAAGCCCA C T -- A
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AAGA ATCCCACCCGA ATGGG
A C AA
GAM336917 TTTGGTCTAAT GFAP NM_002055.2 3 TCCTCTTGAAGAT TG CTA A
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AA CG TAGAAGTTCTCCT
GT ---
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GA TAGA GAGGTTCTCCT
C G GTC
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AA CG TAGAAGTTCTCCT
GT ---
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GA TAGA GAGGTTCTCCT
C G GTC
GAM336919 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336920 GCCTGTAATCC APPBP2 NM_006380.2 3 CCGAGTAGCTGGG A
CAGCTACTTGG ATTACAGGC GCCTGTAATCCCAGCTACTTGG
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GAM336920 GCCTGTAATCC CASP3 NM_032991.1 3 CCATTTATCTGGG T C CT A
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TGG TATTAGGGTC AT ACC
- T TT
GAM336920 GCCTGTAATCC FHL2 NM_001450.2 5 CCAAGTAGCTGGG A A
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GAM336920 GCCTGTAATCC GFAP NM_002055.2 3 CCTGTGTAGCTGG GC TT- A
CAGCTACTTGG GATTATAGAT CTGTAATCCCAGCTAC GG
GATATTAGGGTCGATG CC
TA TGT
GAM336920 GCCTGTAATCC IGF1 NM_000618.2 3 CCAAATTGCTGGG TAC A
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TTA
GAM336920 GCCTGTAATCC IGF1 NM_000618.2 3 CTGAGTAGCTGGG TG A
CAGCTACTTGG ATTACAGGC GCCTGTAATCCCAGCTACT G
CGGACATTAGGGTCGATGA C
GT
GAM336920 GCCTGTAATCC PRND NM_012409.1 3 CCAAAGTGCTGGG T - A
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TGGACATTAGGGTCG TGAA CC
- A
GAM336920 GCCTGTAATCC PRND NM_012409.1 3 CCAAGTAGGTGGG G A
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GAM336920 GCCTGTAATCC PRND NM_012409.1 3 CCGAGTAGCTGGG A
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A G G
GAM336921 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GTGACGTGAGGTCGGACCCG
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GAM336921 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG TAA A
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GAM336921 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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A G G
GAM336922 CACTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GTGACGTGAGGTCGGACCCG
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GAM336922 CACTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG TAA A
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GAM336922 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CAC A
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GAM336922 CACTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
GAM336923 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
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GGTAGGTC TCCTG
GAM336923 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336923 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336923 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM336923 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336923 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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ACGTGAGGTCGGACCCGTTG
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GAM336923 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM336923 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGTTG

GAM336924 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336925 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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GAM336925 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM336925 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM336925 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336926 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
GCCTGGGCAAC GGAGGGCAAT TGC CTCC AGCCTGGGCAAC
ACG GAGG TCGGACCCGTTG
TA G G
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G

GAM336926 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM336926 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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CTG
GAM336926 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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GAM336926 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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TGACGTGAGGTCGGACCC TG
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GAM336926 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336926 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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ACGTGAGGTCGGACCCGTTG
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GAM336926 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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TACGGCA
GAM336926 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM336927 TTAGAAAGAAT FOS NM_005252.2 3 TTCCTGGCAATAG AGAA- TCC A
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AGTCTT ATAACGGTC
GTGTG CTT
GAM336931 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336931 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336931 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM336931 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC

TGACGTGAGGTCGGACCCG
CTG
GAM336931 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM336931 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM336931 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336931 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM336931 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM336931 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM336932 GGCTGGAGAGT ADAM17 NM_021832.1 3 GGGCCCTGATTTG GAG - A
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TTGAC TCGTTTAGTCC GGG
GGG C
GAM336932 GGCTGGAGAGT APPBP2 NM_006380.2 3 TGACATTTGGATT GTA AG--- T A
AAATCAGGTCT AATCTCCAGCT GGCTGGAGA AATC GTC
TCGACCTCT TTAG CAG
AA- GTTTA T
GAM336932 GGCTGGAGAGT GFAP NM_002055.2 3 AGACCTGAGCTCC C A AAA A
AAATCAGGTCT CCACC GG TGG GAGT TCAGGTCT
CC ACC CTCG AGTCCAGA
- C ---
GAM336932 GGCTGGAGAGT GLUL NM_002065.3 3 AGACCTGACGTAC GG AA A
AAATCAGGTCT TCTGGTT GGCT AGAGTA TCAGGTCT
TTGG TCTCAT AGTCCAGA
-- GC
GAM336932 GGCTGGAGAGT OGDH NM_002541.1 3 AGATCTGATTTAT TG -- A
AAATCAGGTCT TTATTTTGGTT GGC GA GAGTAAATCAGGTCT
TTG TT TTTATTTAGTCTAGA
GT TA
GAM336932 GGCTGGAGAGT PRNP NM_000311.1 3 AGACCTGAGATGC - AG AA A
AAATCAGGTCT TGGTCAAGCC GGCT GG AGTA TCAGGTCT
CCGA CT TCGT AGTCCAGA
A GG AG

GAM336933 TCTTGTGAAAT AVP NM_000490.2 5 GGGGTCCACCTGT T AA- CT A
CTGTGGACCCT GTGCACCAGG TCT GTG AT GTGGACCCT
GGA CAC TG CACCTGGGG
C GTG TC
GAM336934 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM336934 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336934 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM336934 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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CTG
GAM336934 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM336934 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM336934 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336934 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM336934 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM336934 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM336937 TAAGGAGCACA IL1B NM_000576.2 3 AATTTGGACTGGT T - AAC- A
CAACCTAGATT GTGCTCTCTTT AAG GAGCACAC CTAGATT
TTC CTCGTGTG GGTTTAA
T T GTCA
GAM336938 TAAGGAGCACA IL1B NM_000576.2 3 AATTTGGACTGGT T - AAC- A
CAACCTAGATT GTGCTCTCTTT AAG GAGCACAC CTAGATT

TTC CTCGTGTG GGTTTAA
T T GTCA
GAM336939 TTTCATTCATT CASP3 NM_032991.1 3 TCCATGAAGGCAG T TCA - A
TCTTTCATGGA AGCCATGGAC TTCAT TTT CTTTCATGGA
AGGTA AGA GGAAGTACCT
C CCG C
GAM336939 TTTCATTCATT FPRL1 NM_001462.1 5 TGGTGAGAGAAAG - - GGA A
TCTTTCATGGA TGAAATGAAA TTTCATT CATTT CTTTCAT
AAAGTAA GTGAA GAGAGTG
A A GT-
GAM336939 TTTCATTCATT GLUL NM_002065.3 5 TCCACGAAGAAAG A T A--- A
TCTTTCATGGA CAACGAATGAAA TTTCATTC TT CTTTC TGGA
AAAGTAAG AA GAAAG ACCT
C C AAGC
GAM336941 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336942 AAAGACTTGGC HD NM_002111.3 3 CAGGGCTGTGATG AAA G -- A
TGTCAGCCCTG GGCGAGTCCCG GACTTG CTGTCA GCCCTG
CTGAGC GGTAGT CGGGAC
GCC G GT
GAM336945 AGTGAGCTATG FHL2 NM_001450.2 5 AGTGGCACGATCT AT A GT A
ATCATGCCGGT CAGCTCACT AGTGAGCT GATC TGCCG
TCACTCGA CTAG ACGGT
CT C GA
GAM336945 AGTGAGCTATG IGF1 NM_000618.2 3 AGTGGCATGATCT AT GT A
ATCATGCCGGT CGGCTCACT AGTGAGCT GATCATGCCG
TCACTCGG CTAGTACGGT
CT GA
GAM336945 AGTGAGCTATG PRND NM_012409.1 3 AACGGCATGATTT T GT A
ATCATGCCGGT TGGCTCACT AGTGAGCTA GATCATGCCG
TCACTCGGT TTAGTACGGC
T AA
GAM336946 GGAGCTGTAGT APP NM_000484.1 3 ATGTGGGAAGAAA AGC AG A
TTTTCCCACAT CAAACCC GG TGT TTTTTCCCACAT
CC ACA AAGAAGGGTGTA
CAA --
GAM336946 GGAGCTGTAGT BACE NM_138973.1 3 ATGTTGGGAAAAA GT - A
TTTTCCCACAT CTGGCTTT GGAGCT AGTTTTTCCCA CAT
TTTCGG TCAAAAAGGGT GTA
-- T
GAM336946 GGAGCTGTAGT IGF1 NM_000618.2 3 ATGTGGGAAGCAT CTGT T A
TTTTCCCACAT TTGATTTTC GGAG AGT TTTCCCACAT
CTTT TTA GAAGGGTGTA
TAGT C
GAM336946 GGAGCTGTAGT PRNP NM_000311.1 3 ATGTGGGAAACCC ---- TGT TT A
TTTTCCCACAT TTTTGCGTGGTCC GGA GC AG TTTCCCACAT
CCT CG TC AAAGGGTGTA
GGTG TTT CC

GAM336947 CAGTGGATGAT MAPT NM_016835.1 3 CCACAGAAACCCT TGATGT A
GTTTTCTGTGG GTTTTATTG CAGTGGA TTTCTGTGG
GTTATTT AAAGACACC
TGTCCC
GAM336950 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336951 AGATGACACAG APP NM_000484.1 3 TTTCCTGATCACT A C AGC A
AGCTCAGGAAA ATGCATTT AGATG CA AG TCAGGAAA
TTTAC GT TC AGTCCTTT
- A ACT
GAM336956 GTCTTCCTCCG APPBP2 NM_006380.2 5 GGAGGTGGGGGCC G ----- A
TCCCCACCTCC TTCGGGAGGAGGA TCTTCCTCC GTCCCCACCTCC
G AGGAGGAGG CGGGGGTGGAGG
G GCTTC
GAM336956 GTCTTCCTCCG BAX NM_138763.1 3 AGGGGTGGGGATT --- - C A
TCCCCACCTCC GGGGGACATGGGC GTCT TCCTCCG TCCCCACCTC
CGGG AGGGGGT AGGGGTGGGG
TAC T A
GAM336956 GTCTTCCTCCG HD NM_002111.3 3 GGAGCTCGGGACG TCC- CAC A
TCCCCACCTCC GATAGTAGAC GTCT TCCGTCCC CTCC
CAGA AGGCAGGG GAGG
TGAT CTC
GAM336956 GTCTTCCTCCG MPO NM_000250.1 5 GGAGGTGGGGTCC T TCCGT A
TCCCCACCTCC TTGGAAGC G CTTCC CCCCACCTCC
C GAAGG GGGGTGGAGG
- TTCCT
GAM336956 GTCTTCCTCCG NGB NM_021257.2 3 CCAGGTGGGGAGG C- G CC A
TCCCCACCTCC GGCTGGGGAC GTCTTC TCC TCCCCACCT
CAGGGG GGG AGGGGTGGA
TC G CC
GAM336956 GTCTTCCTCCG NGB NM_021257.2 3 GGAGGTGGGAGAG -- CGTC A
TCCCCACCTCC GATGGGGC GTCT TCCTC CCCACCTCC
CGGG AGGAG GGGTGGAGG
GT A---
GAM336957 TTAAACTTCCC APLP1 NM_005166.2 3 CTAGGGCAGCAGG AC C A
TGCTGCCCCAG GAGTCTTGA TTAA TTCCCTGCTGCCC AG
AGTT GAGGGACGACGGG TC
CT A
GAM336958 AGGTGGAGTTT ADAM10 NM_001110.1 3 ATGGGAAAACTTC AGG TTTGC A
TGCTTTCCCAT ACTCCAAAG TGGAGT TTTCCCAT
ACCTCA AAAGGGTA
GAA CTTCA
GAM336958 AGGTGGAGTTT BACE NM_138973.1 3 ATGGGAAAGGGTG AG G--- A
TGCTTTCCCAT AGGACTTCACAA GTGGAGTTTT CTTTCCCAT
CACTTCAGGA GAAAGGGTA
AA GTGG
GAM336958 AGGTGGAGTTT DHCR24 NM_014762.1 3 GTGGGAAAGTGGA A G TG A
TGCTTTCCCAT GTCCACCC GGTGGA TTT CTTTCCCAT

CCACCT GAG GAAAGGGTG
C - GT
GAM336959 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM336961 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
GGACACTTGTA GCAGG TCTGCTGTG CACTTGT
GGACGACAC GTGGACG
CG---
GAM336961 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC GA- -- A
GGACACTTGTA AGTAACAGTATT TGCTGT TGGA CACTTGTA
ATGACA ATCT GTGAACAT
TT ATG TT
GAM336961 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
GGACACTTGTA AGTAACAGTATTT TGCTGT TGGA CACTTGTA
C ATGACA ATCT GTGAACAT
CTTT ATG TT
GAM336961 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
GGACACTTGTA TCACAACAAGA TCT TGTGATGGA TTGT
AGA ACACTACCT AACG
ACA TCAAA
GAM336961 TCTGCTGTGAT PSEN2 NM_000447.1 5 CCAAGTGTCCGGG CT GA T A
GGACACTTGTA ATTCAGA TCTG GT TGGACACTTG
AGAC TA GCCTGTGAAC
T- GG C
GAM336961 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 ACAATGTCCAAGA A-- C A
GGACACTTGTA CACAGCAGA TCTGCTGTG TGGACA TTGT
AGACGACAC ACCTGT AACA
AGA -
GAM336961 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 GACAATGTCCAAG A-- C A A
GGACACTTGTA ACACAGCAGA TCTGCTGTG TGGACA TTGT
AGACGACAC ACCTGT AACA
AGA - G
GAM336962 ATAACTGTGAA BACE2 NM_138991.1 3 TAATTGCCTTTGA GTGA A
GAGGCAATTGT GGTTAT ATAACT AGAGGCAATTG
TATTGG TTTCCGTTAAT
AG--
GAM336963 AGCTCCAGGAG APLP1 NM_005166.2 3 CCTCCCCTCTTCC A CT CA A
CTGGCAGGAGG TGGAGCC GCTCCAGGAG GG GGAGG
CGAGGTCCTT CC CCTCC
C CT --
GAM336963 AGCTCCAGGAG BAX NM_004324.2 3 CCTTCTGCCCTCC A - CT A
CTGGCAGGAGG CTGGAGCC GCTCCAGG AG GGCAGGAGG
CGAGGTCC TC CCGTCTTCC
C C --
GAM336963 AGCTCCAGGAG CTSK NM_000396.2 5 TTTCCAGCCGATC - GC A A
CTGGCAGGAGG ACTGGAGCT AGCTCCAG GA TGGC GGAGG
TCGAGGTC CT GCCG CCTTT
A A- A

GAM336963 AGCTCCAGGAG GFAP NM_002055.2 3 CCTCCTGCCACCT TC G --- A
CTGGCAGGAGG GCTGCTGCTGCT AGC CAG AGC TGGCAGGAGG
TCG GTC TCG ACCGTCCTCC
TC G TCC
GAM336963 AGCTCCAGGAG GFAP NM_002055.2 3 CGTCCTGCCACCT A AGC GG A
CTGGCAGGAGG GGGGCA GCTCCAGG TGGCAGGA
CGGGGTCC ACCGTCCT
A --- GC
GAM336963 AGCTCCAGGAG MME NM_007287.1 3 CTTGTTGCCACAG GAGC G A
CTGGCAGGAGG CTGGAGCT AGCTCCAG TGGCAG AGG
TCGAGGTC ACCGTT TTC
GAC- G
GAM336963 AGCTCCAGGAG NCSTN NM_015331.1 3 TTTCTTGCCAGCT A CCAG A
CTGGCAGGAGG CAGCA GCT GAGCTGGCAGGAGG
CGA CTCGACCGTTCTTT
A ----
GAM336963 AGCTCCAGGAG S100B NM_006272.1 3 AATCCGAGCCAGC A A- GG A
CTGGCAGGAGG TCTGGGGGCT AGCTCC GGAGCTGGC GGA
TCGGGG TCTCGACCG CCT
G AG AA
GAM336964 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336965 TGACAGAGGTA GAL NM_015973.2 3 AGCCTCCTGGGCA T G ACA A
CATAGGAGGCT TGTTTGTCT GACAGA GT TAGGAGGCT
CTGTTT TA GTCCTCCGA
T G CGG
GAM336965 TGACAGAGGTA MME NM_000902.2 3 TGCACCTATGTAG A G AG T A
CATAGGAGGCT CTCTGCA TG CAGAG TACATAGG GC
AC GTCTC ATGTATCC CG
- G A- T
GAM336966 TGACAGAGGTA GAL NM_015973.2 3 AGCCTCCTGGGCA T G ACA A
CATAGGAGGCT TGTTTGTCT GACAGA GT TAGGAGGCT
CTGTTT TA GTCCTCCGA
T G CGG
GAM336966 TGACAGAGGTA MME NM_000902.2 3 TGCACCTATGTAG A G AG T A
CATAGGAGGCT CTCTGCA TG CAGAG TACATAGG GC
AC GTCTC ATGTATCC CG
- G A- T
GAM336967 TTCCCTTAGGT CAV1 NM_001753.3 3 GGTCATTTTATGT GTC A A
CTGGAATGGTA TAAGGGAA TTCCCTTAG TGGAATGGT
AAGGGAATT ATTTTACTG
GT- G
GAM336968 AGAGATAAAGA APBA1 NM_001163.2 3 AGCCAACCTTAAA AG - ----- A A
GGTTTAGGCAG CCTCTTCTATTGC AG ATA AAGAGGTTTA GGC
T TC TAT TTCTCCAAAT CCG
GT C TCCAA A
GAM336968 AGAGATAAAGA CNTF NM_000614.2 3 CTGCACCTCTTTG AGA----- TTAG A
GGTTTAGGCAG TCACAGGGTG GATAAAGAGGT GCAG

CTGTTTCTCCA CGTC
GTGGGACA ----
GAM336969 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336970 TGTGACTCGTA IGF1 NM_000618.2 3 GGGATTACAGGCA T A A A
CTTGTAATCCT TGAGCCACC GTG CTCGT CTTGTAATCCT
CAC GAGTA GGACATTAGGG
C C C
GAM336970 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T ACTC A
CTTGTAATCCT CCCACCACC GTG GTACTTGTAATCCT
CAC CGTGGACATTAGGG
C CACC
GAM336970 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T A A
CTTGTAATCCT TGAGCCACC GTG CTCGTACTTGTAATCCT
CAC GAGTGTGGACATTAGGG
C C
GAM336970 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T CT--- A
CTTGTAATCCT TGTGCCATCATG GTGA CGTACTTGTAATCCT
TACT GTGTGGACATTAGGG
G ACCGT
GAM336971 TGTGACTCGTA IGF1 NM_000618.2 3 GGGATTACAGGCA T A A A
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CAC GAGTA GGACATTAGGG
C C C
GAM336971 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T ACTC A
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CAC CGTGGACATTAGGG
C CACC
GAM336971 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T A A
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CAC GAGTGTGGACATTAGGG
C C
GAM336971 TGTGACTCGTA PRND NM_012409.1 3 GGGATTACAGGTG T CT--- A
CTTGTAATCCT TGTGCCATCATG GTGA CGTACTTGTAATCCT
TACT GTGTGGACATTAGGG
G ACCGT
GAM336972 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM336974 TGACTCAGTGG ACE NM_152831.1 3 CTCTCCATCTTCC A ---- CC A
AAGATCCAGAG ACGAAATGGGCCA TG CTCA GTGGAAGAT AGAG
AC GGGT CACCTTCTA TCTC
C AAAG CC
GAM336974 TGACTCAGTGG IGF1 NM_000618.2 5 CTCTGGATTTCCT CT T- A A
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ACT GTT CCT TTAGGTCTC
TC TT -

GAM336975 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
GCCTGGGCAAC GGAGGGCAAT TGC CTCC AGCCTGGGCAAC
ACG GAGG TCGGACCCGTTG
TA G G
GAM336975 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM336975 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM336975 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
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CTG
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GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
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GAM336975 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM336975 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM336975 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM336975 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM336975 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM336976 ATGCCTGTAAT APPBP2 NM_006380.2 3 CGAGTAGCTGGGA AT - T A
CCCAGCACTTT TTACAGGCTC GCCTGTAATCCCAGC ACTT
CGGACATTAGGGTCG TGAG
CT A C
GAM336976 ATGCCTGTAAT IGF1 NM_000618.2 3 AAATTGCTGGGAT CTTT A
CCCAGCACTTT TACAGGCAT ATGCCTGTAATCCCAGCA
TACGGACATTAGGGTCGT
TAAA
GAM336976 ATGCCTGTAAT IGF1 NM_000618.2 3 TGAGTAGCTGGGA A - T A
CCCAGCACTTT TTACAGGCAC TGCCTGTAATCCCAGC ACTT

ACGGACATTAGGGTCG TGAG
C A T
GAM336976 ATGCCTGTAAT PRND NM_012409.1 3 AAAGTGCTGGGAT A
CCCAGCACTTT TACAGGTGT ATGCCTGTAATCCCAGCACTTT
TGTGGACATTAGGGTCGTGAAA

GAM336976 ATGCCTGTAAT PRND NM_012409.1 3 CGAGTAGCTGGGA - T A
CCCAGCACTTT TTACAGGTGT ATGCCTGTAATCCCAGC ACTT
TGTGGACATTAGGGTCG TGAG
A C
GAM336978 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
GGACACTTGTA GCAGG TCTGCTGTG CACTTGT
GGACGACAC GTGGACG
CG---
GAM336978 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC GA- -- A
GGACACTTGTA AGTAACAGTATT TGCTGT TGGA CACTTGTA
ATGACA ATCT GTGAACAT
TT ATG TT
GAM336978 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
GGACACTTGTA AGTAACAGTATTT TGCTGT TGGA CACTTGTA
C ATGACA ATCT GTGAACAT
CTTT ATG TT
GAM336978 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
GGACACTTGTA TCACAACAAGA TCT TGTGATGGA TTGT
AGA ACACTACCT AACG
ACA TCAAA
GAM336978 TCTGCTGTGAT PSEN2 NM_000447.1 5 CCAAGTGTCCGGG CT GA T A
GGACACTTGTA ATTCAGA TCTG GT TGGACACTTG
AGAC TA GCCTGTGAAC
T- GG C
GAM336978 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 ACAATGTCCAAGA A-- C A
GGACACTTGTA CACAGCAGA TCTGCTGTG TGGACA TTGT
AGACGACAC ACCTGT AACA
AGA -
GAM336978 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 GACAATGTCCAAG A-- C A A
GGACACTTGTA ACACAGCAGA TCTGCTGTG TGGACA TTGT
AGACGACAC ACCTGT AACA
AGA - G
GAM336979 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
GGACACTTGTA GCAGG TCTGCTGTG CACTTGT
GGACGACAC GTGGACG
CG---
GAM336979 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC GA- -- A
GGACACTTGTA AGTAACAGTATT TGCTGT TGGA CACTTGTA
ATGACA ATCT GTGAACAT
TT ATG TT
GAM336979 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
GGACACTTGTA AGTAACAGTATTT TGCTGT TGGA CACTTGTA
C ATGACA ATCT GTGAACAT
CTTT ATG TT

GAM336979 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
GGACACTTGTA TCACAACAAGA TCT TGTGATGGA TTGT
AGA ACACTACCT AACG
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GAM336979 TCTGCTGTGAT PSEN2 NM_000447.1 5 CCAAGTGTCCGGG CT GA T A
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T- GG C
GAM336979 TCTGCTGTGAT TNFRSF6 NM_152872.1 3 ACAATGTCCAAGA A-- C A
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AGA -
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GAM336980 TCTGCTGTGAT HD NM_002111.3 3 GCAGGTGGCCACA ATGGA A
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GAM336980 TCTGCTGTGAT HTR2C NM_000868.1 3 TACAAGTGTTTCT TC-- GA- -- A
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GAM336980 TCTGCTGTGAT IGF1 NM_000618.2 3 GCAAAAACTTCCA GC- CAC-- A
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T- GG C
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CTTT ATG TT
GAM336981 TCTGCTGTGAT IGF1 NM_000618.2 3 TACTAGTCCATCA -- ACTTG A
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AGA CGATACTACCTG
TC ATCAT
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AGAC TA GCCTGTGAAC
T- GG
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TACAG ATCCTGAGA TGGT
TC G --
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GACTCCGT TCTCTC CTTC
G CA--
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G GACTCCGTCCTCT TGGGT
TAGCGAATT ---
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G A---
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G TC-

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CTG CC T
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CT CG CC CCCGAGTCCTC
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- - GA
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- TG A
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ACTCTACCA AGTA GATG
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ACACGTGT TGTCCG
ATTT TGC
GAM336992 CCGTAAAATGT CAV2 NM_001233.2 3 AAGATGTTTCATT CC----- TTC A
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TATATGT ---
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GAM336995 ATTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GAM336995 ATTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A A
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- AA TT
GAM337000 GTATGTATTTA HD NM_002111.3 3 TAGACACATCTAT A T-- - T A
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C TTT C T
GAM337000 GTATGTATTTA MME NM_000902.2 3 GTGAACCAAGATC A-- ---- TT A
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TA G G

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GAM337001 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GAM337004 GAGGCGGGAAG RAGE NM_014226.1 5 ATCCTAGTGCGGG AAG - G A
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GAM337007 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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GAM337007 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
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C -- GAGAG A -
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GAM337007 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM337009 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ATTT TGC
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GAM337011 TGCTAGGTTTT BACE NM_138973.1 3 GGAGAAGGAAAAG G TC A
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GAM337013 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ATTT TGC
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GAM337015 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM337015 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GAM337015 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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AGTG GTA
GAM337018 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM337019 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM337022 TCAGTCGTTTC ACE NM_152831.1 3 GCTGGGAGACACA TC GTTTCTC- A
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TCAG AGAGGGTCG
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GAM337022 TCAGTCGTTTC FLNB NM_001457.1 3 GTTGGGGGAGAGA TCA G A
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CGA -
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C - GG TAGG
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G- C CC
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GACC T T
GAM337025 TCATCCTTTTC FPRL1 NM_001462.1 5 CACAGGTTGTAGA - - T A
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A T C
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GAM337027 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
GAM337027 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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GAM337027 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM337027 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
GAM337027 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
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GAM337027 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM337027 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GAM337028 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G

GAM337028 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
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CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337028 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM337028 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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TGACGTGAGGTCGGACCC TG
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GAM337028 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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A TGTCGTC GGG ACCTCGTCC
A TCCAC T C
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CA GACTC TATT
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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C -- GAGAG A -
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GAM337033 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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GT C G
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GAM337041 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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TACGGCA GT

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TTA C AC
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ATTT TGC
GAM337046 AGTGGCTTTGA MME NM_007288.1 3 AAATTATAGTTTC - T GA A
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A ATTCCTCACCAGG GT TGG C
A GGGG GT A
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GG TCA CGACCCTAATGTCCG
AC T
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GAM337060 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
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C -- GAGAG A -

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TCAA C G- T
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C -- GAGAG A -
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A C ACC
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AAG- CT
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TA G G
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TA G G
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GT C GT T
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GAM337077 GGTTCTCAAAT PLAU NM_002658.1 3 AGATGTCCCTTTC TCT AT A
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GAM337077 GGTTCTCAAAT PSEN1 NM_000021.2 3 TGTGTCCCTCGGT ---- - AA T A
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CCA AGA GT GCTCCCTGTG
TCAA C G- T
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C- AT GG
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- GG GG
GAM337138 TGAGGCAGGAG ABCD1 NM_000033.2 5 ATCCTTCCAGCCA A- C AGG A
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GCCC --
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TCCGTCCTC CCGT TCTCC
TG CT C
GAM337140 TGAGGACAGGA AVP NM_000490.2 5 TCTCTGGTGCAGC A ---- T A
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ACTCCTGTCC CCGACG CTC
- TGGT T
GAM337140 TGAGGACAGGA IL1B NM_000576.2 3 GCTAAGAGGATCT - GTG-- A
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ACT CCTGTCCTCTAG TCG
A GAGAA
GAM337140 TGAGGACAGGA MAPK10 NM_138980.1 5 TTTTACAAATTTC ----- - TT A
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TTTTT A T-
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TGGACT - T
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C G CCACG
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ACGGTA G G
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- CCT C
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TCCTCC CGAGGTGTCT
TAC- GC
GAM337161 AGGGGGTTTAG HD NM_002111.3 3 AAAATGTGAAGCT C GGGT A
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TCCCCCAAGTCGA GTGT
A AAAA
GAM337162 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337162 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337162 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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TGACGTGAGGTCGGACCC TG
CC

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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM337162 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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GACG GAGGTAGGA TCCCTC
C A GT A
GAM337166 ACTGCACTCCA FHL2 NM_001450.2 5 TGTCGCCCAGGCT T - GC A
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TGACGTGAGGT GGACCC CT
C G GT
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C G
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TGT GAGG GGACCCCTCG
CTG T --
GAM337167 TTTGCAGCTTC CNTF NM_000614.2 3 TCTGAACTTTGGA G T T A
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AGG GTCGAAGGTTT AAG CT
G C T
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TGA GG
GAM337168 TGAGATGAACC APPBP2 NM_006380.2 5 CTGGGACGGAACC T TAC---- A
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GCTCT CTTGGGCC GGGTC
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CTTT CGTCCTTATA CTCG
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- G ACA
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C A GT A
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C CT
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G CCCGTATC

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CT CT-
GAM337174 GCAGGTGTGCA CNTF NM_000614.2 3 GGGGTGTGATTTG G TG A A
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CGT CGT GTTTAGTGT GGG
G GT G
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CG TCCGC CGTTTAGTGTT
AC C CCA
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CGTTC CACGTTTAGTG GA
- AG T
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A AGT A TT
GAM337177 GTGAAGAAGTT APPBP2 NM_006380.2 3 AAGGATGATTTTA GTG CT---- A
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TTTTTCAAC AGTAGGAA
TAA AATTTT
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AC GGG
GAM337179 CTGTGGGTGAG OGDH NM_002541.1 3 CCTCCCCACCAGT - GA- - A A
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T GAC C C
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T CGT
GAM337180 AGTGCTTTGAT TNFRSF6 NM_152875.1 3 TCTTTCTCAGGCA - TA- T A
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A CGG T
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TTACGAAA CTA ACTCTTTC
A CGG T
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GTAG CGTG GGACCCGTT
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GAM337183 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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TT CACTC
GAM337183 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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GAM337185 ATTGTTCTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG - A
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T C
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CA TTA
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G C G
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G C G
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GAM337192 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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GAM337193 TATTTGTTTTT S100B NM_006272.1 3 TATCCAGCATTAT TATT- ---- A
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TCGTC TTAT

GAM337194 CTGGCTCCCAG ABCD1 NM_000033.2 3 AGGGGGAGCTGTC - GA - A
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GT GGG C C
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CCC- CA
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CGT-- T
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C CC CC--
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AGTCA GTACCCGGACCT
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GAM337200 TGCGCCCCTGT CRAT NM_144782.1 5 CGGCCCAGAGGGT - GTA AA A
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GCGCGGG GG GAGACCCG
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G TGCGG GACGTGAGG CCCGTT
G T TCGGA

GAM337202 TTGAGGTCATC IL1A NM_000575.3 5 CAACACCATTGAA T G A T A
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ACTC GG AG TTACCACAAC
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GAM337203 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TA G G

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C -- GAGAG A -
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C -- GAGAG A -
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GAM337243 TGCTACATTTC IGF1 NM_000618.2 3 CTTAGAATAAAAG C C T A
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C CA
GAM337254 TTTCCTGTTTT BACE NM_138973.1 3 GTCTCCATTTTTC TT---- G A
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TGT A
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AC C GAGTCAAA GAG TCGTCG
T A AG G G
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CCGAGTCA ACGAGTCGTT
T TGT TA
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ACCG AGTCAAA AGT GTCAT
G GA A
GAM337255 TGGCTCAGTTT S100B NM_006272.1 3 CACTACCGGGGGC TTT AGC-- A
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CCG CAA TCCAACGGC CA
C T TG -
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ATTT TGC
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GTAAC CC G
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GTAAC CC G
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TATTC GT GTCAAATTAG
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ACGGTA G G
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GAM337273 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TAAAA C A
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C GTTTCG TG-
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GAM337283 GGCACTGAGAA MAPT NM_173727.1 3 ATCCTGTTTGCTA T-- A--- A
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TTG GTTA
GAM337285 GGAGGAGGTGT APPBP2 NM_006380.2 3 CTCATTTCTGTAT G A A A
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GAM337285 GGAGGAGGTGT GLUL NM_002065.3 3 TTAATTTCTTCAC -- GAA A
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- A C
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AC CG
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TT A TT
GAM337291 ATAAGCACAGG HD NM_002111.3 3 GACAGCAGCCTCC ATA ------ - A
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GAM337291 ATAAGCACAGG HTR2C NM_000868.1 3 GGCAGAACCTAGT ATA - -- A
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TAC T GA
GAM337291 ATAAGCACAGG LRP1 NM_002332.1 3 GACAGGCCCTCCC ATA C TT A
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ACC - CG
GAM337291 ATAAGCACAGG TRPM2 NM_003307.1 5 GGCGGTGGAGACT ATAA ---- A
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GAM337292 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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GAM337293 TTCAGTTCTTG GFAP NM_002055.2 3 CTGTGGGCAGGTG T - G - A
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GG AAG T
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C C T
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C C GT
GAM337300 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG T A A
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TGACGTGAGGT GGAC CGCTG
C C
GAM337300 ACTGCACTCCA HD NM_002111.3 3 TTTAGTCAGGAGA A CA G C A
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GACGTGAG AGGACT ATT
A -- G T
GAM337300 ACTGCACTCCA IGF1 NM_000618.2 3 GCACTGTCCCCCA T ------ AC A
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T TGACGTGAGGT GGAC TCAC
C CCCCTG G-
GAM337300 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG T A TG A
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TGACGTGAGGT GGAC C TG
C C GT

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ACACGTGT TGTCCG
ATTT TGC
GAM337302 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM337303 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
GAM337303 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337303 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM337303 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM337303 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGTTG

GAM337304 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
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ACGGTA G G
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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AC TTTT
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ACACGTGT TGTCCG
ATTT TGC

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GTAG CGTG GGACCCGTT
GTC TCCTG
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GTGACGTGAGGTCGGACCCG
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GAM337311 CATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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G G
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GTAG CGTG GGACCCGTT
GTC TCCTG
GAM337313 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
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GTGACGTGAGGTCGGACCCG
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GAM337313 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
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GT CGT TGGACCCGTT
TT CACTC
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GAM337313 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GAM337313 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GAM337313 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
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TAACG GAGG TCGGACCC TG
G G GT
GAM337314 ATTGCACTTCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG A
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GAM337314 ATTGCACTTCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG T A
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TGACGTGAGGTCGGACCC CTG
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AACGTGAGGTCGGACCC TG
C GT
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AACG AG GGACCCACTG
A GT- GA
GAM337315 AGGTGGCACTG ACE NM_152831.1 3 TTCACCTCCTTGG C GT- - A
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TCCACCGT GCG CC CCACTT
C GTT T
GAM337315 AGGTGGCACTG APBB2 NM_173075.1 3 CCCACCCCTCCTA A GG TGT A
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TCA GTGAT CCCCACCC
A A- CCT
GAM337315 AGGTGGCACTG FOS NM_005252.2 3 CCGGCACCCACAA A G - G A
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G - A G
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TCC C GA AC CCCCACCC
GT CA A -
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ACC TGT
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TTCC TCCTT TTACGAC
TCG -- A
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TTCC CTTC TG TTTACGACT
- G- GC
GAM337317 GAGGTGAAGGA TFCP2 NM_005653.2 3 CCAGTGGCTGCTC ---- AA A A
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CTCCACTTCCTT GT GTGAC
CCTC CG C
GAM337318 GAGGTGAAGGA APBB2 NM_173075.1 3 ACAGCATTTTCCT TGA CA A A
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TTCC TCCTT TTACGAC
TCG -- A
GAM337318 GAGGTGAAGGA SNCA NM_000345.2 3 TCAGCATTTCGGT T GA -- A
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TTCC CTTC TG TTTACGACT
- G- GC
GAM337318 GAGGTGAAGGA TFCP2 NM_005653.2 3 CCAGTGGCTGCTC ---- AA A A
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CTCCACTTCCTT GT GTGAC
CCTC CG C

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TTCC TCCTT TTACGAC
TCG -- A
GAM337319 GAGGTGAAGGA SNCA NM_000345.2 3 TCAGCATTTCGGT T GA -- A
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TTCC CTTC TG TTTACGACT
- G- GC
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CCTC CG C
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CA ACC-
GAM337320 TCCCCAAGCCT GFAP NM_002055.2 3 ACGCTGGTAGAGA - AGC G A
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GGGGGTTCGGG C TG TCG
- - A T
GAM337321 ACCTGCATTCC FHL2 NM_001450.2 5 GTCGCCCAGGCTG AC C- A
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GACGTGAGGTCGGAC GCTG
GT CC
GAM337321 ACCTGCATTCC IGF1 NM_000618.2 3 GTCCCCCAGGCTG AC CT- A
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GACGTGAGGTCGGAC CTG
GT CCC
GAM337321 ACCTGCATTCC MAPT NM_173727.1 5 AGCAGCAGGCTGG T-- T AC A
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GAM337324 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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ACGGTA G G
GAM337324 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
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GAM337324 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
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GAM337324 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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GAM337326 CTTTGGCCACG ABCD1 NM_000033.2 3 ATTCGTAGCCATC CT ---- A
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GAM337326 CTTTGGCCACG DHCR24 NM_014762.1 3 AGACATGTCCCCG T AAT A
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GAM337327 CTTTGGCCACG ABCD1 NM_000033.2 3 ATTCGTAGCCATC CT ---- A
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AACCGGTGCCTCT ATGCTTA
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GAM337328 CTTTGGCCACG DHCR24 NM_014762.1 3 AGACATGTCCCCG T AAT A
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T AGA

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ACACGTGT TGTCCG
ATTT TGC
GAM337331 TTGCACTCCAG APPBP2 NM_006380.2 3 TGTTGCCCAGGCT A - A
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G G
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GACGTGAGGTCGGACCC TGT
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GAM337331 TTGCACTCCAG PRND NM_012409.1 3 TGTTGCCCAGGCT A
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AGC GGTCGGACC GTTGT
TCT- G
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ACACGTGT TGTCCG
ATTT TGC
GAM337334 GAGAGTGCTTT BACE NM_138971.1 3 ATTCTCCAACCCA GT- CC A
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TTCTTATGAAACCCA TCT
ACC TA
GAM337334 GAGAGTGCTTT SLC17A7 NM_020309.1 3 TGCCTCAGGCCTA -- GT- C A
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GAM337336 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM337337 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
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GAM337337 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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GAM337337 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GAM337337 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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TCG CCTAC TC GGTCGTCTT
A G TTAA G
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TCACCCTACTTC TTG TC
-- A CTC
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TC CCCTACCTCG GTC TCT
- AA C CT

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GAM337341 AGTGGGATGGA PRND NM_012409.1 3 CTTCTGCTTCCAC TG --- GTC A
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TT CCT ACCT TCGTCTTC
GT GGC ---
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TTGTC CGACGTCCACCAG
G - TC
GAM337344 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
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C A GT A
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TA G G
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TA G G
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TA G G
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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C A GT A
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C G GT
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C CT
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TG G GAGGTAGGACC TCTC
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CA C G
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TGACGTGAGGT GGACCC TTG
C G
GAM337355 ACTGCACTCCA TNF NM_000594.2 3 GCTCCCCAGGGGA ACT - AT A
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TGT GAGG GGACCCCTCG
CTG T --
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CGTT CGTCCATCTG CTGA
C C AA
GAM337356 AGCAGCGCAGG RAGE NM_014226.1 3 TGTCCCTTCCCAG A TA T T A
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A -- T T
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C A GT A
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TGACGTGAGGT GGACCC CT
C G GT
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C CT
GAM337357 ACTGCACTCCA PLAU NM_002658.1 3 CCTCTGGCCAGGA TG A- -- C A
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CTG T --
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GAM337358 AGGCTTTTGGA HTR2A NM_000621.1 3 GCAATTGCTTCTC - -- TA A
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A CA TA
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ACCGTGGT CCTT TTCC
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GAM337361 GTGGCACCATT IGF1 NM_000618.2 3 TTTTAGTATAATG GAGT A
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GAM337363 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ATTT TGC
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C CC TC GA
GAM337364 AGAAGGCTCGC NCSTN NM_015331.1 3 CCCCTGAGGACAG AG- G C- A
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C T T
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GAM337366 ACTGCACTCCA IGF1 NM_000618.2 3 CTGTCCCCCAGGC T -- A
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AC - - C
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C C - G
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GAM337373 TGGAGGCAGGT NGB NM_021257.2 3 CCAGCCATCTGCA AG A- A
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GAM337397 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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ACGGTA G G
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C -- GAGAG A -
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C -- GAGAG A -
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C -- GAGAG A -

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GAM337447 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
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GAM337447 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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GACG AGGTCGGAC CC GTT
C -- GAGAG A -
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GAM337448 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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TA G G
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GAM337459 CTGGTGAGGAA ADAMTS5 NM_007038.1 3 TACTCTGCTTCTC C GA T A
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CCG ---
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GAM337461 AATCCCAGCTA IGF1 NM_000618.2 3 AGCCTCCCAAATT TACTC A
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- TA
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GAM337478 TATGTCACTCC FLNB NM_001457.1 3 GTCATTTGGCAAA TAT - CA-- A
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TT CACTC
GAM337482 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
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CGGG TT C A
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CACCCGAC TC CC ATGGGT
C CAC T
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CATC CGGC TCCGACGGG
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A ATTCCGTGAC GAT TCG CC
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C GC
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CCTCCTC TCC ACC CGACC
G C - C
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TCCT GT GA
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G G - - C
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CC
GAM337516 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
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C -- GAGAG A -
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G G T G
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C- -

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TCG TCTCCATAGGTCCGT
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GAM337528 GGCTAGAAAGC NPY NM_000905.2 3 TTGCTCTCTGGCC CT A A A
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C AACTTGG --
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ATTT TGC
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ATTT TGC
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C -- GAGAG A -
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C -- GAGAG A -
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T TTT GT
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TA G G
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GAM337567 TGTAAACATCC APPBP2 NM_006380.2 3 CTTTAAGTAGGGA G CG G A
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GAM337567 TGTAAACATCC CASP3 NM_032991.1 3 CTTCCAGTCAGGT ACAT CC A
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GAM337568 TGTAAACATCC APPBP2 NM_006380.2 3 CTTTAAGTAGGGA G CG G A
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ATTT TGC

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ATTT TGC
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TACGGCA
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GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337619 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM337620 AATCATCATTA APBB2 NM_173075.1 3 GAAACTTCAAAAT AA TT A A
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A AGTAGT TAAAACTTCAAA
AA -- G
GAM337620 AATCATCATTA MAPT NM_005910.2 3 GGGACTTCAAAAT AA - A A
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A GGTAGTGA TAAAACTTCAGG
AG C G
GAM337621 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
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ACACGTGT TGTCCG
ATTT TGC
GAM337623 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM337624 TCTAAGAGAAA APPBP2 NM_006380.2 3 TTTGAACTTCCCA TAA- AAA- A
GGAAGTTCAGA ACCTTGTTTGA TC GAG GGAAGTTCAGA
AG TTC CCTTCAAGTTT
TTTG CAAC
GAM337624 TCTAAGAGAAA CNTF NM_000614.2 3 GTTGATTTAAACT AAAGG T A A
GGAAGTTCAGA CTTAGA TCTAAGAG AAGT CAG
AGATTCTC TTTA GTT
AAA-- - G
GAM337624 TCTAAGAGAAA CNTF NM_000614.2 3 TCTGAACTTTGGA A- AGAAAG A
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AGG TC TTTCAAGTCT
GG GAAGG-
GAM337624 TCTAAGAGAAA CRH NM_000756.1 3 TTTGAAACAACTT TC GAAG A
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GTTCTCTTTC AAGTTT
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G C CC
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GGAT TCAAGTCT
GAGGTGAGG-
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G G
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GTAG CGTG GGACCCGTT
GTC TCCTG
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GTGACGTGAGGTCGGACCCG
C

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GTGACGTGAGGTCGGACCCG
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GT CGT TGGACCCGTT
TT CACTC
GAM337625 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
AGCCTGGGCAA GTGCAGTG CATTGCACTCCAGCCTGGG
GTGACGTGAGGTCGGACCC
CC
GAM337625 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
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GTGACGTGAGGTCGGACCC
CCT
GAM337625 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
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GTAGCG GGACCCGT
GCGA--- G
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337626 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337626 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337626 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CTG
GAM337626 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC

TGACGTGAGGTCGGACCCG
CT
GAM337626 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337626 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM337626 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM337626 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM337626 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337627 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337627 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
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A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337627 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337627 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
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TGACGTGAGGTCGGACCCG
CTG
GAM337627 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM337627 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337627 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -

GAM337627 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM337627 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM337627 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337628 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
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ACACGTGT TGTCCG
ATTT TGC
GAM337629 TGTGCACAACA APP NM_000484.1 3 CGTGCCTGTTTTA ACAT TTG A
TGCAGGTTTGT TGTGCACA TGTGCACA GCAGGT
ACACGTGT TGTCCG
ATTT TGC
GAM337630 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337630 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337630 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337630 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CTG
GAM337630 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
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TGACGTGAGGTCGGACCCG
CT
GAM337630 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337630 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM337630 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC

ACGTGAGGTCGGACCCGTTG
CA
GAM337630 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
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TACGGCA
GAM337630 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
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TGACGTGAGGTCGGACCCGTTG

GAM337631 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
GCCTGGGCAAC GGAGGGCAAT TGC CTCC AGCCTGGGCAAC
ACG GAGG TCGGACCCGTTG
TA G G
GAM337631 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337631 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337631 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CTG
GAM337631 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM337631 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337631 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM337631 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM337631 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM337631 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337632 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337632 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337632 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA
CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337632 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CTG
GAM337632 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM337632 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337632 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM337632 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM337632 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
GCCTGGGCAAC GAGTGCAACGGCA TGCACTCCAGCCTGGGCAAC
T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM337632 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337633 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC A - A
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ACG GAGG TCGGACCCGTTG
TA G G
GAM337633 ACTGCACTCCA APPBP2 NM_006380.2 3 GTTGCCCAGGCTG AC---- A - A
GCCTGGGCAAC GGAGGGCAATGGC TGC CTCC AGCCTGGGCAAC
A ACG GAGG TCGGACCCGTTG
ACGGTA G G
GAM337633 ACTGCACTCCA BACE2 NM_012105.3 3 TTGCCCAGGGTCC ACT----- TCCAG A
GCCTGGGCAAC TGTGCCTGGATGG GCAC CCTGGGCAA

CGTG GGACCCGTT
GGTAGGTC TCCTG
GAM337633 ACTGCACTCCA FHL2 NM_001450.2 5 GTCGCCCAGGCTG AAC A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CTG
GAM337633 ACTGCACTCCA FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
GCCTGGGCAAC AGTGCAGT ACTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG
CT
GAM337633 ACTGCACTCCA IGF1 NM_000618.2 3 GTCCCCCAGGCTG CA A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGG AC
TGACGTGAGGTCGGACCC TG
CC
GAM337633 ACTGCACTCCA MME NM_000902.2 5 TTGACCGAGAGCA A AC ----- - C A
GCCTGGGCAAC GGCTGGAGCAGC CTGC TCCAGCCTG GG CAA
GACG AGGTCGGAC CC GTT
C -- GAGAG A -
GAM337633 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC A
GCCTGGGCAAC GAGTGCAAC TGCACTCCAGCCTGGGCAAC
ACGTGAGGTCGGACCCGTTG
CA
GAM337633 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG AC----- A
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T ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM337633 ACTGCACTCCA PRND NM_012409.1 3 GTTGCCCAGGCTG A
GCCTGGGCAAC GAGTGCAGT ACTGCACTCCAGCCTGGGCAAC
TGACGTGAGGTCGGACCCGTTG

GAM337634 CATTGCACTCC APPBP2 NM_006380.2 3 TTGCCCAGGCTGG A - A
AGCCTGGGCAA GAGGGCAATG CATTGC CTCC AGCCTGGGCAA
GTAACG GAGG TCGGACCCGTT
G G
GAM337634 CATTGCACTCC BACE2 NM_138992.1 3 TTGCCCAGGGTCC --- TCCAG A
AGCCTGGGCAA TGTGCCTGGATG CATT GCAC CCTGGGCAA
GTAG CGTG GGACCCGTT
GTC TCCTG
GAM337634 CATTGCACTCC FHL2 NM_001450.2 5 CGCCCAGGCTGGA A A
AGCCTGGGCAA GTGCAGTG CATTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
C
GAM337634 CATTGCACTCC FHL2 NM_001450.2 5 TCGCCCAGGCTGG AA A
AGCCTGGGCAA AGTGCAGTG CATTGCACTCCAGCCTGGGC
GTGACGTGAGGTCGGACCCG
CT
GAM337634 CATTGCACTCC HD NM_002111.3 3 TTGCCCAGGTCTC TT CTCCA A
AGCCTGGGCAA ACTGCTTTG CA GCA GCCTGGGCAA
GT CGT TGGACCCGTT
TT CACTC

GAM337634 CATTGCACTCC IGF1 NM_000618.2 3 CCCCCAGGCTGGA CA A
AGCCTGGGCAA GTGCAGTG CATTGCACTCCAGCCTGGG
GTGACGTGAGGTCGGACCC
CC
GAM337634 CATTGCACTCC IGF1 NM_000618.2 3 TCCCCCAGGCTGG CAA A
AGCCTGGGCAA AGTGCAGTG CATTGCACTCCAGCCTGGG
GTGACGTGAGGTCGGACCC
CCT
GAM337634 CATTGCACTCC PRND NM_012409.1 3 GTGCCCAGGAGCG ACTCCAG A A
AGCCTGGGCAA GCGATG CATTGC CCTGGGCA
GTAGCG GGACCCGT
GCGA--- G
GAM337634 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA A
AGCCTGGGCAA AGTGCAACG TTGCACTCCAGCCTGGGCAA
AACGTGAGGTCGGACCCGTT
GC
GAM337634 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG CA----- A
AGCCTGGGCAA AGTGCAACGGCAT TTGCACTCCAGCCTGGGCAA
G AACGTGAGGTCGGACCCGTT
GTACGGC
GAM337634 CATTGCACTCC PRND NM_012409.1 3 TTGCCCAGGCTGG A
AGCCTGGGCAA AGTGCAGTG CATTGCACTCCAGCCTGGGCAA
GTGACGTGAGGTCGGACCCGTT

GAM NAME	TARGET	GAM RNA SEQUENCE	GAM FUNCTION	GAM TAR POS	DIS
GAM25	IGF1	AATTGCTTGAACCCA GGAAGTG	Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM25 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM25 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

A function of GAM25 is therefore inhibition of IGF1, a GAM25 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM25 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 has been established by previous studies. By the solid- phase method, Li et al. (1983) synthesized human somatomedin C, which has 70 amino acid residues and 3 disulfide bridges. Using cDNA probes in the analysis of somatic cell hybrids, Brissenden et al. (1984) and Tricoli et al. (1984) independently assigned the IGF1 structural gene to chromosome 12. Tricoli et al. (1984) regionalized the locus tentatively to 12q22- qter, where the KRAS2 (OMIM Ref. No. 190070) gene is situated. This proximity, as well as that of the HRAS1 (OMIM Ref. No. 190020) and IGF2 (OMIM Ref. No. 147470) genes on 11p and that of the NRAS (OMIM Ref. No. 164790) and NGFB (OMIM Ref. No. 162030) genes in band 1p22, suggested to Brissenden et al. (1984) that a functional or evolutionary relationship may exist between members of the RAS family of protooncogenes and growth factor genes. Chromosomal abnormalities in the region of these genes have been associated with specific forms of neoplasia. Both IGF1 and IGF2 have a striking structural homology to proinsulin. Deficiency of IGF1 was proposed as the nature of the basic defect in the African pygmy (OMIM Ref. No. 265850) and possibly also in the Laron type of dwarfism (OMIM Ref. No. 262500). The homology of chromosomes 11 and 12 is supported by the finding of yet another pair of structurally homologous loci on these 2 chromosomes. See 146000 for description of the work of Mullis et al. (1991) suggesting that the IGF1 gene may be the site of the mutation causing one form of hypochondroplasia. Using stored sera from men followed in the Baltimore Longitudinal Study on Aging, Harman et al. (2000) investigated whether the circulating IGF1 level is an independent predictor of prostate cancer and compared its predictive value with those of IGF2, IGFBP3, and prostate- specific antigen (PSA; 176820). High IGF1 and low IGF2 were independently associated with increased risk for prostate cancer, but PSA level was a much stronger predictor of prostate cancer than either IGF1 or IGF2. The absence

of a relationship of IGF1 to prostate size is inconsistent with increased ascertainment in men with large prostates as the source of greater prostate cancer risk associated with IGF1. The authors concluded that IGF2 may inhibit both prostate growth and development of prostate cancer. Low birthweight is associated with later risk of type 2 diabetes and related disorders. Vaessen et al. (2002) studied the relationship between low birthweight and a polymorphism in the IGF1 gene that raises risk of type 2 diabetes and myocardial infarction. They recorded birthweight and obtained DNA for 463 adults. Individuals who did not have the wildtype allele of the polymorphism had a 215- gram lower birthweight than those homozygous for the wildtype allele. The data lent support to the hypothesis that genetic variation affecting fetal growth could account for the association between low birthweight and susceptibility to diabetes and cardiovascular disease in later life. Postnatal growth and development are coordinated by genetic and environmental influences and numerous growth factors. Le Roith et al. (2001) reviewed the essential role that the GH- IGFI axis plays in these processes. Although the GH- IGFI axis is a closely coordinated system, both GH and IGFI have independent actions, many of which have become apparent more recently following the characterization of clinical syndromes and the development of mouse models. Genetic manipulation of mice has enabled investigators to reexamine many of the established hypotheses regarding the GH- IGFI axis. Results gleaned from a mouse model created by tissue- specific gene deletion of liver IGFI (Yakar et. al, 1999; Sjogren et al. 1999) enabled investigators to reevaluate the original 'somatomedin hypothesis.' Animal model experiments lend further support to the function of IGF1. Aging skeletal muscles suffer a steady decline in mass and functional performance, and compromised muscle integrity as fibrotic invasions replace contractile tissue. The same programmed deficits in muscle structure and function are found in numerous neurodegenerative syndromes and disease- related cachexia. Musaro et al. (2001) generated a model of persistent, functional myocyte hypertrophy using a tissue- restricted transgene encoding a locally acting isoform of Igf1 that is expressed in skeletal muscle. Transgenic embryos developed normally, and postnatal increases in muscle mass and strength were not accompanied by the additional pathologic changes seen in other Igf1 transgenic models. Expression of Gata2 (OMIM Ref. No. 137295), a transcription factor normally undetected in skeletal muscle, marked hypertrophic myocytes that escaped age- related muscle atrophy and retained the proliferative response to muscle injury characteristic of younger animals. The observations were thought to suggest usefulness of localized expression of this transgene as a clinical strategy for the treatment of age- or disease- related muscle frailty.

It is appreciated that the abovementioned animal model for IGF1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the

publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny, G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N. : Localized Igf- 1 transgene expression sustains hypertrophy and regeneration in senescent skeletal muscle. Nature Genet. 27: 195-200, 2001. ; and

Le Roith, D.; Scavo, L.; Butler, A. : What is the role of circulating IGF- I? Trends Endocr. Metab. 12: 48- 52, 2001.

Further studies establishing the function and utilities of IGF1 are found in John Hopkins OMIM database record ID 147440, and in cited publications listed in Table 9, hereby incorporated herein.

GAM25	MME	AATTGCTTGAACCCA GGAAGTG	Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM25 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM25 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM25 is therefore inhibition of MME, a GAM25 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM25 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME has been established by previous studies. Common acute lymphocytic leukemia antigen is an important cell surface marker in the diagnosis of human acute lymphocytic leukemia (ALL). It is present on leukemic cells of pre- B phenotype, which represent 85% of cases of ALL. CALLA is not restricted to leukemic cells, however, and is found on a variety of normal tissues. CALLA is a glycoprotein that is particularly abundant in kidney, where it is present on the brush border of proximal tubules and on glomerular epithelium. Letarte et al. (1988) cloned a cDNA coding for CALLA and showed that the amino acid sequence deduced from the cDNA sequence is identical to that of human membrane- associated neutral endopeptidase (NEP; EC 3.4.24.11), also known as enkephalinase. NEP cleaves peptides at the amino side of hydrophobic residues and inactivates several peptide hormones including glucagon, enkephalins, substance P, neurotensin, oxytocin, and bradykinin. By cDNA transfection analysis, Shipp et al. (1989) confirmed that CALLA is a functional neutral endopeptidase of the type that has

previously been called enkephalinase. Barker et al. (1989) demonstrated that the CALLA gene, which encodes a 100- kD type II transmembrane glycoprotein, exists in a single copy of greater than 45 kb which is not rearranged in malignancies expressing cell surface CALLA. D'Adamio et al. (1989) demonstrated that the CALLA gene spans more than 80 kb and is composed of 24 exons. Animal model experiments lend further support to the function of MME. Amyloid-beta peptide (OMIM Ref. No. 104760), the pathogenic agent of Alzheimer disease (OMIM Ref. No. 104300), is a physiologic metabolite in the brain. Iwata et al. (2001) examined the role of neprilysin, a candidate amyloid- beta degrading peptidase, in the metabolism using neprilysin gene- disrupted mice. Neprilysin deficiency resulted in defects both in the degradation of exogenously administered amyloid- beta and in the metabolic suppression of the endogenous amyloid- beta levels in a gene dose-dependent manner. The regional levels of amyloid- beta in the neprilysin- deficient mouse brain were in the distinct order of hippocampus, cortex, thalamus/striatum, and cerebellum, where hippocampus has the highest level and cerebellum the lowest, correlating with the vulnerability to amyloid- beta deposition in brains of humans with Alzheimer disease. Iwata et al. (2001) concluded that even partial downregulation of neprilysin activity, which could be caused by aging, can contribute to Alzheimer disease by promoting amyloid- beta accumulation.

It is appreciated that the abovementioned animal model for MME is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard, N. P.; Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C. : Metabolic regulation of brain A- beta by neprilysin. Science 292: 1550- 1552, 2001. ; and

Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. J.; Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R. : Common acute lymphocytic leukemia antigen is identical to neutr.

Further studies establishing the function and utilities of MME are found in John Hopkins OMIM database record ID 120520, and in cited publications listed in Table 9, hereby incorporated herein.

GAM25 A A NCSTN AATTGCTTGAACCCA GGAAGTG NCSTN (Accession NM_015331.1) is another GAM25 target gene. NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM25 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM25 is therefore inhibition of NCSTN, a GAM25 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM25 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN has been established by previous studies. Nicastrin is a type 1 transmembrane glycoprotein that interacts with both presenilin- 1 (PS1; OMIM Ref. No. 104311) and presenilin- 2 (PS2; 600759) and has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, 104760) and some aspects of notch (OMIM Ref. No. 190198)/glp- 1 signaling in vivo. Nicastrin regulates gamma- secretase cleavage of the amyloid precursor protein by forming complexes with presenilins, in which most mutations causing familial early- onset Alzheimer disease (EOAD) have been found. The nicastrin gene maps to 1q23, a region that shows evidence for linkage to (Kehoe et al. 1999) and association with (Hiltunen et al. 2001) late- onset Alzheimer disease (LOAD). Dermaut et al. (2002) evaluated the contribution of genetic variations in NCSTN in 2 large series of patients with EOAD (onset at or before age 65 years) and LOAD (onset after age 65 years). In 78 familial EOAD cases, they found 14 NCSTN single-nucleotide polymorphisms (SNPs): 10 intronic SNPs, 3 silent mutations, and 1 missense mutation (N417Y). N417Y was thought not to be pathogenic, since it did not alter amyloid- beta secretion in an in vitro assay and its frequency was similar in case and control subjects. However, SNP haplotype estimation in 2 population- based series of Dutch patients with EOAD (n = 116) and LOAD (n = 240) indicated that the frequency of 1 SNP haplotype (designated HapB) was higher in the group with familial EOAD (7%), compared with the LOAD group (3%) and control group (3%). In patients with familial EOAD without the APOE epsilon- 4 allele (107741.0016), the HapB frequency further increased, to 14%, resulting in a 4- fold increased risk (odds ratio = 4.1). These results were considered compatible with an important role of gamma- secretase dysfunction in the etiology of familial EOAD.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Hiltunen, M.; Mannermaa, A.; Thompson, D.; Easton, D.; Pirskanen, M.; Helisalmi, S.; Koivisto, A. M.; Lehtovirta, M.;

Ryynanen, M.; Soininen, H. : Genome- wide linkage disequilibrium mapping of late- onset Alzheimer's disease in Finland. Neurology 57: 1663- 1668, 2001. ; and

Kehoe, P.; Wavrant- De Vrieze, F.; Crook, R.; Wu, W. S.; Holmans, P.; Fenton, I.; Spurlock, G.; Norton, N.; Williams, H.; Williams, N.; Lovestone, S.; Perez- Tur, J.; Hutton, J.; and 10.

Further studies establishing the function and utilities of NCSTN are found in John Hopkins OMIM database record ID 605254, and in cited publications listed in Table 9, hereby incorporated herein.

GAM25 OLR1 AATTGCTTGAACCCA GGAAGTG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

(OLR1, Accession NM_002543.1) is another GAM25 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM25 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM25 is therefore inhibition of OLR1, a GAM25 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM25 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 has been established by previous studies. Endothelial cell dysfunction or activation elicited by oxidatively modified low density lipoprotein (OMIM Ref. No. Ox- LDL) has been implicated in the pathogenesis of atherosclerosis. Vascular endothelial cells internalize and degrade Ox- LDL through a putative receptor- mediated pathway that does not involve macrophage scavenger receptors (see OMIM Ref. No. MSR1; 153622). To identify genes encoding Ox- LDL receptors, Sawamura et al. (1997) transfected mammalian cells with a cDNA expression library derived from bovine aortic endothelial cells and assayed for uptake of labeled Ox- LDL. They recovered a cDNA encoding an Ox- LDL receptor, which they designated lectin- like Ox- LDL receptor- 1 (LOX1). Immunofluorescence studies showed that bovine LOX1 is expressed on the cell surface. Sawamura et al. (1997) cloned a cDNA encoding the human homolog of LOX1 by screening a human lung cDNA library with the bovine LOX1 cDNA. Cells stably expressing human LOX1 showed uptake of labeled Ox- LDL. The predicted 273- amino acid human LOX1 protein is 72% identical to bovine LOX1. Its structure is similar to that of C- type lectins such as CD94 (KLRD1) and NKR- P1 (KLRB1). Northern blot analysis revealed that human LOX1 is expressed as a 2.8- kb mRNA in various tissues, with the most abundant expression in placenta. Yamanaka et al. (1998) determined that LOX1 is expressed in vascular- rich organs but not in lymphocytes. Yamanaka et al. (1998) found that the LOX1 gene spans approximately 15 kb and

consists of 6 exons. By fluorescence in situ hybridization, they mapped the gene to 12p12- p13, where genes of the natural killer cell receptors are clustered.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Sawamura, T.; Kume, N.; Aoyama, T.; Moriwaki, H.; Hoshikawa, H.; Aiba, Y.; Tanaka, T.; Miwa, S.; Katsura, Y.; Kita, T.; Masaki, T. : An endothelial receptor for oxidized low- density lipoprotein. Nature 386: 73- 77, 1997. ; and

Yamanaka, S.; Zhang, X.- Y.; Miura, K.; Kim, S.; Iwao, H. : The human gene encoding the lectin- type oxidized LDL receptor (OLR1) is a novel member of the natural killer gene complex with.

Further studies establishing the function and utilities of OLR1 are found in John Hopkins OMIM database record ID 602601, and in cited publications listed in Table 9, hereby incorporated herein.

GAM31 HTR2C TCAAGTAATCCAGGA A A TAGGCTG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is a GAM31 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM31 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM31 is therefore inhibition of HTR2C, a GAM31 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM31 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C has been established by previous studies. Hall (1947) found that DBA/2 mice exhibited genetic susceptibility to audiogenic seizures (AGSs) stimulated by a doorbell mounted in an iron tub. Thereafter, audiogenic seizures were among the intensively studied phenotypes in behavioral genetics. Brennan et al. (1997) found that null mutant mice lacking serotonin 5- HT- 2C receptors are extremely susceptible to AGSs. The onset of susceptibility was between 2 and 3 months of age, with complete penetrance in adult animals. Heisler et al. (2002) hypothesized that 5- HT receptors are expressed in POMC (OMIM Ref. No. 176830) neurons and that action at these receptors mediates a component of the anorexic effect of d- FEN (D- fenfluramine). Heisler et al. (2002) found that up to 80% of alpha- MSH neurons express HTR2C mRNA and that the pattern of coexpression was greatest in the caudal arcuate nucleus of the hypothalamus. Heisler et al.

(2002) demonstrated that direct activation of HTR2C by agonist in rats decreased their food intake and showed increased induction of FOS- like immunoreactivity in a pattern persistent with d- FEN- induced FOS- like immunoreactivity expression in the arcuate nucleus and paraventricular nucleus of the hypothalamus. Heisler et al. (2002) demonstrated that d- FEN directly activates POMC neurons, indicating that central 5- HT systems directly activate POMC neurons.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Heisler, L. K.; Cowley, M. A.; Tecott, L. H.; Fan, W.; Low, M. J.; Smart, J. L.; Rubinstein, M.; Tatro, J. B.; Marcus, J. N.; Holstege, H.; Lee, C. E.; Cone, R. D.; Elmquist, J. K. : Activation of central melanocortin pathways by fenfluramine. Science 297: 609-611, 2002. ; and

Tecott, L. H.; Sun, L. M.; Akana, S. F.; Strack, A. M.; Lowenstein, D. H.; Dallman, M. F.; Julius, D. : Eating disorder and epilepsy in mice lacking 5- HT2C serotonin receptors. Nature 3.

Further studies establishing the function and utilities of HTR2C are found in John Hopkins OMIM database record ID 312861, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 ACE AAGGTGGTGTCATGT TTTGGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM44 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM44 is therefore inhibition of ACE, a GAM44 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE has been established by previous studies. Angiotensin I- converting enzyme (EC 3.4.15.1), or kininase II, is a dipeptidyl carboxypeptidase that plays an important role in blood pressure regulation and electrolyte balance by hydrolyzing angiotensin I into angiotensin II, a potent vasopressor, and aldosterone- stimulating peptide. The enzyme is also able to inactivate bradykinin, a potent vasodilator. Howard et al. (1990) found that the testis- specific form of ACE has its own promoter within intron 12, is encoded by the 3- prime region of the

gene, and is found only in postmeiotic spermatogenic cells and sperm. Exner et al. (2001) focused on the fact that black patients with heart failure have a poorer prognosis than white patients and performed a study comparing racial groups.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Howard, T. E.; Shai, S. Y.; Langford, K. G.; Martin, B. M.; Bernstein, K. E. : Transcription of testicular angiotensin-converting enzyme (ACE) is initiated within the 12th intron of the somatic ACE gene. Molec. Cell. Biol. 10: 4294- 4302, 1990. ; and

Exner, D. V.; Dries, D. L.; Domanski, M. J.; Cohn, J. N. : Lesser response to angiotensin- converting- enzyme inhibitor therapy in black as compared with white patients with left ventricu.

Further studies establishing the function and utilities of ACE are found in John Hopkins OMIM database record ID 106180, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 APBB2 AAGGTGGTGTCATGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTTGGGG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM44 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM44 is therefore inhibition of APBB2, a GAM44 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 has been established by previous studies. The cytoplasmic domain of the Alzheimer disease locus amyloid protein precursor (APP; 107640) binds 4 human phosphotyrosine- binding (PTB) proteins; see APBA1 (OMIM Ref. No. 602414). By use of a yeast 2- hybrid screening of a human brain cDNA library, McLoughlin and Miller (1996) identified 3 of these proteins: the human homolog of Fe65 (APBB1; 602709), an Fe65- like sequence (APBB2), and an X11- like sequence (APBA2; 602712). From a human fetal brain cDNA library, Guenette et al. (1996) also cloned APBB2 based on its interaction with the carboxy terminus of APP. They showed that the APBB2 protein interacts with another amyloid protein precursor, APLP2 (OMIM Ref. No. 104776), but not with APLP1 (OMIM Ref. No. 104775). The APBB2 gene encodes a 730-

amino acid polypeptide that is 51% identical to rat Fe65. Northern blot analysis revealed that APBB2 has widespread expression in human tissues. By use of a radiation hybrid panel, Blanco et al. (1998) mapped the human APBB2 gene to chromosome 4, between the markers D4S405 (OMIM Ref. No. 4.6 cR) and D4S496 (10.1 cR).

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Blanco, G.; Irving, N. G.; Brown, S. D. M.; Miller, C. C. J.; McLoughlin, D. M. : Mapping of the human and murine X11- like genes (APBA2 and Apba2), the murine Fe65 gene (Apbb1), and the human Fe65-like gene (APBB2): genes encoding phosphotyrosine- binding domain proteins that interact with the Alzheimer's disease amyloid precursor protein. Mammalian Genome 9: 473- 475, 1998. ; and

Guenette, S. Y.; Chen, J.; Jondro, P. D.; Tanzi, R. E. : Association of a novel human FE65- like protein with the cytoplasmic domain of the beta- amyloid precursor protein. Proc. Nat. Acad.

Further studies establishing the function and utilities of APBB2 are found in John Hopkins OMIM database record ID 602710, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 APPBP2 AAGGTGGTGTCATGT TTTGGGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM44 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM44 is therefore inhibition of APPBP2, a GAM44 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 has been established by previous studies. Epithelial cell surfaces are divided into apical and basolateral domains. The basolateral sorting of cell surface proteins depends on the presence of peptide- based basolateral sorting signals (BaSS) in the cytoplasmic domains of proteins. Amyloid precursor protein (APP; 104760), a basolateral protein implicated in the pathogenesis of Alzheimer disease (AD; 104300), contains a tyrosine- based BaSS. Mutation of the tyrosine results in nonpolarized transport of APP. Using APP- BaSS as bait in a yeast 2- hybrid screen of a HeLa cell

cDNA library, followed by negative selection with a tyr- ala mutant APP- BaSS as bait and 5- prime RACE, Zheng et al. (1998) isolated a cDNA encoding amyloid beta precursor protein- binding protein- 2 (OMIM Ref. No. APPBP2), which they called PAT1 (protein interacting with APP tail- 1). The deduced 585- amino acid hydrophilic APPBP2 protein, which is identical to the uncharacterized KIAA0228 protein identified by Nagase et al. (1996), lacks signal or transmembrane sequences but contains N- and C- terminal globular structures, a coiled coil domain, several protein kinase C phosphorylation sites, and 4 imperfect C- terminal tandem repeats. Binding analysis determined that APPBP2 binds specifically to the tyrosine-containing APP- BaSS and to to the complete cytoplasmic domain of APP; it does not bind to mutant APP- BaSS. Western blot analysis showed that APPBP2 is present as a 70- kD protein in both cytosolic and, together with APP, membrane- associated cell fractions. Immunofluorescence microscopy demonstrated that APPBP2 is present in the Golgi region and that its distribution overlaps that of APP. SDS- PAGE and immunoblotting showed that APPBP2 interacts with microtubules and is functionally associated with APP transport and/or processing. By Northern blot analysis, Nagase et al. (1996) detected ubiquitous expression of KIAA0228 as an approximately 6.5-kb transcript.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.; Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N. : Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysis of cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329, 1996. ; and

Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W. : PAT1, a microtubule- interacting protein, recognizes the basolateral sorting signal of amyloid precursor protein. Proc. Nat. Aca.

Further studies establishing the function and utilities of APPBP2 are found in John Hopkins OMIM database record ID 605324, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 DHCR24 AAGGTGGTGTCATGT A A TTTGGGG 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM44 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM44 is therefore inhibition of DHCR24, a GAM44 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 has been established by previous studies. Sarkar et al. (2001) showed that the gene encoding seladin- 1, a human homolog of the Diminuto/Dwarf1 gene described in plants and C. elegans, has adenoma- specific overexpression. Northern blot analysis revealed that seladin- 1 mRNA was overexpressed in the adenoma tissue of 14 patients with Cushing syndrome in comparison to the adjacent nontumorous adrenal gland. In situ hybridization using a seladin- 1 cRNA probe showed its abundant expression in the tumor cells, whereas the nontumorous cells showed a low level of expression. Almost no apoptotic cell was detected in the tumor or in the normal adrenal cortex where seladin- 1 expression was abundant. The authors noted that their results were compatible with a recent report that seladin- 1 acts as an antiapoptotic factor in neurons (Greeve et al. 2000). In addition, expression of seladin- 1 in the normal adrenal cortex was most abundant in the zona fasciculata, suggesting its possible regulation by ACTH/cAMP. The authors concluded that the overexpression of seladin- 1 in the adenoma could be due to the abundant expression of ACTH receptor and hypothesized that seladin- 1 might be involved in the molecular events of adrenocortical tumorigenesis by facilitating steroid synthesis and cell growth. In a severely affected infant with desmosterolosis (OMIM Ref. No. 602398), Waterham et al. (2001) identified 3 mutations in the DHCR24 gene. The mutation inherited from the mother was a 1412A- C change resulting in a tyr471- to- ser (Y471S) substitution. Expression studies in S. cerevisiae showed nondetectable activity of this variant, consistent with the severe phenotype of the patient. Two mutations on the same allele were inherited from the father: an 881A- C change resulting in an asn294- to- thr substitution (N294T), and a 918G- C change resulting in a lys306- to- asn (K306N) substitution (606418.0002). Expression studies in S. cerevisiae of the N294T and K306N variants showed 14.4% and 49.8% of wildtype activity, respectively. Expression studies in S. cerevisiae of an allele with both mutations from the father showed less than 1% of wildtype activity. To determine whether one of the mutations inherited from the father was a common polymorphic variant, 50 alleles of controls were analyzed but neither mutation was detected.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Sarkar, D.; Imai, T.; Kambe, F.; Shibata, A.; Ohmori, S.; Siddiq, A.; Hayasaka, S.; Funahashi, H.; Seo, H. : The human homolog

of Diminuto/Dwarf1 gene (hDiminuto): a novel ACTH- responsive gene overexpressed in benign cortisol- producing adrenocortical adenomas. J. Clin. Endocr. Metab. 86: 5130- 5137, 2001. ; and

Greeve, I.; Hermans- Borgmeyer, I.; Brellinger, C.; Kasper, D.; Gomez- Isla, T.; Behl, C.; Levkau, B.; Nitsch, R. M. : The human DIMINUTO/DWARF1 homolog seladin- 1 confers resistance to A.

Further studies establishing the function and utilities of DHCR24 are found in John Hopkins OMIM database record ID 606418, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 PRND AAGGTGGTGTCATGT TTTGGGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM44 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM44 is therefore inhibition of PRND, a GAM44 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND has been established by previous studies. Lu et al. (2000) characterized the expression and structure of DPL by matrix-assisted laser desorption ionization (MALDI) mass spectrometry and electrospray mass spectrometry. Unlike PRP, DPL has a second disulfide bond that may contribute to the stability of its uniquely folded alpha- helical core. Lu et al. (2000) noted that PRP is most highly expressed in brain, whereas DPL is enriched in testis. Biochemical analysis determined that DPL resembles PRP in terms of solubility and protease sensitivity and undergoes cooperative and reversible unfolding during thermal denaturation. Silverman et al. (2000) showed that recombinant Dpl refolded under standard conditions adopts an alpha- helical conformation. When expressed in mouse neuroblastoma cells, Dpl possessed 2 N- linked oligosaccharides and was attached to the cell surface via a GPI anchor, much like the cellular prion protein. Dpl was present in brain samples of Rcm0 mice, which develop progressive ataxia with loss of Purkinje cells at around 70 weeks of age, but was absent in equivalent samples from asymptomatic Zurich and wildtype mice. Schroder et al. (2001) investigated whether there are any polymorphisms within the PRND gene that might cause or be involved in the development of transmissible spongiform encephalopathies. They screened the complete open reading frame of the human gene from 58 patients who had died of genetic or sporadic Creutzfeldt- Jakob disease (CJD; 123400), Alzheimer disease (OMIM Ref. No. 104300), or other neurologic disorders, and from 111 controls. They found 5

novel polymorphisms and 1 frameshift mutation. One silent polymorphism, which did not lead to an altered amino acid sequence, was also observed. Statistical analysis revealed a significant difference in the distribution of the PRND genotype at codon 174 between sporadic CJD patients and healthy controls. Like other investigators, they found no evidence that the strong association between sporadic CJD and the PRNP polymorphism at codon 129 (176640.0005) is influenced by different PRND genotypes.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo, G.; Vaccari, G.; Williams, J. L.; Harbitz, I. Ferretti, L. : Genomic organization, comparative analysis, and genetic polymorphisms of the bovine and ovine prion Doppel genes (PRND). Mammalian Genome 12: 729- 733, 2001. ; and

Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.; Sy, M.- S.; Chen, S. G. : Expression and structural characterization of the recombinant human doppel protein. Biochemistr.

Further studies establishing the function and utilities of PRND are found in John Hopkins OMIM database record ID 604263, and in cited publications listed in Table 9, hereby incorporated herein.

GAM44 PSEN1 AAGGTGGTGTCATGT PSEN1 (Accession NM_000021.2) is another GAM44 target gene. A A

TTTGGGG PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM44 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM44 is therefore inhibition of PSEN1. Accordingly, utilities of GAM44 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM55 CAV2 CTGCCATTTCCAGGA Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM55 target A A

GATCACC gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM55 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM55 is therefore inhibition of CAV2, a GAM55 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM55 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 has been established by previous studies. Scherer et al. (1996) identified a protein related to caveolin- 1 (CAV1; 601047) through microsequencing of adipocyte- derived caveolin- enriched membranes. They called the novel protein caveolin- 2. They stated that caveolins- 1 and - 2 are similar in most respects. For both caveolin- 1 and caveolin- 2, mRNAs are most abundantly expressed in white adipose tissue and are induced during adipocyte differentiation. Caveolin- 2 localizes with caveolin- 1, indicating that caveolin- 2 also localizes to caveolae. However, caveolin- 1 and caveolin- 2 differ in their functional interactions with heterotrimeric G proteins, possibly explaining why caveolins 1 and 2 are coexpressed within a single cell. Specifically, Scherer et al. (1996) found that whereas residues 82 to 101 of murine caveolin- 1 functionally suppressed the basal GTPase activity of purified heterotrimeric G proteins, the corresponding region of caveolin- 2 (which is 30% identical) had a stimulatory effect. Engelman et al. (1998) reviewed the molecular genetics of the caveolin gene family. They compared the genomic organization of the CAV1, CAV2, and CAV3 (OMIM Ref. No. 601253) genes. The CAV1 gene contains 3 exons, while the human CAV2 gene contains 2 exons. The boundary of the last exon of CAV1 and CAV2 are analogous, suggesting that they arose through gene duplication. The genes encoding murine caveolin- 1 and - 2 are colocalized within the A2 region of mouse chromosome 6 (Engelman et al. 1998). By FISH, Engelman et al. (1998) mapped CAV1 and CAV2 to 7q31.1- q31.2. (CA)n microsatellite repeat marker analysis of the CAV genomic clones indicated that they contain the marker D7S522, located at 7q31.1. Thus, the 2 genes map to 7q31 in a region of conserved synteny with murine 6- A2 (2,3:Engelman et al. 1998, 1998).

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Engelman, J. A.; Zhang, X. L.; Galbiati, F.; Lisanti, M. P. : Chromosomal localization, genomic organization, and developmental expression of the murine caveolin gene family (Cav- 1, - 2, and - 3): Cav- 1 and Cav- 2 genes map to a known tumor suppressor locus (6- A2/7q31). FEBS Lett. 429: 330- 336, 1998. ; and

Scherer, P. E.; Okamoto, T.; Chun, M.; Nishimoto, I.; Lodish, H. F.; Lisanti, M. P. : Identification, sequence, and expression of

caveolin- 2 defines a caveolin gene family. Proc. Nat. Ac.

Further studies establishing the function and utilities of CAV2 are found in John Hopkins OMIM database record ID 601048, and in cited publications listed in Table 9, hereby incorporated herein.

GAM55 B A ABCD1 TGGCATC GGTGGGTTTCCTTAA ABCD1 (Accession NM_000033.2) is another GAM55 target gene. ABCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM55 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM55 is therefore inhibition of ABCD1. Accordingly, utilities of GAM55 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM55 A APBA1 TGGCATC GGTGGGTTTCCTTAA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member B 1 (X11) (APBA1, Accession NM_001163.2) is another GAM55 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM55 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM55 is therefore inhibition of APBA1, a GAM55 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM55 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 has been established by previous studies. Abnormal processing of the membrane- spanning amyloid precursor protein (APP; 104760), resulting in the production of increased amounts of fibrillogenic beta- amyloid peptide (OMIM Ref. No. A- beta), is considered to be one of the key metabolic events underlying Alzheimer disease (OMIM Ref. No. 104300). One pathway for A- beta production involves the reinternalization of membrane- bound APP into lysosomes where APP containing intact A- beta are generated. In common with a number of cell surface receptors, the C- terminal cytoplasmic domain of APP contains an asn- pro- thr- tyr (NPTY) motif that mediates re- internalization via clathrin- coated pits (Chen et al. 1990). This motif has also been demonstrated to be a consensus sequence for binding to phosphotyrosine- binding/- interacting domain (PTB)- bearing proteins (van der Geer and Pawson, 1995). Several groups

demonstrated that the cytoplasmic domain of APP binds to 4 human PTB proteins: X11, X11- like (APBA2; 602712), Fe65 (APBB1; 602709), and Fe65- like (APBB2; 602710). PTB- domain proteins are believed to be involved in signal transduction processes, and the interaction of APP with the 4 human PTB proteins suggest a role for APP in such signal transaction mechanisms. Furthermore, as the 4 proteins interact with the YENPTY motif in APP, these PTB proteins may modulate processing of APP and hence formation of A- beta. Blanco et al. (1998) pointed out that it is generally agreed that there are as yet unidentified susceptibility genes for Alzheimer disease. The genes APBA1, APBA2, APBB1, and APBB2 represent such candidate genes. By searching for proteins that bind to Munc18- 1 (OMIM Ref. No. 602926), Okamoto and Sudhof (1997) isolated rat cDNAs encoding Mint1 and Mint2. They determined the full- length human MINT1 cDNA sequence (GenBank AF029106) using human MINT1 ESTs. The deduced 837- amino acid MINT1 protein contains an N- terminal domain that binds to Munc18- 1, a middle phosphotyrosine- binding (PTB) domain that binds to phosphatidylinositol phosphates, and 2 C- terminal PDZ domains. The rat Mint1 protein is largely membrane- bound and copurifies with synaptic plasma membranes, but it is not a component of synaptic vesicles. The authors suggested that in the brain Mint1 is part of a multimeric complex containing Munc18- 1 and syntaxin- 1 (OMIM Ref. No. 186590) that likely functions as an intermediate in synaptic vesicle docking/fusion.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Blanco, G.; Irving, N. G.; Brown, S. D. M.; Miller, C. C. J.; McLoughlin, D. M. : Mapping of the human and murine X11- like genes (APBA2 and Apba2), the murine Fe65 gene (Apbb1), and the human Fe65- like gene (APBB2): genes encoding phosphotyrosine- binding domain proteins that interact with the Alzheimer's disease amyloid precursor protein. Mammalian Genome 9: 473- 475, 1998. ; and

Okamoto, M.; Sudhof, T. C. : Mints, Munc18- interacting proteins in synaptic vesicle exocytosis. J. Biol. Chem. 272: 31459- 31464, 1997.

Further studies establishing the function and utilities of APBA1 are found in John Hopkins OMIM database record ID 602414, and in cited publications listed in Table 9, hereby incorporated herein.

GAM55	APPBP2	GGTGGGTTTCCTTAA TGGCATC	Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM55 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide	B	A

sequence of GAM55 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM55 is therefore inhibition of APPBP2, a GAM55 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM55 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM55	MAPK10	GGTGGGTTTCCTTAA TGGCATC	Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is another GAM55 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM55 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM55 is therefore inhibition of MAPK10, a GAM55 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM55 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 has been established by previous studies. Using a yeast 2- hybrid screen, McDonald et al. (2000) identified JNK3 as a binding partner of beta- arrestin- 2 (ARBB2; 107941). These results were confirmed by coimmunoprecipitation from mouse brain extracts and cotransfection in COS7 cells. The upstream JNK activators apoptosis signal- regulating kinase- 1 (ASK1; 602448) and MKK4 (OMIM Ref. No. 601335) were also found in complex with ARBB2. Cellular transfection of ARBB2 caused cytosolic retention of JNK3 and enhanced JNK3 phosphorylation stimulated by ASK1. Moreover, stimulation of the angiotensin II type 1A receptor (AGTR1; 106165) activated JNK3 and triggered the colocalization of ARBB2 and active JNK3 to intracellular vesicles. Thus, McDonald et al. (2000) concluded that ARBB2 acts as a scaffold protein, which brings the spatial distribution and activity of this MAPK module under the control of a G protein- coupled receptor. Yoshida et al. (2001) mapped the MAPK10 gene to 4q21- q22 by fluorescence in situ hybridization and radiation hybrid mapping. They found loss of expression EST markers in the 4q21- q22 region that correspond to the JNK3 gene in 10 of 19 cell lines derived from brain tumors. Together with previous evidence that the Jnk3 signaling pathway mediates apoptosis in

central nervous tissue in Jnk3- deficient mice (Yang et al. 1997), the results suggested that loss of expression of the JNK3 gene may play an important role in the development of brain tumors in humans

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

McDonald, P. H.; Chow, C.- W.; Miller, W. E.; Laporte, S. A.; Field, M. E.; Lin, F.- T.; Davis, R. J.; Lefkowitz, R. J. : Beta-arrestin 2: a receptor- regulated MAPK scaffold for the activation of JNK3. Science 290: 1574- 1577, 2000. ; and

Yoshida, S.; Fukino, K.; Harada, H.; Nagai, H.; Imoto, I.; Inazawa, J.; Takahashi, H.; Teramoto, A.; Emi, M. : The c- Jun NH2-terminal kinase 3 (JNK3) gene: genomic structure, chromosomal a.

Further studies establishing the function and utilities of MAPK10 are found in John Hopkins OMIM database record ID 602897, and in cited publications listed in Table 9, hereby incorporated herein.

GAM66 ARHA TTTGCACCTGAGACA Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GATAGCC is a GAM66 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM66 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM66 is therefore inhibition of ARHA, a GAM66 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM66 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA has been established by previous studies. The small guanosine triphosphatase (GTP) Rho regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. In their Figure 3C, Maekawa et al. (1999) diagrammed proposed signaling pathways for Rho- induced remodeling of the actin cytoskeleton. They demonstrated that active Rho signals to its downstream effector ROCK1 (OMIM Ref. No. 601702), which phosphorylates and activates LIM kinase (see OMIM Ref. No. 601329). LIM kinase, in turn, phosphorylates cofilin (OMIM Ref. No. 601442), inhibiting its actin- depolymerizing activity. Rao et al. (2001) investigated the role of Rho kinase in the modulation of aqueous humor outflow facility. The treatment of human trabecular meshwork and canal of Schlemm cells with a Rho kinase- specific inhibitor led to significant but reversible changes in cell shape

and decreased actin stress fibers, focal adhesions, and protein phosphotyrosine staining. Based on the Rho kinase inhibitor- induced changes in myosin light chain phosphorylation and actomyosin organization, the authors suggested that cellular relaxation and loss of cell- substratum adhesions in the human trabecular meshwork and canal of Schlemm cells could result in either increased paracellular fluid flow across the canal of Schlemm or altered flow pathway through the juxtacanalicular tissue, thereby lowering resistance to outflow. They suggested Rho kinase as a potential target for the development of drugs to modulate intraocular pressure in glaucoma patients.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Maekawa, M.; Ishizaki, T.; Boku, S.; Watanabe, N.; Fujita, A.; Iwamatsu, A.; Obinata, T.; Ohashi, K.; Mizuno, K.; Narumiya, S. : Signaling from Rho to the actin cytoskeleton through protein kinases ROCK and LIM- kinase. Science 285: 895- 898, 1999. ; and

Rao, P. V.; Deng, P.- F.; Kumar, J.; Epstein, D. L. : Modulation of aqueous humor outflow facility by the Rho kinase- specific inhibitor Y- 27632. Invest. Ophthal. Vis. Sci. 42: 1029- 1037.

Further studies establishing the function and utilities of ARHA are found in John Hopkins OMIM database record ID 165390, and in cited publications listed in Table 9, hereby incorporated herein.

GAM83 ACE AAGGTGGTGTCATGT TTTGGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM83 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM83 is therefore inhibition of ACE, a GAM83 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM83 APBB2 AAGGTGGTGTCATGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTTGGGG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM83 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM83 is therefore inhibition of APBB2, a GAM83 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM83 APPBP2 AAGGTGGTGTCATGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TTTGGGG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM83 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM83 is therefore inhibition of APPBP2, a GAM83 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM83 DHCR24 AAGGTGGTGTCATGT 24- dehydrocholesterol Reductase (DHCR24, Accession A A
TTTGGGG NM_014762.1) is another GAM83 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM83 is therefore inhibition of DHCR24, a GAM83 target gene which catalyzes the reduction of sterol

intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM83 PRND AAGGTGGTGTCATGT TTTGGGG A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM83 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM83 is therefore inhibition of PRND, a GAM83 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM83 PSEN1 AAGGTGGTGTCATGT TTTGGGG A A PSEN1 (Accession NM_000021.2) is another GAM83 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM83 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM83 is therefore inhibition of PSEN1. Accordingly, utilities of GAM83 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM99 BACE TGGAGAGATAAGCCA AGTATCC A A Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM99 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM99 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM99 is therefore inhibition of BACE, a GAM99 target gene which is responsible for the proteolytic

processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM99 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE has been established by previous studies. Cerebral deposition of amyloid beta peptide is an early and critical feature of Alzheimer disease (AD; 104300). Amyloid beta generation depends on proteolytic cleavage of amyloid precursor protein (APP; 104760) by 2 proteases, beta- secretase and gamma- secretase. Vassar et al. (1999) reported the cloning of a human transmembrane aspartic protease that had all the known characteristics of the beta-secretase. Using an expression cloning strategy, they identified a clone that shared significant sequence similarity with members of the pepsin subfamily of aspartic proteases. This clone encoded a novel protein, designated BACE for 'beta- site APP- cleaving enzyme.' The BACE open reading frame encodes a protein of 501 amino acids containing a 21- amino acid signal peptide followed by a proprotein domain spanning amino acids 22 to 45. The lumenal domain of the mature protein is followed by 1 predicted transmembrane domain and a short cytosolic C- terminal tail of 24 amino acids. BACE was predicted to be a type 1 transmembrane protein with the active site on the lumenal side of the membrane, where beta-secretase cleaves APP. The BACE protein shares greatest amino acid identity (30%) with cathepsin E (OMIM Ref. No. 116890). Rat and mouse BACE orthologs have 96% amino acid sequence identity with the human BACE protein. Northern blot analysis of human BACE mRNA in adult peripheral tissues and various subregions of the brain detected 3 transcripts of approximately 7.0, 4.4, and 2.6 kb. By in situ hybridization, expression of BACE mRNA in rat brain was observed at higher levels in neurons than in glia, supporting the idea that neurons are the primary source of the extracellular A-beta deposited in amyloid plaques. Vassar et al. (1999) ascribed the difference between the apparent and calculated molecular weight (approximately 70 and 51 kD, respectively) of the BACE protein to N-linked glycosylation. Immunostaining demonstrated intracellular localization of BACE to the Golgi and endosomes. Transient overexpression of BACE did not affect APP expression, but decreased alpha- secretase cleavage and increased beta- secretase activity in cells expressing wildtype or Swedish mutant (104760.0008) APP. BACE overexpression induced cleavage only at the known beta- secretase positions, asp1 and glu11. Vassar et al. (1999) concluded that their data provided strong evidence that the BACE aspartic protease is the long- sought beta- secretase. Animal model experiments lend further support to the function of BACE. Luo et al. (2001) found that mice deficient in BACE1 are healthy, fertile, and appear normal in gross anatomy, tissue histology, hematology, and clinical chemistry. Bace1 - /- mice who are also hemizygous for an amyloid precursor protein transgene lack brain beta- amyloid and beta- secretase- cleaved APP C- terminal fragments. These results provided validation of BACE1 as the major beta- secretase in vivo and suggested that therapeutic

inhibition of BACE1 for the treatment of Alzheimer disease may be free of mechanism- based toxicity.

It is appreciated that the abovementioned animal model for BACE is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz, E. A.; Dents, P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff, R.; Luo, Y.; Fisher, S.; and 12 others : Beta- secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE. Science 286: 735- 741, 1999. ; and

Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis, P.; Fan, W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.; Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.

Further studies establishing the function and utilities of BACE are found in John Hopkins OMIM database record ID 604252, and in cited publications listed in Table 9, hereby incorporated herein.

GAM99 CTSK TGGAGAGATAAGCCA CTSK (Accession NM_000396.2) is another GAM99 target gene. CTSK A A
AGTATCC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM99 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM99 is therefore inhibition of CTSK. Accordingly, utilities of GAM99 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM99 TNF TGGAGAGATAAGCCA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A
AGTATCC Accession NM_000594.2) is another GAM99 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM99 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM99 is therefore inhibition of TNF, a GAM99 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly,

utilities of GAM99 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF has been established by previous studies. Ruuls and Sedgwick (1999) reviewed the problem of unlinking TNF biology from that of the MHC. Dysregulation and, in particular, overproduction of TNF have been implicated in a variety of human diseases, including sepsis, cerebral malaria, and autoimmune diseases such as multiple sclerosis (OMIM Ref. No. 126200), rheumatoid arthritis, systemic lupus erythematosus (OMIM Ref. No. 152700), and Crohn disease (see OMIM Ref. No. 266600), as well as cancer. Susceptibility to many of these diseases is thought to have a genetic basis, and the TNF gene is considered a candidate predisposing gene. However, unraveling the importance of genetic variation in the TNF gene to disease susceptibility or severity is complicated by its location within the MHC, a highly polymorphic region that encodes numerous genes involved in immunologic responses. Ruuls and Sedgwick (1999) reviewed studies that had analyzed the contribution of TNF and related genes to susceptibility to human disease, and they discussed how the presence of the TNF gene within the MHC may potentially complicate the interpretation of studies in animal models in which the TNF gene is experimentally manipulated. Animal model experiments lend further support to the function of TNF. Bruce et al. (1996) used targeted gene disruption to generate mice lacking either the p55 or the p75 TNF receptors; mice lacking both p55 and p75 were generated from crosses of the singly deficient mice. The TNFR- deficient (TNFR- KO) mice exhibited no overt phenotype under unchallenged conditions. Bruce et al. (1996) reported that damage to neurons caused by focal cerebral ischemia and epileptic seizures was exacerbated in the TNFR- KO mice, indicating that TNF serves a neuroprotective function. Their studies indicated that TNF protects neurons by stimulating antioxidative pathways. Injury- induced microglial activation was suppressed in TNFR- KO mice. They concluded that drugs which target TNF signaling pathways may prove beneficial in treating stroke or traumatic brain injury.

It is appreciated that the abovementioned animal model for TNF is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Ruuls, S. R.; Sedgwick, J. D. : Unlinking tumor necrosis factor biology from the major histocompatibility complex: lessons from human genetics and animal models. Am. J. Hum. Genet. 65: 294- 301, 1999. ; and

Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P. J.; Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P. : Altered neuronal and microglial responses to excitotoxic and is.

Further studies establishing the function and utilities of TNF are found in John Hopkins OMIM database record ID 191160, and in cited publications listed in Table 9, hereby incorporated herein.

GAM106 A FPRL1 A ATTAGCTATAGCAAA AGGCTTA FPRL1 (Accession NM_001462.1) is a GAM106 target gene. FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM106 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM106 is therefore inhibition of FPRL1. Accordingly, utilities of GAM106 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM106 A S100B A ATTAGCTATAGCAAA AGGCTTA S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is another GAM106 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM106 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM106 is therefore inhibition of S100B, a GAM106 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM106 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B has been established by previous studies. See 176940. The beta- subunit of S100 protein is expressed in glial cells at levels at least tenfold higher than in most other cell types. The brain also contains small amounts of the alpha subunits at levels approximately one- tenth that of the beta subunit. Allore et al. (1988) used genomic and cDNA probes in connection with a panel of rodent- human somatic cell hybrids to assign the S100B gene to 21q22. They suggested that this is a candidate gene for the neurologic disturbances in Down syndrome when present in trisomic state. By in situ hybridization, Duncan et al. (1989) localized the S100B gene to 21q22.2- q22.3. Allore et al. (1990) isolated overlapping genomic clones spanning the region coding for S100B and its flanking sequences. The intron/exon organization is similar to that of the

genes coding for several other members of the S100 protein subfamily. The S100B gene is composed of 3 exons, the first of which specifies the 5- prime untranslated region. Morii et al. (1991) isolated the S100A (OMIM Ref. No. 176940) and S100B genes from a human genomic DNA library. Endonuclease mapping and DNA sequencing showed that both comprise 3 exons and 2 introns. Two Ca(2)- binding domains were independently encoded by exons 2 and 3. By spot- blot hybridization analysis of flow- sorted chromosomes, Morii et al. (1991) showed that the S100A and S100B genes are located on chromosome 1 and chromosome 21, respectively. Using restriction endonuclease fragment length variations (RFLV) in multipoint backcrosses, Shimizu et al. (1992) mapped the S100b gene in relation to other genes on mouse chromosome 10. The S100B gene is expressed at high levels in brain primarily by astrocytes. Addition of the disulfide- bonded dimeric form of the protein to primary neuronal and glial cultures and established cell lines induces axonal extension and alterations in astrocyte proliferation and phenotype. Reeves et al. (1994) demonstrated that the same effects of the S100B protein are exerted in vivo. They found that both astrocytosis and neurite proliferation occurred in transgenic mice expressing elevated levels of S100b. They suggested that these transgenic mice represent a useful model for studies of the role of S100B in glial-neuronal interactions in normal development and function of the brain and for analyzing the significance of elevated levels of the protein in Down syndrome and Alzheimer disease.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Reeves, R. H.; Yao, J.; Crowley, M. R.; Buck, S.; Zhang, X.; Yarowsky, P.; Gearhart, J. D.; Hilt, D. C. : Astrocytosis and axonal proliferation in the hippocampus of S100b transgenic mice. Proc. Nat. Acad. Sci. 91: 5359- 5363, 1994. ; and

Shimizu, A.; Sakai, Y.; Ohno, K.; Masaki, S.; Kuwano, R.; Takahashi, Y.; Miyashita, N.; Watanabe, T. : A molecular genetic linkage map of mouse chromosome 10, including the Myb, S100b, P.

Further studies establishing the function and utilities of S100B are found in John Hopkins OMIM database record ID 176990, and in cited publications listed in Table 9, hereby incorporated herein.

GAM112 APP TGATATATAATCAGC APP (Accession NM_000484.1) is a GAM112 target gene. APP A A

CCATGAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM112 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM112 is therefore inhibition of APP. Accordingly, utilities of GAM112 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM144 AVP CTGTGCCTGTGACGA AVP (Accession NM_000490.2) is a GAM144 target gene. AVP A A
GGGATGA BINDING SITE1 and AVP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by AVP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE1 and AVP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM144 is therefore inhibition of AVP. Accordingly, utilities of GAM144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM144 MAPT CTGTGCCTGTGACGA Microtubule- associated Protein Tau (MAPT, Accession A A
GGGATGA NM_173727.1) is another GAM144 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM144 is therefore inhibition of MAPT, a GAM144 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT has been established by previous studies. The microtubule- associated proteins (MAPs) coassemble with tubulin (see OMIM Ref. No. 602529) into microtubules in vitro. Microtubule- associated protein tau appears to be enriched in axons. Neve et al. (1986) identified tau cDNA clones in a human fetal brain cDNA library. The clones recognized a 6- kb message that was expressed in human brain but not in other human tissues and exhibited a developmental shift in size. By screening cDNA libraries prepared from the frontal cortex of an Alzheimer disease patient and from fetal human brain, Goedert et al. (1988) isolated the cDNA for a core protein of the paired helical filament of Alzheimer disease (OMIM Ref. No. 104300). The partial amino acid sequence of this core protein was used to design synthetic oligonucleotide probes. The cDNA encodes a protein of 352 amino acids that contains a characteristic amino acid repeat in its carboxyl- terminal half. Because of extensive homology to the

sequence of the mouse microtubule- associated protein tau, they stated that this protein must constitute the human equivalent of mouse tau. Tau protein mRNA was found in normal amounts in the frontal cortex from patients with Alzheimer disease. Hutton et al. (1998) studied 13 families in which an autosomal dominant inherited dementia, frontotemporal dementia with parkinsonism (OMIM Ref. No. 600274), had been shown to be linked to chromosome 17. The authors stated that this disorder has historically been termed Pick disease (OMIM Ref. No. 172700). Most cases showed neuronal and/or glial inclusions that stained positively with antibodies raised against tau, although the tau pathology varied considerably in both its quantity (or severity) and characteristics. This form of dementia, symbolized FTDP17 by them, had been mapped to a 2- cM region on 17q21.11. Since the tau gene was known to lie within this region and because the disorder was recognized to be a 'tauopathy,' Hutton et al. (1998) sequenced the MAPT gene in the thirteen 17- linked families and identified 3 missense mutations (gly272 to val, 157140.0002; pro301 to leu, 157140.0001; and arg406 to trp, 157140.0003) and 3 mutations in the 5- prime splice site of exon 10. All of the splice site mutations destabilized a potential stem- loop structure that is probably involved in regulating the alternative splicing of exon 10 (Goedert et al. 1989). This caused more frequent usage of the 5- prime splice site and an increased proportion of tau transcripts that include exon 10. The increase in exon 10 mRNA was expected to increase the proportion of tau containing 4 microtubule-binding repeats, which is consistent with the neuropathology described in families with FTDP17. Hong et al. (1998) indicated that more than 10 exonic and intronic mutations of the MAPT gene had been identified in about 20 FTDP17 families. They found that analyses of soluble and insoluble tau proteins from brains of FTDP17 patients indicated that different pathogenic mutations differentially altered distinct biochemical properties and stoichiometry of brain tau isoforms. Functional assays of recombinant tau proteins with different FTDP17 missense mutations implicated all but 1 of these mutations in disease pathogenesis by reducing the ability of tau to bind microtubules and promote microtubule assembly. In a study of frontotemporal dementia in the Netherlands during the period January 1994 to June 1998, Rizzu et al. (1999) found 37 patients who had one or more first- degree relatives with dementia. A mutation in the MAPT gene was found in 17.8% of the group of patients with FTDP17 and in 43% of patients with FTDP17 who also had a positive family history of the disorder. Three distinct missense mutations, G272V (157140.0002), P301L (157140.0001), and R406W (157140.0003), accounted for 15.6% of the mutations. These 3 missense mutations, and a single amino acid deletion, K280del, that was detected in 1 patient, strongly reduced the ability of tau to promote microtubule assembly. In some FTDP17 families, MAPT mutations have not been found, suggesting locus and/or allelic heterogeneity. Rizzu et al. (1999) suggested that the MAPT mutations may result in disturbances in the interactions of the protein tau with microtubules, resulting

in hyperphosphorylation of tau protein, assembly into filaments, and subsequent cell death. Verpillat et al. (2002) found that the tau H1/H1 genotype was significantly overrepresented in 100 patients with frontotemporal dementia compared to controls (odds ratio for H1/H1 = 1.95). In addition, there was a significant negative effect in carriers of both the H1/H1 genotype and the APOE2 allele (OMIM Ref. No. 107741). The association of intronic mutations in the MAPT gene in frontotemporal dementia with parkinsonism (e.g. 157140.0004) highlights the involvement of aberrant pre- mRNA splicing in the pathogenesis of neurodegenerative disorders. To establish a model system for studying the role of pre- mRNA splicing in neurodegenerative diseases, Jiang et al. (2000) constructed a MAPT minigene that reproduced alternative splicing in both cultured cells and in vitro biochemical assays. They demonstrated that mutations in a nonconserved intronic region of the human MAPT gene led to increased splicing between exons 10 and 11. Systematic biochemical analyses indicated the importance of U1 snRNP (OMIM Ref. No. 180740) and, to a lesser extent, U6 snRNP (OMIM Ref. No. 180692) in differentially recognizing wildtype versus intron- mutant MAPT pre-mRNAs. Goedert et al. (1998) reviewed the role of tau mutations in frontotemporal dementias. Heutink (2000) reviewed the role of tau protein in frontotemporal dementia and other neurodegenerative disorders. Hutton (2001) reviewed the known missense and splice site mutations in the tau gene that are associated with disease and described different mechanisms involved in pathogenesis, including disruption of the interaction between tau and tubulin, deposition of abnormal tau filaments, and the generation of abnormal ratios of tau isoforms. Animal model experiments lend further support to the function of MAPT. Lewis et al. (2000) demonstrated that expression of human tau containing the most common mutation, P301L (157140.0001), results in motor and behavioral deficits in transgenic mice, with age- and gene- dose- dependent development of neurofibrillary tangles (NFT).

It is appreciated that the abovementioned animal model for MAPT is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Hutton, M.; Lendon, C. L.; Rizzu, P.; Baker, M.; Froelich, S.; Houlden, H.; Pickering- Brown, S.; Chakraverty, S.; Isaacs, A.; Grover, A.; Hackett, J.; Adamson, J.; and 39 others : Association of missense and 5- prime- splice- site mutations in tau with the inherited dementia FTDP- 17. Nature 393: 702- 705, 1998. ; and

Rizzu, P.; Van Swieten, J. C.; Joosse, M.; Hasegawa, M.;

Stevens, M.; Tibben, A.; Niermeijer, M. F.; Hillebrand, M.; Ravid, R.; Oostra, B. A.; Goedert, M.; van Duijn, C. M.; Heutink, P.

Further studies establishing the function and utilities of MAPT are found in John Hopkins OMIM database record ID 157140, and in cited publications listed in Table 9, hereby incorporated herein.

GAM144 A A TGFB1 CTGTGCCTGTGACGA GGGATGA TGFB1 (Accession NM_000660.1) is another GAM144 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM144 is therefore inhibition of TGFB1. Accordingly, utilities of GAM144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM175 A A CNTF GACCCTGTGTTCAAG GTTAGGG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a GAM175 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM175 is therefore inhibition of CNTF, a GAM175 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF has been established by previous studies. Takahashi et al. (1994) identified an apparent polymorphism of the CNTF gene. An acceptor splice site mutation caused aberrant mRNA splicing and abolished expression of CNTF protein. The specific change was a G- to- A transition at position - 6 of the acceptor splice site leading to insertion of 4 additional ribonucleotides at the beginning of the next exon. This caused a frameshift from amino acid 39, resulting in a stop codon 24 amino acids downstream. (The normal open reading frame codes for 200 amino acids.) The aberrant mRNA was predicted to code for a truncated protein of 62 amino acids. Analysis of tissue samples and transfection of CNTF minigenes into cultured cells demonstrated to Takahashi et al. (1994) that the mutated allele expressed only the mutated mRNA species. Studies with an antiserum that recognized both the normal and mutated CNTF showed complete lack of CNTF immunoreactivity in peripheral nerve tissue

from a homozygous mutant subject. In 391 Japanese people tested, 61.9% were normal homozygotes, 39.8% heterozygotes, and 2.3% mutant homozygotes. The distribution of the 3 genotypes were similar in healthy and neurologic disease subjects, indicating that human CNTF deficiency is not causally related to neurologic diseases In 7 of 288 patients with multiple sclerosis (OMIM Ref. No. 126200), Giess et al. (2002) identified homozygosity for the CNTF null mutation. The 7 patients demonstrated a significantly earlier age of onset of disease (17 years) compared to patients carrying at least 1 functional CNTF allele (27 years). Six of the 7 patients with the null allele (85%) had marked motor or brainstem symptoms and incomplete remission, which was detected in only 21% of the other patients with MS. Giess et al. (2002) noted that the null allele is very rare, and that the frequency of the homozygous null allele in this group is the same as in control groups, thus indicating that the genotype itself is not a risk factor for development of MS. However, they suggested that trophic support of neurons and oligodendrocytes by CNTF may be critical to reduce early damage caused by inflammatory mediators, and that lack of functional CNTF may lead to earlier onset of clinical symptoms in MS

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Barbin, G.; Manthorpe, M.; Varon, S. : Purification of the chick eye ciliary neuronotrophic factor. J. Neurochem. 43: 1468-1478, 1984. ; and

Takahashi, R.; Yokoji, H.; Misawa, H.; Hayashi, M.; Hu, J.; Deguchi, T. : A null mutation in the human CNTF gene is not causally related to neurological diseases. Nature Genet. 7: 79- 84.

Further studies establishing the function and utilities of CNTF are found in John Hopkins OMIM database record ID 118945, and in cited publications listed in Table 9, hereby incorporated herein.

GAM175 A GFAP A GACCCTGTGTTCAAG GTTAGGG GFAP (Accession NM_002055.2) is another GAM175 target gene. GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM175 is therefore inhibition of GFAP. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM189 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM189 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM189 is therefore inhibition of APPBP2, a GAM189 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM189 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM189 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM189 is therefore inhibition of BACE2, a GAM189 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 has been established by previous studies. Deposition in the brain of the 39- to 43- amino acid amyloid- beta peptide is a hallmark of Alzheimer disease (AD; 104300), a frequent complication of Down syndrome (OMIM Ref. No. 190685) patients after age 30 years. Amyloid- beta is generated by proteolytic processing of the amyloid precursor protein (APP; 104760) by beta- and gamma- secretase at the N and C termini, respectively. Presenilin- 1 (OMIM Ref. No. 104311) is involved in the gamma- secretase activity. BACE (OMIM Ref. No. 604252), a transmembrane aspartyl protease, possesses beta-secretase activity. By differential display RT- PCR of poorly and highly metastatic breast cancer cell lines, followed by screening a bone marrow stroma cell cDNA library, Xin et al. (2000) obtained a cDNA encoding BACE2, which they termed ALP56. Sequence analysis predicted that the 518- amino acid protein has 2 pepsin- like active centers, a signal sequence, a propeptide, and a long C- terminal

extension including a transmembrane domain. Northern blot analysis detected 2.5- and 2.0- kb transcripts in metastatic tumors injected in SCID mice (see OMIM Ref. No. 202500). In situ hybridization analysis demonstrated high expression in breast, colon, and prostate cancer biopsies, as well as in normal prostate. Northern blot analysis of normal tissue revealed expression in prostate, pancreas, and placenta. Further exposure detected expression in all tissues tested except brain and lymphocytes. Western blot analysis showed expression of a 60- kD protein as well as apparent autocleavage products of 17 and 14 kD. By searching EST databases with the BACE sequence and identifying mapped sequences, Saunders et al. (1999) identified a cDNA encoding BACE2 and mapped the gene to 21q22.2-q22.3. Using FISH, Acquati et al. (2000) confirmed the localization of BACE2 to 21q22.3, within the Down syndrome critical region.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Xin, H.; Stephans, J. C.; Duan, X.; Harrowe, G.; Kim, E.; Grieshammer, U.; Kingsley, C.; Giese, K. : Identification of a novel aspartic- like protease differentially expressed in human breast cancer cell lines. Biochim. Biophys. Acta 1501: 125- 137, 2000. ; and

Saunders, A. J.; Kim, T.- W.; Tanzi, R. E. : BACE maps to chromosome 11 and a BACE homolog, BACE2, reside in the obligate Down syndrome region of chromosome 21. Science 286: 1255A only.

Further studies establishing the function and utilities of BACE2 are found in John Hopkins OMIM database record ID 605668, and in cited publications listed in Table 9, hereby incorporated herein.

GAM189 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A TGGGCAA another GAM189 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM189 is therefore inhibition of FHL2, a GAM189 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 has been established by previous studies. LIM proteins contain a highly

conserved double zinc finger motif called the LIM domain. By searching sequence databases with a partial human SLIM1 (FHL1; 300163) cDNA, Morgan and Madgwick (1996) identified partial SLIM3 cDNAs. Genini et al. (1997) used subtractive cloning to isolate a gene that is downregulated during transformation of normal myoblasts to rhabdomyosarcoma cells. The gene, termed DRAL for 'down-regulated in rhabdomyosarcoma LIM protein,' encodes a 279- amino acid polypeptide with an observed mass of 32 kD. The protein sequence contains 4 complete LIM domains and the second half of a fifth LIM domain. DRAL appears to be a member of the LIM- only class of proteins, which consist primarily of LIM domains and little else. Southern blotting revealed a single- copy gene that is conserved among vertebrates. Northern blotting revealed that the DRAL gene is expressed at highest levels in heart and ovary, and at lower levels in skeletal muscle, prostate, testis, small intestine, and colon. Results of Northern blotting of tumor cell lines suggested to Genini et al. (1997) that this gene may be downregulated during transformation of a variety of cell types. Genini et al. (1997) used in situ hybridization to map the human FHL2 gene to 2q12- q14. By fluorescence in situ hybridization, Chan et al. (1998) mapped the FHL2 gene to 2q12- q13. Using the yeast 2- hybrid system, Tanahashi and Tabira (2000) screened for proteins interacting with an Alzheimer disease gene, presenilin- 2 (OMIM Ref. No. 600759), and cloned DRAL. DRAL interacted with a hydrophilic loop region (amino acids 269- 298) in the endoproteolytic N- terminal fragment of PS2, but not that of PS1 (OMIM Ref. No. 104311), although residues 269 to 298 of PS2 and the corresponding PS1 sequence differ by only 3 amino acids. Each of 9 PS2 point mutations within a region from residues 275 to 296 abolished the binding. The in vitro interaction was confirmed by affinity column assay and the physiologic interactions between endogenous PS2 and DRAL by coimmunoprecipitation from human lung fibroblast MRC5 cells. The authors suggested that DRAL functions as a link between PS2 and an intracellular signaling pathway.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- G.; Schafer, B. W. : Subtractive cloning and characterization of DRAL, a novel LIM- domain protein down- regulated in rhabdomyosarcoma. DNA Cell Biol. 16: 433- 442, 1997. ; and

Tanahashi, H.; Tabira, T. : Alzheimer's disease- associated presenilin 2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9: 2281- 2289, 2000.

Further studies establishing the function and utilities of FHL2 are found in John Hopkins OMIM database record ID 602633, and in

cited publications listed in Table 9, hereby incorporated herein.

GAM189 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM189 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM189 is therefore inhibition of HD. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM189 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM189 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM189 is therefore inhibition of IGF1, a GAM189 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM189 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM189 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM189 is therefore inhibition of PRND, a GAM189 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM193 APPBP2 TATTGCTAAGAATTC AGGTAGT A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM193 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM193 is therefore inhibition of APPBP2, a GAM193 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM193 IGF1 TATTGCTAAGAATTC AGGTAGT A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM193 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM193 is therefore inhibition of IGF1, a GAM193 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM193 NPY TATTGCTAAGAATTC AGGTAGT A A Neuropeptide Y (NPY, Accession NM_000905.2) is another GAM193 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM193 is therefore inhibition of NPY,

a GAM193 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY has been established by previous studies. Hansel et al. (2001) identified a role for NPY in promoting proliferation of postnatal neuronal precursor cells. NPY is synthesized in the postnatal olfactory epithelium by sustentacular cells, previously proposed to function only in structural support. Mice with a targeted deletion of NPY contained half as many dividing olfactory neuronal precursor cells as did controls. Furthermore, NPY-deficient mice developed significantly fewer olfactory neurons by adulthood. NPY acts on multipotent neuronal precursor or basal cells to activate rapidly and transiently the extracellular signal-regulated kinase (ERK) 1/2 (OMIM Ref. No. 601795) subgroup of mitogen- activated protein kinases. The NPY Y1 receptor subtype (OMIM Ref. No. 162641) appears to mediate this effect. The ability of NPY to induce neuronal precursor proliferation is mediated by protein kinase C (PKC; 176960), indicating an upstream PKC-dependent activation of ERK1/2. These results indicate that NPY may regulate neuronal precursor proliferation in the adult mammal. Animal model experiments lend further support to the function of NPY. Neuropeptide Y is a neuromodulator implicated in the control of energy balance and is overproduced in the hypothalamus of ob/ob mice. To determine the role of NPY in the response to leptin (OMIM Ref. No. 164160) deficiency, Erickson et al. (1996) generated ob/ob mice deficient in NPY. In the absence of NPY, ob/ob mice were less obese because of reduced food intake and increased energy expenditure, and were less severely affected by diabetes, sterility, and somatotropic defects. These results were interpreted as indicating that NPY is a central effector of leptin deficiency.

It is appreciated that the abovementioned animal model for NPY is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Erickson, J. C.; Hollopeter, G.; Palmiter, R. D. : Attenuation of the obesity syndrome of ob/ob mice by the loss of neuropeptide Y. Science 274: 1704- 1706, 1996. ; and

Hansel, D. E.; Eipper, B. A.; Ronnett, G. V. : Neuropeptide Y functions as a neuroproliferative factor. Nature 410: 940- 943, 2001.

Further studies establishing the function and utilities of NPY are found in John Hopkins OMIM database record ID 162640, and in cited publications listed in Table 9, hereby incorporated herein.

GAM205 A B2M GTGGAGTTCTCTGCT AGTCCTA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

GAM205 A target gene. A function of GAM205 is therefore inhibition of B2M, a GAM205 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M has been established by previous studies. Hemodialysis- related amyloidosis (HRA) is a form of systemic amyloidosis with a predilection for the synovium and bone that occurs with a disturbingly high frequency among patients on long- term hemodialysis. The clinical features include carpal tunnel syndrome, erosive arthropathy, spondyloarthropathy, lytic bone lesions, and pathologic fractures. Gejyo et al. (1985) found that protein that accumulates in amyloid- laden tissue obtained from a chronic hemodialysis patient with carpal tunnel syndrome was identical to B2M in several characteristics. Connors et al. (1985) demonstrated the in vitro creation of amyloid fibers from B2M. Gorevic et al. (1985, 1986) reported the amino acid sequence of the HRA subunit protein and identified it as beta- 2- microglobulin. The occurrence of amyloidosis in these patients can be prevented by periodic use of high- permeability membranes or intermittent hemofiltration. Charra et al. (1984) reported that 38 of 52 patients receiving hemodialysis for more than 8 years for chronic renal failure not due to amyloid nephropathy developed carpal tunnel syndrome. Tissues excised at surgical decompression contained amyloid. In 95% of these patients, shoulder pain, which was presumed to be due to amyloid deposits, was present. McClure et al. (1986) demonstrated the beta- 2- microglobulin nature of the amyloid in the 3 patients with carpal tunnel syndrome requiring decompression surgery after long- term hemodialysis treatment for chronic renal failure not due to amyloid nephropathy. Zingraff et al. (1990) described a patient with severe renal insufficiency who had beta- 2- microglobulin amyloidosis despite the fact that dialysis had never been performed. The possibility that some B2M variants are more amyloidogenic than others should be explored. Animal model experiments lend further support to the function of B2M. The defect in hereditary hemochromatosis (HFE; 235200) resides in a gene in the class I MHC

region. This fact lends significance to the findings of de Sousa et al. (1994), who reported a comparative histologic and quantitative analysis of iron distribution in the tissues of mice homozygous and heterozygous for knockout of the beta- 2- microglobulin gene. Progressive hepatic iron overload, indistinguishable from that observed in human hemochromatosis, was found only in mice homozygous for the mutated B2M gene.

It is appreciated that the abovementioned animal model for B2M is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Gorevic, P. D.; Casey, T. T.; Stone, W. J.; DiRaimondo, C. R.; Prelli, F. C.; Frangione, B. : Beta- 2 microglobulin is an amyloidogenic protein in man. J. Clin. Invest. 76: 2425- 2429, 1985. ; and

de Sousa, M.; Reimao, R.; Lacerda, R.; Hugo, P.; Kaufmann, S. H. E.; Porto, G. : Iron overload in beta- 2- microglobulin-deficient mice. Immun. Lett. 39: 105- 111, 1994.

Further studies establishing the function and utilities of B2M are found in John Hopkins OMIM database record ID 109700, and in cited publications listed in Table 9, hereby incorporated herein.

GAM205 PLCD1 GTGGAGTTCTCTGCT Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is A A AGTCCTA another GAM205 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM205 is therefore inhibition of PLCD1, a GAM205 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 has been established by previous studies. Phosphoinositide- specific phospholipase C acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5- trisphosphate, by hydrolyzing inositol phospholipids. Molecules belonging to the PLC

family are divided into subfamilies, PLC- beta (see OMIM Ref. No. 600810), PLC- gamma (see OMIM Ref. No. 172420), and PLC- delta, whose amino acid sequences are highly conserved in 2 distinct regions designated X and Y. PLC- delta- 1 is distinguished from PLC- gamma by lack of the SH2 and SH3 domains that are essential for activation of PLC- gamma by tyrosine protein kinases, and from PLC- beta by lack of the C- terminal region of PLC- beta that is responsible for binding and activation by G proteins. Cheng et al. (1995) cloned cDNA for human PLC- delta- 1 and localized the gene to chromosome 3 by means of a human/rodent somatic cell panel (Lyu et al. 1996). In the course of a large- scale sequencing analysis of genomic DNA in the vicinity of the homozygous deletion on chromosome 3p found in a lung cancer cell line, Ishikawa et al. (1997) found that the gene encoding phospholipase C, delta- 1 (PLCD1) is located just distal to the region removed by the deletion. They found that the gene consists of 15 exons and spans about 22 kb. By fluorescence in situ hybridization, they localized the PLCD1 gene to 3p22- p21.3. Shimohama et al. (1998) examined the entire sequences corresponding to protein- coding exons 2- 15 of the hamster PLC- delta- 1 gene in genomic DNA derived from the leukocytes of 13 unrelated patients with early- onset sporadic Alzheimer disease (OMIM Ref. No. 104300). In 1 of these patients whose clinical features and course did not differ from those of the other 12 cases, they found a change of codon CGC (arg) to CAC (his), located in the pleckstrin homology domain of the PLCD1 gene. They stated that this was the first mutation found in the human PLC genes. Site- directed mutagenesis of the glutathione- S- transferase (GST/PLCD1) fusion protein changing arg105 to his resulted in a 4- fold decrease in the affinity of specific binding and a reduction in hydrolyzing activity to about 40% of that of the wildtype enzyme. This remarkable loss of function could be interpreted in terms of a conformational change in the pleckstrin homology domain. Shimohama et al. (1998) found that the arg105- to- his mutation was present in heterozygous state in the patient with AD. The mutation was not found in DNA extracted from leukocytes of 23 unrelated patients with familial AD, 23 unrelated patients with early- onset sporadic AD, 46 unrelated patients with late- onset sporadic AD, and 456 nondemented control subjects. Thus the change did not appear to be a common polymorphism. However, determination of the possible pathologic role required transgenic studies of the mutant gene to determine the role of the enzyme and the mutation and a search for other mutations in the pleckstrin homology domain of PLC genes in human subjects with genetic disorders. They pointed out that mutations in the pleckstrin homology domain of the BTK gene occur in patients with Bruton agammaglobulinemia (OMIM Ref. No. 300300).

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Cheng, H. F.; Jiang, M. J.; Chen, C. L.; Liu, S. M.; Wong, L. P.; Lomasney, J. W.; King, K. : Cloning and identification of amino acid residues of human phospholipase C delta 1 essential for catalysis. J. Biol. Chem. 270: 5495- 5505, 1995. ; and

Ishikawa, S.; Takahashi, T.; Ogawa, M.; Nakamura, Y. : Genomic structure of the human PLCD1 (phospholipase C delta 1) locus on 3p22- p21.3. Cytogenet. Cell Genet. 78: 58- 60, 1997.

Further studies establishing the function and utilities of PLCD1 are found in John Hopkins OMIM database record ID 602142, and in cited publications listed in Table 9, hereby incorporated herein.

GAM206 MME TGCACTTGTCTTTAC CCTAGAG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is a GAM206 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM206 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM206 is therefore inhibition of MME, a GAM206 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM206 HD TTTCTGGAGGGCAAG TGCAGGG HD (Accession NM_002111.3) is another GAM206 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM206 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM206 is therefore inhibition of HD. Accordingly, utilities of GAM206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM240 MME TGGCACATAGTAAGT GTTCAGT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is a GAM240 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the A A

nucleotide sequence of GAM240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM240 is therefore inhibition of MME, a GAM240 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM240	DLST	ATCACTATTAATGTG TGCTAGT	Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM240 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM240 is therefore inhibition of DLST, a GAM240 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST has been established by previous studies. The alpha- keto acid dehydrogenase complexes (pyruvate dehydrogenase complex, alpha-ketoglutarate dehydrogenase complex, and branched chain alpha- keto acid dehydrogenase complex) are a family of multienzyme complexes. They are localized in mitochondria and catalyze the oxidative decarboxylation of alpha- keto acids. These 3 alpha- keto acid dehydrogenase complexes are composed of 3 different enzymes: alpha-keto acid dehydrogenase (E1), dihydrolipoamide acyltransferase (E2), and dihydrolipoamide dehydrogenase (E3). Dihydrolipoamide succinyltransferase, which is a component of the structural core of the alpha- keto glutarate dehydrogenase complex, was studied by Nakano et al. (1993), who isolated a cDNA from a human fibroblast cDNA library. They found that the DLST gene contains 3 exons and 4 introns and that the nucleotide sequence at the 5- prime donor and 3- prime acceptor sites of all introns conformed to the gt- ag rule. Amino acid sequences of the 3 exons supported their previous observation (Nakano et al. 1993) that human dihydrolipoamide succinyltransferase lacks a sequence motif for an E1 (OMIM Ref. No. 312170) and/or E3 (OMIM Ref. No. 246900) binding site. By fluorescence in situ hybridization, they found that the DLST gene is located on 14q24.2- q24.3 and that a related sequence is located on 1p31. The gene for the dihydrolipoamide acyltransferase of the branched chain alpha- keto acid dehydrogenase complex (DBT; 248610),

the site of the mutation in type 2 maple syrup urine disease, is located on 1p31. Nakano et al. (1993) mentioned the possibility that mutation of the DLST gene may be a cause of familial Alzheimer disease that maps to 14q24.3 (AD3; 104311). Ali et al. (1994) mapped the DLST gene (symbolized by them KGDHC) to 14q24.3 by isotopic in situ hybridization. The cDNA they used also cross- hybridized to an apparent E2k pseudogene on 1p31. Northern analysis demonstrated that the gene is ubiquitously expressed in peripheral tissues and brain. Ali et al. (1994) mentioned Machado- Joseph disease as another candidate for mutation in the DLST gene. DLST is the E2 component of the alpha- ketoglutarate dehydrogenase complex. In contrast to the E2 components of the other 2 alpha- keto acid dehydrogenase complexes, the pyruvate dehydrogenase complex, and the branched-chain alpha- keto acid dehydrogenase complex, the alpha- KGDC E2 has a unique structure consisting of 2 domains and lacking a sequence motif of an E3 and/or E1 binding site (Patel and Harris, 1995).

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Nakano, K.; Takase, C.; Sakamoto, T.; Ohta, S.; Nakagawa, S.; Ariyama, T.; Inazawa, J.; Abe, T.; Matuda, S. : An unspliced cDNA for human dihydrolipoamide succinyltransferase: characterization and mapping of the gene to chromosome 14q24.2- q24.3. Biochem. Biophys. Res. Commun. 196: 527- 533, 1993. ; and

Patel, M. S.; Harris, R. A. : Mammalian alpha- keto acid dehydrogenase complexes: gene regulation and genetic defects. FASEB J. 9: 1164- 1172, 1995.

Further studies establishing the function and utilities of DLST are found in John Hopkins OMIM database record ID 126063, and in cited publications listed in Table 9, hereby incorporated herein.

GAM259 HD GTCAGCAAGGAGGGG HD (Accession NM_002111.3) is a GAM259 target gene. HD BINDING A A
TGGACAA SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM259 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM259 is therefore inhibition of HD. Accordingly, utilities of GAM259 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM269 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGTGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM269 target gene. APPBP2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM269 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM269 is therefore inhibition of APPBP2, a GAM269 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM269 FHL2 CATTGCACTCCAGCC A A TGGGTGA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM269 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM269 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM269 is therefore inhibition of FHL2, a GAM269 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM269 IGF1 CATTGCACTCCAGCC A A TGGGTGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM269 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM269 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM269 is therefore inhibition of IGF1, a GAM269 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM269 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM269 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM269 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

TGGGTGA

Another function of GAM269 is therefore inhibition of PRND, a GAM269 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM269 TNFRSF5 CATTGCACTCCAGCC TNFRSF5 (Accession NM_152854.1) is another GAM269 target gene. A A

TGGGTGA TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM269 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM269 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM270 SNCA AAGGTAGATAAAGGC SNCA (Accession NM_000345.2) is a GAM270 target gene. SNCA A A

TTCACGT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM270 is therefore inhibition of SNCA. Accordingly, utilities of GAM270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with SNCA.

GAM281 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM281 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM281 is therefore inhibition of APPBP2, a GAM281 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM281 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM281 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of BACE2, a GAM281 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM281 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM281 target gene.
A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of

BCHE. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM281 A A CTSB TGGGCAA CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM281 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of CTSB. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM281 A A CTSK TGGGCAA CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM281 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of CTSK. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM281 A A FHL2 TGGGCAA CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM281 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of FHL2, a GAM281 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM189.

GAM281 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM281 target gene. HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of HD. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM281 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM281 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of IGF1, a GAM281 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM281 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM281 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of IL1A, a GAM281 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A has

been established by previous studies. There are 2 structurally distinct forms of IL1: IL1(alpha), which is the acidic form with pI5, and IL1(beta) (IL1B; 147720), the neutral form with pI7. Both are 17- kD proteins coded by separate genes. The IL1A gene has 10,206 bp with 7 exons and 6 introns (Furutani et al. 1986). By Southern transfer analysis of DNAs from human- rodent somatic cell hybrids, Modi et al. (1988) assigned the IL1A gene to chromosome 2. Regional localization to 2q13- q21 was achieved by in situ hybridization. Lafage et al. (1989) confirmed assignment to 2q13 by in situ hybridization. The IL1A and IL1B proteins, which are synthesized by a variety of cell types including activated macrophages, keratinocytes, stimulated B lymphocytes, and fibroblasts, are potent mediators of inflammation and immunity. Lord et al. (1991) demonstrated that both the alpha and beta forms, but particularly the beta form, are transcribed in polymorphonuclear leukocytes stimulated with LPS. Both IL1A and IL1B stimulate osteoclast activity in vitro and are potent bone resorbing factors. Sabatino et al. (1988) studied the effects of 72- hour subcutaneous infusions of interleukins 1- alpha and - beta on plasma, calcium, and bone morphology. Both interleukins 1 caused a marked, dose-dependent increase in plasma calcium. Increased numbers of osteoclasts and bone resorption surfaces were observed on quantitative histomorphometry of bone. The results suggest a role for IL1 in the modulation of extracellular fluid calcium homeostasis. Hogquist et al. (1991) demonstrated that interleukin- 1 is involved in apoptosis (cell death). Both the alpha and the beta forms are released as a consequence of cell injury regardless of the insult Ki et al. (2001) analyzed the IL1A - 889 C/T genotype of 126 Korean patients with AD and found no significant difference in allele frequencies between patients and controls. Interestingly, there were no T/T homozygotes in the entire study population

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Hogquist, K. A.; Nett, M. A.; Unanue, E. R.; Chaplin, D. D. : Interleukin 1 is processed and released during apoptosis. Proc. Nat. Acad. Sci. 88: 8485- 8489, 1991. ; and

Ki, C.- S.; Na, D. L.; Kim, D. K.; Kim, H. J.; Kim, J.- W. : Lack of association of the interleukin- 1- alpha gene polymorphism with Alzheimer's disease in a Korean population. (Letter) Ann.

Further studies establishing the function and utilities of IL1A are found in John Hopkins OMIM database record ID 147760, and in cited publications listed in Table 9, hereby incorporated herein.

GAM281 A NGB A CACTGCACTCCAGCC TGGGCAA Neuroglobin (NGB, Accession NM_021257.2) is another GAM281 target gene. NGB BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of NGB, a GAM281 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB has been established by previous studies. By EST database searching for globin- like sequences, Burmester et al. (2000) identified cDNAs encoding human and mouse neuroglobin, symbolized NGB. Sequence analysis predicted that the 151- amino acid mouse and human proteins share 94% identity with each other but less than 25% identity with other vertebrate globins. RNA dot blot analysis revealed predominant expression in the brain, with strongest signals observed in the frontal lobe, the subthalamic nucleus, and the thalamus. In situ hybridization analysis demonstrated expression in mouse brain neuronal cells. RT- PCR detected only trace amounts of Ngb in other mouse tissues. Biochemical purification and size- exclusion chromatographic analysis showed that Ngb is a 16- kD monomer, found in low concentrations in mouse brain, that reversibly binds oxygen with an affinity nearly as high as that of MB but higher than that of HB. Genomic sequence analysis of a PAC clone determined that the NGB gene has a 4 exon/3 intron structure, distinct from that of other globin genes, and a promoter region that contains several putative SP1 (OMIM Ref. No. 189906)- binding sites. Five- prime RACE identified at least 3 transcription starting points but no TATA box, suggesting a housekeeping promoter. In an accompanying editorial, Moens and Dewilde (2000) noted that regions of the brain with lower expression of NGB (e.g. hippocampus) have lower resistance to ischemia and are frequently affected by neurofibrillary tangles in Alzheimer disease.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Burmester, T.; Weich, B.; Reinhardt, S.; Hankeln, T. : A vertebrate globin expressed in the brain. Nature 407: 520- 523, 2000. ; and

Moens, L.; Dewilde, S. : Globins in the brain. Nature 407: 461- 462, 2000.

Further studies establishing the function and utilities of NGB

are found in John Hopkins OMIM database record ID 605304, and in cited publications listed in Table 9, hereby incorporated herein.

GAM281 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM281 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM281 is therefore inhibition of PRND, a GAM281 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM282 APLP1 TGAGAGAGCAAGTGA Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A ATTTCCC NM_005166.2) is a GAM282 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM282 is therefore inhibition of APLP1, a GAM282 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 has been established by previous studies. Wasco et al. (1992) isolated a cDNA from a mouse brain library that encodes a protein whose predicted amino acid sequence is 42% identical and 64% similar to that of the amyloid beta protein precursor (APP; 104760). This 653- amino acid amyloid precursor- like protein (APLP) was also similar to APP in overall structure. Wasco et al. (1993) studied a panel of DNAs from human/rodent somatic cell lines to determine that the APLP locus is located on chromosome 19. Further study of somatic cell hybrids containing parts of chromosome 19 excluded the short arm of chromosome 19 as the site of APLP and placed it between the centromere and 19q13.2. The finding was of interest because of the existence of some families with late- onset (more than 65 years of age) Alzheimer disease that mapped to chromosome 19 and the fact that at least some families with Alzheimer disease have a mutation

in the APP gene on chromosome 21. Lenkkeri et al. (1998) determined the entire sequence of human APLP1 from a cosmid clone. The gene is 11.8 kb long and contains 17 exons. Since congenital nephrotic syndrome (CNF; 256300) maps close to APLP1, and because of the proposed interference of amyloid with basement membrane assembly, APLP1 had been considered a candidate gene for CNF. Lenkkeri et al. (1998) amplified all exon regions of the APLP1 gene by PCR and sequenced them from DNA of CNF patients. No differences were observed between CNF patients and controls, suggesting that mutations in APLP1 are not involved in the etiology of CNF.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Lenkkeri, U.; Kestila, M.; Lamerdin, J.; McCready, P.; Adamson, A.; Olsen, A.; Tryggvason, K. : Structure of the human amyloid-precursor- like protein gene APLP1 at 19q13.1. Hum. Genet. 102: 192-196, 1998. ; and

Wasco, W.; Brook, J. D.; Tanzi, R. E. : The amyloid precursor-like protein (APLP) gene maps to the long arm of human chromosome 19. Genomics 15: 237- 239, 1993.

Further studies establishing the function and utilities of APLP1 are found in John Hopkins OMIM database record ID 104775, and in cited publications listed in Table 9, hereby incorporated herein.

GAM282 A NPY A TGAGAGAGCAAGTGA ATTTCCC Neuropeptide Y (NPY, Accession NM_000905.2) is another GAM282 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM282 is therefore inhibition of NPY, a GAM282 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM282 A APBB2 A CTGGCTCTACCCTCT CACTTCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B (Fe65- (APBB2, Accession NM_173075.1) is another GAM282 target gene. APBB2 BINDING SITE is a target binding site found in the 5`

untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM282 is therefore inhibition of APBB2, a GAM282 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM282 PLAU CTGGCTCTACCCTCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1)
B A

CACTTCA is another GAM282 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM282 is therefore inhibition of PLAU, a GAM282 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU has been established by previous studies. Urokinase is the urinary plasminogen activator (uPA; EC 3.4.2.73). (Tissue plasminogen activator, 173370, is a second type; it has a single polypeptide chain of 70,000 daltons and is unrelated to urokinase immunologically.) Urokinase is a protein that has a molecular weight of about 54,000 daltons and is composed of 2 disulfide- linked chains, A and B, of molecular weights 18,000 and 33,000, respectively. Salerno et al. (1984) developed separate monoclonal antibodies for the A and B chains and by using them identified a single- chain biosynthetic precursor in a rabbit reticulocyte cell-free protein- synthesizing system directed by human kidney total polyadenylated RNA. Thus, the precursor must be cleaved in a way that the insulin precursor is cleaved. By combined somatic cell genetics, in situ hybridization, and Southern hybridization, Tripputi et al. (1985) localized the human urokinase gene to 10q24-qter. By use of specific cDNA probes in the study of human- mouse somatic cell hybrids, Rajput et al. (1985) mapped the human tissue plasminogen activator and urokinase genes to chromosomes 8 and 10,

respectively. By Southern blot analysis of DNA from mouse- Chinese hamster and mouse- rat somatic cell hybrids, Rajput et al. (1987) assigned the mouse equivalent (Plau) to mouse chromosome 14. Ahmed et al. (2001) stated that PLAU is 1 of 3 genes that are nested in the introns of PCDH15 (OMIM Ref. No. 605514), which maps to 10q21-q22. Animal model experiments lend further support to the function of PLAU. Rijneveld et al. (2002) generated mice deficient in Upa or Upar. Intranasal exposure to a beta- 2 integrin- dependent pathogen, Streptococcus pneumoniae, resulted in locally elevated levels of Upa in wildtype mouse lungs. In Upar - /- mice, there was less granulocyte accumulation but more bacteria in lungs, as well as reduced survival, compared with wildtype mice.

It is appreciated that the abovementioned animal model for PLAU is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Salerno, G.; Verde, P.; Nolli, M. L.; Corti, A.; Szots, H.; Meo, T.; Johnson, J.; Bullock, S.; Cassani, G.; Blasi, F. : Monoclonal antibodies to human urokinase identify the single- chain pro- urokinase precursor. Proc. Nat. Acad. Sci. 81: 110- 114, 1984. ; and

Tripputi, P.; Blasi, F.; Verde, P.; Cannizzaro, L. A.; Emanuel, B. S.; Croce, C. M. : Human urokinase gene is located on the long arm of chromosome 10. Proc. Nat. Acad. Sci. 82: 4448- 44.

Further studies establishing the function and utilities of PLAU are found in John Hopkins OMIM database record ID 191840, and in cited publications listed in Table 9, hereby incorporated herein.

GAM291 APBB2 AGATAGTTCTCTGTT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GTTGGGG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM291 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM291 is therefore inhibition of APBB2, a GAM291 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM291 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM291 FHL2 AGATAGTTCTCTGTT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GTTGGGG another GAM291 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM291 is therefore inhibition of FHL2, a GAM291 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM291 PRND AGATAGTTCTCTGTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GTTGGGG another GAM291 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM291 is therefore inhibition of PRND, a GAM291 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM291 TNFSF5 AGATAGTTCTCTGTT TNFSF5 (Accession NM_000074.1) is another GAM291 target gene. A A GTTGGGG TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM291 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM317 ADAM17 TAGGAAGTATTTTTT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AAAAACA factor, (ADAM17, Accession NM_021832.1) is a GAM317 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM317 is therefore inhibition of ADAM17, a GAM317 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 has been established by previous studies. Black et al. (1997) cloned a human cDNA encoding ADAM17, which they called TACE. The gene encodes an 824- amino acid polypeptide containing the features of the ADAM family: a secretory signal sequence, a disintegrin domain, and a metalloprotease domain. Expression studies showed that the encoded protein cleaves precursor tumor necrosis factor- alpha (TNFA; 191160) to its mature form. Northern blot analysis revealed that the gene was expressed as a 5- kb mRNA in all tissues examined. Black et al. (1997) generated mouse T cells with a homozygous deficiency in the TACE gene; these cells showed an 80 to 90% reduction in the release of TNFA. Yamazaki et al. (1998) used PCR of a backcross panel to map the mouse Tace gene to the proximal arm of chromosome 12. Hirohata et al. (1998) used radiation hybrids to map ADAM17 to human chromosome 2p25. Animal model experiments lend further support to the function of ADAM17. Peschon et al. (1998) found that mice lacking the zinc- binding domain of Tace died in utero after embryonic day 17.5 or failed to survive beyond 1 week of age.

It is appreciated that the abovementioned animal model for ADAM17 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Black, R. A.; Rauch, C. T.; Kozlosky, C. J.; Peschon, J. J.;

Slack, J. L.; Wolfson, M. F.; Castner, B. J.; Stocking, K. L.; Reddy, P.; Srinivasan, S.; Nelson, N.; Boiani, N.; Schooley, K. A.; Gerhart, M.; Davis, R.; Fitzner, J. N.; Johnson, R. S.; Paxton, R. J.; March, C. J.; Cerretti, D. P. : A metalloproteinase disintegrin that releases tumour- necrosis factor- alpha from cells. Nature 385: 729- 733, 1997. ; and

Peschon, J. J.; Slack, J. L.; Reddy, P.; Stocking, K. L.; Sunnarborg, S. W.; Lee, D. C.; Russell, W. E.; Castner, B. J.; Johnson, R. S.; Fitzner, J. N.; Boyce, R. W.; Nelson, N.; Kozlosk.

Further studies establishing the function and utilities of ADAM17 are found in John Hopkins OMIM database record ID 603639, and in cited publications listed in Table 9, hereby incorporated herein.

GAM317 APPBP2 TAGGAAGTATTTTTT AAAAAACA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM317 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM317 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM317 is therefore inhibition of APPBP2, a GAM317 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM317 GYPA TAGGAAGTATTTTTT AAAAAACA Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM317 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM317 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM317 is therefore inhibition of GYPA, a GAM317 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA has been established by previous studies. On the basis of studies in the family of a child with a translocation chromosome, German et al. (1968) suggested that the MN

locus is either in the middle of chromosome 2 or near the distal end of the long arm of chromosome 4. Using 'banding techniques,' German and Chaganti (1973) restudied the translocation they reported in 1968 and concluded that MN can be tentatively assigned to the area of band q14 in the proximal portion of the long arm of chromosome 2. Weitkamp et al. (1972) presented data suggesting that the MN locus and the beta hemoglobin locus (OMIM Ref. No. 141900) are linked. (This has, of course, been disproved.) Barbosa et al. (1975) excluded a recombination fraction of less than 0.30 for MN and Hb beta. The results supported a lower recombination fraction for males. Linkage with the Alzheimer locus (OMIM Ref. No. 104300) and with colonic polyposis (OMIM Ref. No. 175100) has been suspected. Recombination data suggested that the MN and acid phosphatase (ACP1; 171500) loci are far apart (Weitkamp et al. 1975). Cook et al. (1978) excluded MNSs from chromosome 9 by exclusion mapping that incorporated data both from families with chromosome markers and from linkage studies with firmly assigned markers. MNSs was subsequently assigned to chromosome 4. In a further study of the propositus of the 2q;4q translocation family, German et al. (1979) showed by banding that the breaks had occurred at 2q14 and 4q29 and that a minute segment had been lost at the site of break. Whether the loss was from chromosome 2 or 4 was not certain because both have several short bands at these sites and only one band was missing in the proband. The proband lacked blood type 's' (GPB; 111740) which he should have received from his 'ss' father, had signs of a modified red cell membrane, and had developmental abnormalities. Since the abnormalities of phenotype appeared at the same time as the chromosomal abnormality, German et al. (1979) suggested that deletion was the basis of all the changes. Since Weitkamp (1978) reported observations indicating strongly that MNSs is not near 2q14, German et al. (1979) concluded that it must be in a band near 4q29. Cook et al. (1980) favored 4q28 over 4q31. For males, Bias and Meyers (1979) found a maximal lod score of 3.99 at theta 0.18 for linkage of Stoltzfus (OMIM Ref. No. 111800) and MNS. Acid phosphatase and Kidd both gave lods of 0.32 with Stoltzfus at a male- theta of 0.20. Linkage of Gc and MNSs at recombination frequencies of less than 25% in males and 30% in females was excluded by Weitkamp (1978). For MN versus Gc, Falk et al. (1979) found a male lod score of 3.75 at a recombination fraction of 0.30. In females the maximal lod score was 0.34 at a recombination fraction of 0.42. From analysis of MNSs blood groups in families with chromosome 4 rearrangements, both deletion analysis and family linkage study, Cook et al. (1981) concluded that the MNSs 'locus' lies in the region 4q28- q31. Red cells with the rare En(a-) variant are resistant to falciparum malaria (Pasvol et al. 1982). Such cells lack glycophorin A, the major red cell sialoglycoprotein (Siebert and Fukuda, 1986). The rare U(-) variant of the Ss system, which lacks the other major sialoglycoprotein, glycophorin B, is relatively resistant to invasion. Wr(b)- negative cells are also resistant to invasion by P. falciparum despite the fact that they

have normal amounts of glycophorins A and B on their surface. All of these observations, as well as experiments using antibodies to glycophorins and certain sugars, particularly N- acetylglucosamine, have led to a tentative model of the role of glycophorin in the red cell invasion of P. falciparum (Pasvol and Wilson, 1982). Langlois et al. (1986) studied the frequency of red cells with loss of expression at the glycophorin A locus (GPA). Glycophorin A is present in about 500,000 copies per red cell. The 2 allelic forms of GPA, blood group M and blood group N, are identical except for 2 amino acid substitutions at positions 1 and 5 from the amino terminus (Prohaska et al. 1986). Using monoclonal antibodies, Langlois et al. (1986) identified expression loss mutants. They found a frequency of about 1 in 100,000 cells in normals and a significant increase in the variant cells in cancer patients after exposure to mutagenic chemotherapy drugs. Langlois et al. (1987) demonstrated a linear relationship between frequency of mutations at the glycophorin A locus and radiation exposure in atomic bomb survivors. Grant and Bigbee (1994) discussed the use of the GPA assay to evaluate the creation of somatic mutations by cancer chemotherapy.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Grant, S. G.; Bigbee, W. L. : Bone marrow somatic mutation after genotoxic cancer therapy. (Letter) Lancet 343: 1507- 1508, 1994. ; and

Cook, P. J. L.; Lindenbaum, R. H.; Salonen, R.; de la Chapelle, A.; Daker, M. G.; Buckton, K. E.; Noades, J. E.; Tippett, P. : The MNSs blood groups of families with chromosome 4 rearran.

Further studies establishing the function and utilities of GYPA are found in John Hopkins OMIM database record ID 111300, and in cited publications listed in Table 9, hereby incorporated herein.

GAM317 IL1A TAGGAAGTATTTTTT AAAAACA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM317 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM317 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM317 is therefore inhibition of IL1A, a GAM317 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM317 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM329 APPBP2 TCATAAACTGGCAAG CACTACC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM329 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM329 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM329 is therefore inhibition of APPBP2, a GAM329 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM329 MAPK10 TCATAAACTGGCAAG CACTACC Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM329 target gene. MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPK10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM329 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM329 is therefore inhibition of MAPK10, a GAM329 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM330 FHL2 ACTGCACTCCAGCCT GGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM330 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, A A

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM330 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM330 is therefore inhibition of FHL2, a GAM330 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM330 IGF1 ACTGCACTCCAGCCT GGGTGAC — Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM330 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM330 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM330 is therefore inhibition of IGF1, a GAM330 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM330 PRND ACTGCACTCCAGCCT GGGTGAC — Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM330 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM330 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM330 is therefore inhibition of PRND, a GAM330 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM44.

GAM335 CHAT CCCCAGTCAATGCTT Choline Acetyltransferase (CHAT, Accession NM_020549.2) is a A A

CTCTCCA GAM335 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM335 is therefore inhibition of CHAT, a GAM335 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT has been established by previous studies. Cholinergic systems are implicated in numerous neurologic functions. Alteration in some cholinergic neurons may account for the disturbances of Alzheimer disease. Cholinergic neurons are best characterized by the enzyme choline acetyltransferase (CHAT; EC 2.3.1.6), which catalyzes the biosynthesis of acetylcholine. Barrard et al. (1987) isolated a cDNA clone encoding the complete sequence of porcine CHAT. By use of this clone in the study of DNA from a panel of human- rodent somatic cell hybrids, Cohen- Haguenauer et al. (1990) demonstrated that the CHAT gene is located on human chromosome 10. Strauss et al. (1991) confirmed the mapping to chromosome 10 and regionalized the assignment to 10q11- q22.2 by in situ hybridization. Viegas-Pequignot et al. (1991) used a human choline acetyltransferase genomic sequence and in situ hybridization studies to sublocalize the gene to human chromosome 10q11.2. Toussaint et al. (1992) isolated and partially sequenced a human CHAT genomic clone. The fragment they studied contained the first 4 exons with an AUG initiator codon and potential control regions including TATA, CAAT, GC boxes, and several transcription control sequences. By analyzing cDNAs from mouse spinal cord, Misawa et al. (1992) demonstrated 7 polymorphic forms of CHAT resulting from the alternative splicing of 3 5- prime exons named R, N, and M to exon 1 which contains the ATG initiation codon. Chireux et al. (1995) identified 2 alternative first exons in human choline acetyltransferase. They found regions homologous to rodent exons R and M but found that rodent exon N was not conserved in the human gene. Mutations in genes encoding choline acetyltransferase affecting motility have been described in C. elegans and Drosophila. Ohno et al. (2001) described the first mutations in human CHAT. The mutations were identified in a congenital myasthenic syndrome associated with frequently fatal episodes of apnea (CMS- EA, or FIMG; 254210). Studies of the neuromuscular junction in this disorder showed a stimulation-dependent decrease of the amplitude of the miniature endplate

potential and no deficiency of the acetylcholine receptor. These findings pointed to a defect in acetylcholine resynthesis or vesicular filling and to CHAT as one of the candidate genes. Direct sequencing of CHAT demonstrated 10 recessive mutations in 5 patients with FIMG. One mutation was a frameshifting null mutation: 523insCC (118490.0001). Three missense mutations, I305T (118490.0009), R420C (118490.0010), and E441K (118490.0003), markedly reduced CHAT expression in COS cells. Kinetic studies of 9 bacterially expressed CHAT mutants demonstrated that 1 mutant, E441K, lacked catalytic activity, and 8 mutants had significantly impaired catalytic efficiencies. The 5 patients in whom Ohno et al. (2001) demonstrated mutations of the CHAT gene ranged from age 4 to age 40 at the time of report. Four were male and 1 female. All had myasthenic symptoms since birth or early infancy, negative tests for anti- AChR antibodies, and abrupt episodic crises with increased weakness, bulbar paralysis, and apnea precipitated by undue exertion, fever, or excitement. One of the patients had 3 affected sibs and another had 2; 3 of the 5 affected sibs died during febrile episodes, and 1 died suddenly without apparent cause

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Ohno, K.; Tsujino, A.; Brengman, J. M.; Harper, C. M.; Bajzer, Z.; Udd, B.; Beyring, R.; Robb, S.; Kirkham, F. J.; Engel, A. G. : Choline acetyltransferase mutations cause myasthenic syndrome associated with episodic apnea in humans. Proc. Nat. Acad. Sci. 98: 2017- 2022, 2001. ; and

Misawa, H.; Ishii, K.; Deguchi, T. : Gene expression of mouse choline acetyltransferase: alternative splicing and identification of a highly active promoter region. J. Biol. Chem. 267:.

Further studies establishing the function and utilities of CHAT are found in John Hopkins OMIM database record ID 118490, and in cited publications listed in Table 9, hereby incorporated herein.

GAM335 DLST CCCCAGTCAATGCTT CTCTCCA A A Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM335 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM335 is therefore inhibition of DLST, a GAM335 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM335 TNFRSF5 CCCCAGTCAATGCTT TNFRSF5 (Accession NM_152854.1) is another GAM335 target gene. A A

CTCTCCA TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM335 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM335 TRPM2 CCCCAGTCAATGCTT TRPM2 (Accession NM_003307.1) is another GAM335 target gene. A A

CTCTCCA TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM335 is therefore inhibition of TRPM2, a GAM335 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 has been established by previous studies. Perraud et al. (2001) demonstrated that a 350- amino acid protein, designated NUDT9 (OMIM Ref. No. 606022), and a homologous domain (NUDT9 homology domain) near the C terminus of the LTRPC2 putative cation channel both function as specific ADP- ribose pyrophosphatases. Whole- cell and single- channel analysis of HEK293 cells expressing LTRPC2 showed that LTRPC2 functions as a calcium-permeable cation channel that is specifically gated by free ADP-ribose. The expression of native LTRPC2 transcripts is detectable in many tissues, including the U937 monocyte cell line, in which ADP-ribose induces large cation currents that closely match those mediated by recombinant LTRPC2. Perraud et al. (2001) concluded that intracellular ADP- ribose regulates calcium entry into cells that express LTRPC2. Hara et al. (2002) reported that LTRPC2 is activated by micromolar levels of H2O2 and agents that produce reactive

oxygen/nitrogen species. This sensitivity of LTRPC2 to redox state modifiers was attributable to an agonistic binding of beta-nicotinamide adenine dinucleotide to the MutT motif. Arachidonic acid and calcium were important positive regulators for LTRPC2. Heterologous LTRPC2 expression conferred susceptibility to death on HEK cells. Antisense oligonucleotide experiments revealed physiologic involvement of native LTRPC2 in H2O2- and TNF- alpha (OMIM Ref. No. 191160)- induced calcium influx and cell death. Thus, LTRPC2 represents an important intrinsic mechanism that mediates calcium and sodium overload in response to disturbance of redox state in cell death.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Perraud, A.- L.; Fleig, A.; Dunn, C. A.; Bagley, L. A.; Launay, P.; Schmitz, C.; Stokes, A. J.; Zhu, Q.; Bessman, M. J.; Penner, R.; Kinet, J.- P.; Scharenberg, A. M. : ADP- ribose gating of the calcium- permeable LTRPC2 channel revealed by Nudix motif homology. Nature 411: 595- 599, 2001. ; and

Hara, Y.; Wakamori, M.; Ishii, M.; Maeno, E.; Nishida, M.; Yoshida, T.; Yamada, H.; Shimizu, S.; Mori, E.; Kudoh, J.; Shimizu, S.; Kurose, H.; Okada, Y.; Imoto, K.; Mori, Y. : LTRPC2 Ca(2 .

Further studies establishing the function and utilities of TRPM2 are found in John Hopkins OMIM database record ID 603749, and in cited publications listed in Table 9, hereby incorporated herein.

GAM347 IAPP TCATTGCAACCTCCA CCTCCTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM347 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM347 is therefore inhibition of IAPP, a GAM347 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP has been established by previous studies. IAPP has cysteine residues in positions 2 and 7, a feature found in all known calcitonin gene- related peptides (OMIM Ref. No. 114130). IAPP shows 46% amino acid sequence homology with CGRP II (OMIM Ref. No. 114160). Since IAPP has been demonstrated immunochemically in normal beta cells of several mammals, it probably has an important role in

respect to pancreatic islet function. Cooper et al. (1988) presented evidence that the 37- amino acid peptide may be a hormone present in normal individuals; hence, 'diabetes- associated peptide' is an inappropriate designation. Cooper et al. (1988) synthesized whole amylin by using solid- phase techniques, with formation of the disulfide linkage by oxidation in dilute aqueous solution and recovery of the peptide by lyophilization. The effects of amylin on glucose metabolism were studied by 2 in vitro preparations: isolated rat soleus muscle strips and isolated rat adipocytes. In skeletal muscle, amylin resulted in a marked decrease in insulin- stimulated glycogen synthesis with resulting reduction in insulin- stimulated glucose uptake. In muscle, amylin resulted in a failure of response to the concentration of insulin required to stimulate glucose uptake half- maximally in untreated muscles. No effects were observed in isolated adipocytes. Amylin may be a factor in the etiology of the insulin resistance in type II diabetes mellitus. A correlation has been observed between the extent of islet amyloid deposition and the clinical severity of type II diabetes. Mosselman et al. (1988) isolated and partially characterized the human IAPP gene. By hybridization to DNA from human- rodent somatic cell hybrids, Mosselman et al. (1988) demonstrated that the IAPP gene is located on 12pter- q14. Because of the striking parallelism in the genetic constitution of chromosomes 11 and 12, suggesting an ancient tetraploidization, the mapping of this calcitonin- related gene to 12 is of interest; 2 calcitonin genes are located on 11p. The amyloid in amyloid- producing medullary carcinoma of the thyroid, a feature of multiple endocrine neoplasia type II (OMIM Ref. No. 171400), is derived from calcitonin. Sanke et al. (1988) showed that the islet amyloid polypeptide is derived from an 89- amino acid precursor by proteolytic processing. The processed peptide, 37- amino acids long, is bracketed at its NH(2) and COOH termini by lys- arg and gly- lys- arg, respectively. The data indicated that this amyloid peptide is generated by proteolytic processing similar to that for proinsulin and other islet prohormones and also that the peptide may be carboxyamidated. Mosselman et al. (1989) found that 2 exons, which are approximately 5 kb apart, encode the 89- amino acid pre- pro- IAPP. A putative signal sequence at the amino- terminus of the precursor suggested that IAPP is a secreted protein. From the DNA sequence of a partial cDNA clone and a phage lambda genomic clone of the coding region of the amylin gene, Roberts et al. (1989) concluded that this peptide is synthesized as a precursor peptide called proamylin. The sequences of the genes for amylin and the calcitonin gene- related peptides show strong similarity, especially in their 5- prime coding regions, where these peptides have a conserved intramolecular disulfide bridge, and also in their 3- prime coding regions, where the presence of a glycine codon strongly suggests that the carboxyl- terminal residue, like that of CGRP, is amidated. In a study of the biologic activity of amylin synthesized with or without the disulfide bridge and/or amidation, Roberts et al. (1989) demonstrated that both features are necessary for full

biologic activity, thereby confirming the functional importance of those regions of the molecule that have been conserved at both protein and genetic levels. Animal model experiments lend further support to the function of IAPP. Janson et al. (1996) created homozygous transgenic mice with a high level of expression of human IAPP. Male transgenic mice spontaneously developed diabetes mellitus by 8 weeks of age, which was associated with selective beta- cell death and impaired insulin secretion. Approximately 20% of female transgenic mice spontaneously developed diabetes at 30 weeks of age when beta- cell degeneration and both amorphous and amyloid deposits of IAPP were present. Large deposits of IAPP- derived amyloid did not appear to be important to the cytotoxicity, but early, small amorphous intra- and extracellular aggregates of human IAPP were consistently present at the time of beta- cell death and therefore may be the most cytotoxic form of IAPP.

It is appreciated that the abovementioned animal model for IAPP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Cooper, G. J.; Willis, A. C.; Clark, A.; Turner, R. C.; Sim, R. B.; Reid, K. B. : Purification and characterization of a peptide from amyloid- rich pancreases of type 2 diabetic patients. Proc. Nat. Acad. Sci. 84: 8628- 8632, 1987. ; and

Cooper, G. J. S.; Leighton, B.; Dimitriadis, G. D.; Parry-Billings, M.; Kowalchuk, J. M.; Howland, K.; Rothbard, J. B.; Willis, A. C.; Reid, K. B. M. : Amylin found in amyloid deposits.

Further studies establishing the function and utilities of IAPP are found in John Hopkins OMIM database record ID 147940, and in cited publications listed in Table 9, hereby incorporated herein.

GAM347 ACE CTCCTAGGCTGGAGT GCAGTGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is another GAM347 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM347 is therefore inhibition of ACE, a GAM347 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with

Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM347 ADAM17 CTCCTAGGCTGGAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis B A
GCAGTGG factor, (ADAM17, Accession NM_003183.3) is another GAM347 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM347 is therefore inhibition of ADAM17, a GAM347 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM347 APBB1 CTCCTAGGCTGGAGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A
GCAGTGG 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM347 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM347 is therefore inhibition of APBB1, a GAM347 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 has been established by previous studies. APP, a widely expressed cell surface protein, is cleaved in the transmembrane region by gamma-secretase. Gamma- cleavage of APP produces the extracellular amyloid beta peptide of Alzheimer disease and releases an intracellular tail fragment. Cao and Sudhof (2001) demonstrated that the cytoplasmic tail of APP forms a multimeric complex with the nuclear adaptor protein Fe65 and the histone acetyltransferase TIP60 (OMIM Ref. No.

601409). This complex potently stimulated transcription via heterologous Gal4 or LexA DNA binding domains, suggesting that release of the cytoplasmic tail of APP by gamma- cleavage may function in gene expression. Hu et al. (2002) demonstrated that a protective (minor) second allele alters the splicing of the terminal exon by selection of an alternative acceptor site within exon 14. The resulting isoform, FE65a2, lacks the 55 amino acids of the C-terminal APP binding site, which are replaced by 53 missense residues. Pull- down assays confirmed that the FE65a2 isoform bound to APP less efficiently, suggesting that an attenuated binding of FE65 with APP may be, in part, responsible for resistance to the very late onset disease. Sequence analysis of FE65 in mice, non-human primates, and man revealed that the susceptibility allele, which codes for stronger binding of the FE65 protein to APP, was favored by natural selection leading to our lineage. The authors hypothesized that this allele may contribute to a very late onset form of Alzheimer disease.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Cao, X.; Sudhof, T. C. : A transcriptively active complex of APP with Fe65 and histone acetyltransferase Tip60. Science 293: 115-120, 2001. ; and

Hu, Q.; Cool, B. H.; Wang, B.; Hearn, M. G.; Martin, G. M. : A candidate molecular mechanism for the association of an intronic polymorphism of FE65 with resistance to very late onset d.

Further studies establishing the function and utilities of APBB1 are found in John Hopkins OMIM database record ID 602709, and in cited publications listed in Table 9, hereby incorporated herein.

GAM347	APPBP2	CTCCTAGGCTGGAGT GCAGTGG	Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM347 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM347 is therefore inhibition of APPBP2, a GAM347 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM347 FPRL1 CTCCTAGGCTGGAGT FPRL1 (Accession NM_001462.1) is another GAM347 target gene. B A

GCAGTGG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM347 is therefore inhibition of FPRL1. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM347 IAPP CTCCTAGGCTGGAGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM347 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM347 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

GCAGTGG

Another function of GAM347 is therefore inhibition of IAPP, a GAM347 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP has been established by previous studies. IAPP has cysteine residues in positions 2 and 7, a feature found in all known calcitonin gene- related peptides (OMIM Ref. No. 114130). IAPP shows 46% amino acid sequence homology with CGRP II (OMIM Ref. No. 114160). Since IAPP has been demonstrated immunochemically in normal beta cells of several mammals, it probably has an important role in respect to pancreatic islet function. Cooper et al. (1988) presented evidence that the 37- amino acid peptide may be a hormone present in normal individuals; hence, 'diabetes- associated peptide' is an inappropriate designation. Cooper et al. (1988) synthesized whole amylin by using solid- phase techniques, with formation of the disulfide linkage by oxidation in dilute aqueous solution and recovery of the peptide by lyophilization. The effects of amylin on glucose metabolism were studied by 2 in vitro preparations: isolated rat soleus muscle strips and isolated rat adipocytes. In skeletal muscle, amylin resulted in a marked decrease in insulin- stimulated glycogen synthesis with resulting reduction in insulin- stimulated glucose uptake. In muscle, amylin resulted in a failure of response to the concentration of insulin required to stimulate glucose uptake

half- maximally in untreated muscles. No effects were observed in isolated adipocytes. Amylin may be a factor in the etiology of the insulin resistance in type II diabetes mellitus. A correlation has been observed between the extent of islet amyloid deposition and the clinical severity of type II diabetes. Mosselman et al. (1988) isolated and partially characterized the human IAPP gene. By hybridization to DNA from human- rodent somatic cell hybrids, Mosselman et al. (1988) demonstrated that the IAPP gene is located on 12pter- q14. Because of the striking parallelism in the genetic constitution of chromosomes 11 and 12, suggesting an ancient tetraploidization, the mapping of this calcitonin- related gene to 12 is of interest; 2 calcitonin genes are located on 11p. The amyloid in amyloid- producing medullary carcinoma of the thyroid, a feature of multiple endocrine neoplasia type II (OMIM Ref. No. 171400), is derived from calcitonin. Sanke et al. (1988) showed that the islet amyloid polypeptide is derived from an 89- amino acid precursor by proteolytic processing. The processed peptide, 37- amino acids long, is bracketed at its NH(2) and COOH termini by lys- arg and gly- lys- arg, respectively. The data indicated that this amyloid peptide is generated by proteolytic processing similar to that for proinsulin and other islet prohormones and also that the peptide may be carboxyamidated. Mosselman et al. (1989) found that 2 exons, which are approximately 5 kb apart, encode the 89- amino acid pre- pro- IAPP. A putative signal sequence at the amino- terminus of the precursor suggested that IAPP is a secreted protein. From the DNA sequence of a partial cDNA clone and a phage lambda genomic clone of the coding region of the amylin gene, Roberts et al. (1989) concluded that this peptide is synthesized as a precursor peptide called proamylin. The sequences of the genes for amylin and the calcitonin gene- related peptides show strong similarity, especially in their 5- prime coding regions, where these peptides have a conserved intramolecular disulfide bridge, and also in their 3- prime coding regions, where the presence of a glycine codon strongly suggests that the carboxyl- terminal residue, like that of CGRP, is amidated. In a study of the biologic activity of amylin synthesized with or without the disulfide bridge and/or amidation, Roberts et al. (1989) demonstrated that both features are necessary for full biologic activity, thereby confirming the functional importance of those regions of the molecule that have been conserved at both protein and genetic levels. Animal model experiments lend further support to the function of IAPP. Janson et al. (1996) created homozygous transgenic mice with a high level of expression of human IAPP. Male transgenic mice spontaneously developed diabetes mellitus by 8 weeks of age, which was associated with selective beta- cell death and impaired insulin secretion. Approximately 20% of female transgenic mice spontaneously developed diabetes at 30 weeks of age when beta- cell degeneration and both amorphous and amyloid deposits of IAPP were present. Large deposits of IAPP- derived amyloid did not appear to be important to the cytotoxicity, but early, small amorphous intra- and extracellular aggregates of human IAPP were

consistently present at the time of beta- cell death and therefore may be the most cytotoxic form of IAPP.

It is appreciated that the abovementioned animal model for IAPP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Cooper, G. J.; Willis, A. C.; Clark, A.; Turner, R. C.; Sim, R. B.; Reid, K. B. : Purification and characterization of a peptide from amyloid- rich pancreases of type 2 diabetic patients. Proc. Nat. Acad. Sci. 84: 8628- 8632, 1987. ; and

Cooper, G. J. S.; Leighton, B.; Dimitriadis, G. D.; Parry-Billings, M.; Kowalchuk, J. M.; Howland, K.; Rothbard, J. B.; Willis, A. C.; Reid, K. B. M. : Amylin found in amyloid deposits.

Further studies establishing the function and utilities of IAPP are found in John Hopkins OMIM database record ID 147940, and in cited publications listed in Table 9, hereby incorporated herein.

GAM354 AVP ACACAGGCCCAGAGA AVP (Accession NM_000490.2) is a GAM354 target gene. AVP A A GGCAGTG BINDING SITE1 and AVP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by AVP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE1 and AVP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM354 is therefore inhibition of AVP. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM354 CRAT ACACAGGCCCAGAGA Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A GGCAGTG another GAM354 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of CRAT, a GAM354 target gene which catalyzes the reversible transfer

of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT has been established by previous studies. Carnitine acyltransferases are a group of enzymes that catalyze the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine, thus forming the corresponding acylcarnitine. These enzymes can be distinguished according to their substrate specificity in carnitine palmitoyltransferase (see OMIM Ref. No. CPT1, 600528 and CPT2, 600650), carnitine octanoyltransferase (CROT; 606090), and carnitine acetyltransferase (EC 2.3.1.7). CRAT is a key enzyme for metabolic pathways involved with the control of the acyl- CoA/CoA ratio in mitochondria, peroxisomes, and endoplasmic reticulum Acetylcarnitine, which can be a precursor for acetylcholine synthesis catalyzed by choline acetyltransferase, is thought to slow the rate of mental deterioration in Alzheimer patients, and Kalaria and Harik (1992) found decreased function of CRAT in the brain of Alzheimer patients

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Kalaria, R. N.; Harik, S. I. : Carnitine acetyltransferase activity in the human brain and its microvessels is decreased in Alzheimer's disease. Ann. Neurol. 32: 583- 586, 1992. ; and

van der Leij, F. R.; Huijkman, N. C. A.; Boomsma, C.; Kuipers, J. R. G.; Bartelds, B. : Genomics of the human carnitine acyltransferase genes. Molec. Genet. Metab. 71: 139- 153, 2000.

Further studies establishing the function and utilities of CRAT are found in John Hopkins OMIM database record ID 600184, and in cited publications listed in Table 9, hereby incorporated herein.

GAM354 A A CTSB GGCAGTG ACACAGGCCCAGAGA CTSB (Accession NM_001908.2) is another GAM354 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of CTSB. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM354 MAPT ACACAGGCCCAGAGA Microtubule- associated Protein Tau (MAPT, Accession A A
GGCAGTG NM_173727.1) is another GAM354 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of MAPT, a GAM354 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM354 NCSTN ACACAGGCCCAGAGA NCSTN (Accession NM_015331.1) is another GAM354 target gene. A A
GGCAGTG NCSTN BINDING SITE1 and NCSTN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCSTN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE1 and NCSTN BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of NCSTN, a GAM354 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM354 S100B ACACAGGCCCAGAGA S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A
GGCAGTG NM_006272.1) is another GAM354 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of

S100B, a GAM354 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM354 A A SLC17A7 ACACAGGCCCAGAGA GGCAGTG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM354 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of SLC17A7, a GAM354 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 has been established by previous studies. Bellocchio et al. (2000) demonstrated that BNPI transports glutamate into synaptic vesicles. In addition, they showed that this vesicular glutamate transporter, which they renamed VGLUT1, exhibits a conductance for chloride that is blocked by glutamate. Bellocchio et al. (2000) found that glutamate was transported by BNPI in the absence of sodium. Vesicular glutamate transport has a substantially lower apparent affinity than the plasma membrane excitatory amino acid transporters. Glutamate transport by BNPI is saturated with a K(m) of approximately 2 mM, in the same range as transport by synaptic vesicles. Finally, plasma membrane glutamate transporters recognize both aspartate and glutamate as substrates, whereas vesicular glutamate transport does not recognize aspartate. Vesicular glutamate transport has a biphasic dependence on chloride concentration that may reflect the presence of anion binding site distinct from the site of substrate recognition. Chloride concentrations of approximately 4 to 10 mM appear optimal for transport, with substantially lower activity detected at higher and lower levels. BNPI transports glutamate with all of the functional characteristics previously reported for glutamate transport into native synaptic vesicles from the brain. It localizes to synaptic vesicles, and the mutant C. elegans eat- 4 (a BNPI ortholog) reduces glutamate release. BNPI thus functions as a vesicular glutamate transporter, VGLUT1. Only a subset of glutamate neurons expresses VGLUT1, but a closely related sequence has been identified that

appears to be expressed in brain regions that lack VGLUT1 (Aihara et al. 2000). The 2 isoforms together may therefore account for the uptake of glutamate by synaptic vesicles from all glutamatergic neurons. VGLUT1 (BNPI1) may thus function as both a phosphate transporter, presumably at the plasma membrane, and a glutamate transporter in synaptic vesicles. Bellocchio et al. (2000) stated that the localization of VGLUT1 to synaptic vesicles, the phenotype of the eat- 4 mutant, and biochemical evidence strongly suggest that vesicular glutamate transport is its primary role. Takamori et al. (2000) independently showed that expression of BNPI results in glutamate uptake by intracellular vesicles. Substrate specificity and energy dependence are very similar to glutamate uptake by synaptic vesicles. Stimulation of exocytosis resulted in quantal release of glutamate from BNPI- expressing cells. Furthermore, Takamori et al. (2000) expressed BNPI in neurons containing GABA (see OMIM Ref. No. 137150) and maintained them as cultures of single neurons that form synapses to themselves. After stimulation of these neurons, a component of the postsynaptic current is mediated by glutamate as it is blocked by a combination of the glutamate receptor antagonists, but is insensitive to a GABA- A receptor (see OMIM Ref. No. 137192) antagonist. Takamori et al. (2000) concluded that BNPI functions as a vesicular glutamate transporter and that expression of BNPI suffices to define a glutamatergic phenotype in neurons.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Bellocchio, E. E.; Reimer, R. J.; Fremeau, R. T. Jr.; Edwards, R. H. : Uptake of glutamate into synaptic vesicles by an inorganic phosphate transporter. Science 289: 957- 960, 2000. ; and

Takamori, S.; Rhee, J. S.; Rosenmund, C.; Jahn, R. : Identification of a vesicular glutamate transporter that defines a glutamatergic phenotype in neurons. Nature 407: 189- 194, 2000.

Further studies establishing the function and utilities of SLC17A7 are found in John Hopkins OMIM database record ID 605208, and in cited publications listed in Table 9, hereby incorporated herein.

GAM354 A A — SNCB ACACAGGCCCAGAGA GGCAGTG — Synuclein, Beta (SNCB, Accession NM_003085.2) is another target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM354 is therefore inhibition of SNCB, a GAM354 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB has been established by previous studies. Jakes et al. (1994) examined the composition of proteins found in Alzheimer disease neurofibrillary lesions. They identified 2 abundant proteins, both with apparent molecular weights of 19 kD. One was alpha- synuclein (OMIM Ref. No. 163890). Cloning and sequencing revealed that the other was a novel 134- amino acid protein, which they named beta- synuclein. The sequences of the 2 proteins are 61% identical, establishing the existence of a family of human brain synucleins. Northern blotting detected a strong 1.3- kb signal in adult human brain. Weak hybridization was observed in skeletal muscle. Immunohistochemical localization showed that beta- synuclein is concentrated in presynaptic nerve terminals. Spillantini et al. (1997) found no staining of beta- synuclein in Lewy bodies associated with Parkinson disease. Consistent with this, Lavedan et al. (1998) found no evidence of linkage to SNCB in the probands of 71 families with apparent autosomal dominant Parkinson disease drawn from the various ethnic backgrounds. Lavedan et al. (1998) found that the SNCB gene contains 5 coding exons and at least one 5- prime untranslated exon, with intron- exon junctions similar to those of alpha- synuclein. Spillantini et al. (1995) used PCR panels and fluorescence in situ hybridization to map the SNCB gene to human chromosome 5q35.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Lavedan, C.; Buchholtz, S.; Auburger, G.; Albin, R. L.; Athanassiadou, A.; Blancato, J.; Burguera, J. A.; Ferrell, R. E.; Kostic, V.; Leroy, E.; Leube, B.; Mota- Vieira, L.; and 9 others : Absence of mutation in the beta- and gamma- synuclein genes in familial autosomal dominant Parkinson's disease. DNA Research 5: 401- 402, 1998. ; and

Lavedan, C.; Leroy, E.; Torres, R.; Dehejia, A.; Dutra, A.; Buchholtz, S.; Nussbaum, R. L.; Polymeropoulos, M. H. : Genomic organization and expression of the human beta- synuclein gene.

Further studies establishing the function and utilities of SNCB are found in John Hopkins OMIM database record ID 602569, and in cited publications listed in Table 9, hereby incorporated herein.

GAM361 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TAGGCAA a GAM361 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are

target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM361 is therefore inhibition of FHL2, a GAM361 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM361 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM361 target gene. HD A A
TAGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM361 is therefore inhibition of HD. Accordingly, utilities of GAM361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM361 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TAGGCAA NM_000618.2) is another GAM361 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM361 is therefore inhibition of IGF1, a GAM361 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM361 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TAGGCAA another GAM361 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM361 is therefore inhibition of PRND, a GAM361 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM367 GYPA TGAGGTAAGTATGTT Glycophorin A (includes MN blood group) (GYPA, Accession A A

ATTGGAA NM_002099.2) is a GAM367 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM367 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM367 is therefore inhibition of GYPA, a GAM367 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM367 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM388 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM388 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM388 is therefore inhibition of APP. Accordingly, utilities of GAM388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM401 ACE TCACTGCAACCTCTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

CCTTCCG (ACE, Accession NM_152831.1) is a GAM401 target gene. ACE BINDING

SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM401 is therefore inhibition of ACE, a GAM401 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM401 IAPP TCACTGCAACCTCTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A CCTTCCG another GAM401 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM401 is therefore inhibition of IAPP, a GAM401 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM401 MTNR1A TCACTGCAACCTCTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A CCTTCCG another GAM401 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM401 is therefore inhibition of MTNR1A, a GAM401 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MTNR1A.The function of MTNR1A has been established by previous studies. Reppert and Weaver (1995) reviewed the hormonal properties of melatonin and the characteristics of the melatonin receptors. Brzezinski (1997) likewise gave a comprehensive review of the function of melatonin and its clinical implications. Sleep disruption, nightly restlessness, sundowning, and other circadian disturbances are frequently seen in Alzheimer disease (AD; 104300) patients. Since melatonin is the main endocrine message for circadian rhythmicity from the pineal, Liu et al. (1999) studied melatonin levels in the cerebrospinal fluid (CSF) of 85 AD patients and 82 age- matched controls. In old control subjects (older than 80 years of age), CSF melatonin levels were half those of control subjects 41 to 80 years of age. In AD patients the CSF melatonin levels were only one- fifth of those in control subjects. The authors did not find a diurnal rhythm in CSF melatonin levels in control subjects or AD patients Von Gall et al. (2002) demonstrated that cycling expression of the clock gene Period- 1 (OMIM Ref. No. 602260) in rodent pituitary cells depends on the heterologous sensitization of the adenosine A2B receptor (OMIM Ref. No. 600446), which occurs through the nocturnal activation of melatonin mt1 receptors. Eliminating the impact of the neurohormone melatonin simultaneously suppresses the expression of Period- 1 and evokes an increase in the release of pituitary prolactin. Von Gall et al. (2002) concluded that their observations expose a mechanism by which 2 convergent signals interact within a temporal dimension to establish high- amplitude, precise, and robust cycles of gene expression.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

von Gall, C.; Garabette, M. L.; Kell, C. A.; Frenzel, S.; Dehghani, F.; Schumm- Draeger, P.- M.; Weaver, D. R.; Korf, H.- W.; Hastings, M. H.; Stehle, J. H. : Rhythmic gene expression in pituitary depends on heterologous sensitization by the neurohormone melatonin. Nature Neurosci. 5: 234- 238, 2002. ; and

Weaver, D. R.; Rivkees, S. A.; Carlson, L. L.; Reppert, S. M. : Localization of melatonin receptors in mammalian brain.In: Klein, D. C.; Moore, R. Y.; Reppert, S. M. : Suprachiasmatic.

Further studies establishing the function and utilities of MTNR1A are found in John Hopkins OMIM database record ID 600665, and in cited publications listed in Table 9, hereby incorporated herein.

GAM401 A A NCKAP1 TCACTGCAACCTCTG CCTTCCG NCKAP1 (Accession NM_013436.2) is another GAM401 target gene. NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM401 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM401 NGB TCACTGCAACCTCTG Neuroglobin (NGB, Accession NM_021257.2) is another GAM401 A A

CCTTCCG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM401 is therefore inhibition of NGB, a GAM401 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM408 IGF1 CTGGGATGGAGGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ATTAGAG NM_000618.2) is a GAM408 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM408 is therefore inhibition of IGF1, a GAM408 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM426 CRAT TCTGGATTTGAGAGG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is a A A

CTTTACT GAM426 target gene. CRAT BINDING SITE is a target binding site found

in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM426 is therefore inhibition of CRAT, a GAM426 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM426 DHCR24 TCTGGATTTGAGAGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

CTTTACT NM_014762.1) is another GAM426 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM426 is therefore inhibition of DHCR24, a GAM426 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM492 CAV2 CCGTAAAATGTTCAA Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM492 target A A

ATGTTTT gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM492 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM492 is therefore inhibition of CAV2, a GAM492 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM492 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM492 PRND AAAGCTTTGTTCATT GTATCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM492 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM492 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM492 is therefore inhibition of PRND, a GAM492 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM492 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM495 BACE AAAATGCTTACAGGC AGTAGCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) is a GAM495 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM495 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM495 is therefore inhibition of BACE, a GAM495 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM495 CAV2 AAAATGCTTACAGGC AGTAGCC Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM495 target gene. CAV2 BINDING SITE1 through CAV2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 through CAV2 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of A A

GAM495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM495 is therefore inhibition of CAV2, a GAM495 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM507 BACE2 GAGAGAGGTAGAGGG GAGCAGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM507 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM507 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM507 is therefore inhibition of BACE2, a GAM507 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM507 DLST GAGAGAGGTAGAGGG GAGCAGA Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM507 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM507 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM507 is therefore inhibition of DLST, a GAM507 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM507 A A GFAP GAGAGAGGTAGAGGG GAGCAGA GFAP (Accession NM_002055.2) is another GAM507 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM507 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM507 is therefore inhibition of GFAP. Accordingly, utilities of GAM507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM519 CRYAB A A TGTGGCTTAGGTGAG CATGTGA CRYAB (Accession NM_001885.1) is a GAM519 target gene. CRYAB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CRYAB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRYAB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM519 is therefore inhibition of CRYAB. Accordingly, utilities of GAM519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRYAB.

GAM519 B A CNTF TCCCACAGCTTCCTA GCCACAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM519 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM519 is therefore inhibition of CNTF, a GAM519 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM519 B A GLUL TCCCACAGCTTCCTA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession

GCCACAG NM_002065.3) is another GAM519 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM519 is therefore inhibition of GLUL, a GAM519 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL has been established by previous studies. Glutamine synthetase (EC 6.3.1.2), also called glutamate- ammonia ligase (GLUL), is expressed throughout the body and plays an important role in controlling body pH and in removing ammonia from the circulation. The enzyme clears L- glutamate, the major neurotransmitter in the central nervous system, from neuronal synapses (see OMIM Ref. No. references in Clancy et al. 1996). Gibbs et al. (1987) reported the complete 1,119- bp coding sequence of glutamine synthetase, which they determined from a liver- derived cDNA. Pesole et al. (1991) suggested that glutamine synthetase is a good molecular clock for determining times of divergence even as great as that which occurred between eukaryotes and prokaryotes. One conclusion reached by Pesole et al. (1991) was that organelle- specific enzymes, such as those of the mitochondria, may have originated from a duplication of nuclear genes. The endosymbiotic hypothesis suggests that a transfer of prokaryotic genes to nuclei occurred during the evolution of the primitive eukaryotic cell. In some cases, it is likely that the old prokaryotic gene could not be active in the new nuclear genome environment and was totally lost because its function in the organelle could be dispensed with. Subsequently, a new organelle-specific enzyme could have originated to serve specialized metabolic functions. The presence of glutamine synthetase in mitochondria is linked to the nitrogen metabolism of the species, and in particular to the need for glutamine as a source of ammonia and for particular biochemical pathways for ammonia detoxification.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Gibbs, C. S.; Campbell, K. E.; Wilson, R. H. : Sequence of a human glutamine synthetase cDNA. Nucleic Acids Res. 15: 6293 only, 1987. ; and

Pesole, G.; Bozzetti, M. P.; Lanave, C.; Preparata, G.; Saccone, C. : Glutamine synthetase gene evolution: a good molecular

clock. Proc. Nat. Acad. Sci. 88: 522- 526, 1991.

Further studies establishing the function and utilities of GLUL are found in John Hopkins OMIM database record ID 138290, and in cited publications listed in Table 9, hereby incorporated herein.

GAM520 BACE TCTGGTTTGAGAGAC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

AATGACA is a GAM520 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM520 is therefore inhibition of BACE, a GAM520 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM520 DHCR24 TCTGGTTTGAGAGAC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

AATGACA NM_014762.1) is another GAM520 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM520 is therefore inhibition of DHCR24, a GAM520 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM520 THOP1 TCTGGTTTGAGAGAC Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is A A

AATGACA another GAM520 target gene. THOP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE, and secondary structure complementarity to

the nucleotide sequence of GAM520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM520 is therefore inhibition of THOP1, a GAM520 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 has been established by previous studies. Papastoitsis et al. (1994) purified and characterized the metalloprotease from human Alzheimer disease brain that is able to cleave a synthetic peptide encompassing the amino- terminus of amyloid beta peptide and generate amyloidogenic fragments from recombinant human APP. Sequence comparison revealed that this enzyme has high homology to the previously described rat metalloendopeptidase 24.15 (EC 3.4.24.15). The beta- secretase- like activity of the human enzyme in vitro in combination with its localization in neurons and its co- localization with APP in transport vesicles purified from rabbit optic nerve rendered this enzyme an interesting candidate for amyloidogenic processing of APP. Using a cDNA encoding the rat enzyme, Meckelein et al. (1996) assigned the human gene, symbolized THOP1, to chromosome 19 by hybridization to DNA from human/rodent somatic cell hybrids. By fluorescence in situ hybridization, they localized the gene to 19q13.3. However, after localizing the THOP1 gene to the high-resolution cosmid contig map of human chromosome 19, Torres et al. (1998) found that the FISH mapping to 19q13.3 by Meckelein et al. (1996) was incorrect. Results of the hybridization and FISH mapping of positive clones indicated localization of THOP1 to 19p13.3, thus excluding THOP1 as a candidate gene for AD2.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Papastoitsis, G.; Siman, R.; Scott, R.; Abraham, C. R. : Identification of a metalloprotease from Alzheimer's disease brain able to degrade the beta- amyloid precursor protein and generate amyloidogenic fragments. Biochemistry 33: 192- 199, 1994. ; and

Meckelein, B.; Rohan de Silva, H. A.; Roses, A. D.; Rao, P. N.; Pettenati, M. J.; Xu, P.- T.; Hodge, R.; Glucksman, M. J.; Abraham, C. R. : Human endopeptidase (THOP1) is localized on chr.

Further studies establishing the function and utilities of THOP1 are found in John Hopkins OMIM database record ID 601117, and in cited publications listed in Table 9, hereby incorporated herein.

GAM550	ADAM17	TTTGCACACTTTCCA	A	Disintegrin and Metalloproteinase Domain 17 (tumor necrosis	A

A

AGTTGCC factor, (ADAM17, Accession NM_003183.3) is a GAM550 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM550 is therefore inhibition of ADAM17, a GAM550 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM550 B2M TTTGCACACTTTCCA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A

AGTTGCC GAM550 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM550 is therefore inhibition of B2M, a GAM550 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM550 CTNND2 TTTGCACACTTTCCA Catenin (cadherin- associated protein), Delta 2 (neural A A
AGTTGCC plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM550 target gene. CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTNND2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM550 is therefore inhibition of CTNND2, a GAM550 target gene which interacts with presenilin 1

(PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 has been established by previous studies. Armadillo- like proteins are characterized by a series of armadillo repeats, first defined in the Drosophila 'armadillo' gene product, that are typically 42 to 45 amino acids long. These proteins can be divided into subfamilies based on the number of repeats, their overall sequence similarity, and the dispersion of the repeats throughout their sequences. Members of the p120(ctn)/plakophilin subfamily of Armadillo- like proteins, including CTNND1 (OMIM Ref. No. 601045), CTNND2, PKP1 (OMIM Ref. No. 601975), PKP2 (OMIM Ref. No. 602861), PKP4 (OMIM Ref. No. 604276), and ARVCF (OMIM Ref. No. 602269), have 10 armadillo repeats each In a search for proteins with sequence homology to PKP1, Paffenholz and Franke (1997) identified a human cDNA with 45% amino acid identity to PKP1 in a segment within the armadillo (arm) repeat units. Antibodies raised against the arm repeat region recognized 2 polypeptide bands of approximately 150 and 160 kD in immunoblots of mouse brain and a weak band of approximately 160 kD in mouse skeletal muscle and pancreas. The authors, therefore, named the protein NPRAP for 'neural plakophilin- related arm- repeat protein.' Paffenholz and Franke (1997) isolated 2 partial human cDNA clones from a human fetal brain cDNA library. The longer displays 91% identity to the complete mouse cDNA. Northern blot analysis of a number of human and bovine cell lines and tissues detected CTNND2 expression as 5- and 6- kb transcripts only in human fetal brain RNA

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Paffenholz, R.; Franke, W. W. : Identification and localization of a neurally expressed member of the plakoglobin/armadillo multigene family. Differentiation 61: 293- 304, 1997. ; and

Medina, M.; Marinescu, R. C.; Overhauser, J.; Kosik, K. S. : Hemizygosity of delta- catenin (CTNND2) is associated with severe mental retardation in cri- du- chat syndrome. Genomics 63: 157.

Further studies establishing the function and utilities of CTNND2 are found in John Hopkins OMIM database record ID 604275, and in cited publications listed in Table 9, hereby incorporated herein.

GAM550 IGF1 TTTGCACACTTTCCA AGTTGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM550 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM550 is therefore inhibition of IGF1, a GAM550 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM550 PRNP TTTGCACACTTTCCA AGTTGCC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM550 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM550 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM550 is therefore inhibition of PRNP, a GAM550 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP has been established by previous studies. Mutations in the prion protein gene are associated with Gerstmann- Straussler disease (GSD; 137440), Creutzfeldt- Jakob disease (CJD; 123400), and familial fatal insomnia (OMIM Ref. No. 600072), and aberrant isoforms of the prion protein can act as an infectious agent in these disorders as well as in kuru (OMIM Ref. No. 245300) and in scrapie in sheep. Riek et al. (1998) used the refined NMR structure of the mouse prion protein to investigate the structural basis of inherited human transmissible spongiform encephalopathies. In the cellular form of mouse prion protein, no spatial clustering of mutation sites was observed that would indicate the existence of disease- specific subdomains. A hydrogen bond between residues 128 and 178 provided a structural basis for the observed highly specific influence of a polymorphism at position 129 in human PRNP on the disease phenotype that segregates with the asp178- to- asn (D178N; 176640.0007) mutation. Overall, the NMR structure implied that only some of the disease-related amino acid replacements lead to reduced stability of the cellular form of PRNP, indicating that subtle structural differences in the mutant proteins may affect intermolecular signaling in a variety of different ways. Windl et al. (1999) searched for mutations and polymorphisms in the coding region of the PRNP gene in

578 patients with suspect prion diseases referred to the German Creutzfeldt- Jakob disease surveillance unit over a period of 4.5 years. They found 40 cases with a missense mutation previously reported as pathogenic. Among these, the D178N mutation was the most common. In all of these cases, D178N was coupled with methionine at codon 129, resulting in the typical fatal familial insomnia genotype. Two novel missense mutations and several silent polymorphisms were found. In their Figure 1, Windl et al. (1999) diagrammed the known pathogenic mutations in the coding region of PRNP. Mead et al. (2001) analyzed the PRNP locus for tightly linked susceptibility factors for prion disease. They identified 56 polymorphic sites within 25 kb of the PRNP open reading frame, including sites within the PRNP promoter and the PRNP 3- prime untranslated region. These were characterized in 61 CEPH families, demonstrating extensive linkage disequilibrium around PRNP and the existence of 11 major European PRNP haplotypes. A common haplotype was overrepresented in patients with sporadic Creutzfeldt- Jakob disease. They could demonstrate that, in addition to the strong susceptibility conferred by codon 129, there was a significant independent association between sporadic CJD and a polymorphism upstream of PRNP. Although their sample size was necessarily small, no association was found between these polymorphisms and variant CJD or iatrogenic CJD, in keeping with their having distinct disease mechanisms. Cousens et al. (2001) described a cluster of variant CJD near the Leicestershire village of Queniborough in the U.K. Mead et al. (2001) could find no evidence of a PRNP founder susceptibility effect in that cluster. Animal model experiments lend further support to the function of PRNP. The incubation period and the neuropathology of transmissible spongiform encephalopathies have been extensively used to distinguish prion isolates (or strains) inoculated into panels of inbred mouse strains. Such studies have shown that the bovine spongiform encephalopathy (BSE) agent is indistinguishable from the agent causing variant Creutzfeldt- Jakob disease (vCJD), but differs from isolates of sporadic CJD, reinforcing the idea that the vCJD epidemic in Britain results from consumption of contaminated beef products. Manolakou et al. (2001) presented a mouse model for genetic and environmental factors that modify the incubation period of BSE cross- species transmission. They used 2 mouse strains that carried the same PrP allele, but displayed a 100- day difference in their mean incubation period following intracerebral inoculation with primary BSE isolate. They reported genetic effects on incubation period that map to 4 chromosomal regions in the mouse, and in addition they found significant factors of host environment, namely, the age of the host's mother, the age of the host at infection, and an interaction between the X chromosome and the cytoplasm in the host. Miele et al. (2002) identified 3 genes involved in mitochondrial physiology that were differentially expressed in the postnatal developing brains of normal mice and Prnp - /- mice. Further analysis showed that compared to the hippocampal CA1 regions of Prnp / mice, those of

Prnp - /- mice contained 40% fewer mitochondria, unusual mitochondrial morphology, and significantly increased activity of mitochondrial manganese- dependent antioxidant superoxide dismutase (SOD2; 147460), suggesting greater levels of oxidative assault. These results suggested that there is a relationship between normal cellular PrP expression and quality and quantity of mitochondria.

It is appreciated that the abovementioned animal model for PRNP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Miele, G.; Jeffrey, M.; Turnbull, D.; Manson, J.; Clinton, M. : Ablation of cellular prion protein expression affects mitochondrial numbers and morphology. Biochem. Biophys. Res. Commun. 291: 372-377, 2002. ; and

Cousens, J.; Smith, P. G.; Ward, H.; Everington, D.; Knight, R. S. G.; Zeidler, M.; Stewart, G.; Smith- Bathgate, E. A. B.; Macleod, M.- A.; Mackenzie, J.; Will, R. G. : Geographical dis.

Further studies establishing the function and utilities of PRNP are found in John Hopkins OMIM database record ID 176640, and in cited publications listed in Table 9, hereby incorporated herein.

GAM569 AVP ACACAGGCCCAGAGA AVP (Accession NM_000490.2) is a GAM569 target gene. AVP A A

GGCAGTG BINDING SITE1 and AVP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by AVP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE1 and AVP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM569 is therefore inhibition of AVP. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM569 CRAT ACACAGGCCCAGAGA Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A

GGCAGTG another GAM569 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of CRAT, a GAM569 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM569 CTSB ACACAGGCCCAGAGA A A GGCAGTG CTSB (Accession NM_001908.2) is another GAM569 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of CTSB. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM569 MAPT ACACAGGCCCAGAGA A A GGCAGTG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM569 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of MAPT, a GAM569 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM569 NCSTN ACACAGGCCCAGAGA A A GGCAGTG NCSTN (Accession NM_015331.1) is another GAM569 target gene. NCSTN BINDING SITE1 and NCSTN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCSTN, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE1 and NCSTN BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of NCSTN, a GAM569 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM569 S100B ACACAGGCCCAGAGA S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A GGCAGTG NM_006272.1) is another GAM569 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of S100B, a GAM569 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM569 SLC17A7 ACACAGGCCCAGAGA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A GGCAGTG NM_020309.1) is another GAM569 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of SLC17A7, a GAM569 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM569 SNCB ACACAGGCCCAGAGA Synuclein, Beta (SNCB, Accession NM_003085.2) is another GAM569 A A GGCAGTG target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM569 is therefore inhibition of SNCB, a GAM569 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM572 IGF1 TAAGTGAGTAGGCAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TGTTCT NM_000618.2) is a GAM572 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM572 is therefore inhibition of IGF1, a GAM572 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM584 TRPM2 GGCCCCTTTGTGAGG TRPM2 (Accession NM_003307.1) is a GAM584 target gene. TRPM2 A A CACGCTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM584 is therefore inhibition of TRPM2, a

GAM584 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM588 A A BACE TCCAGTGAAACAGGT CTCTTTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM588 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM588 is therefore inhibition of BACE, a GAM588 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM588 A A TNFRSF5 TCCAGTGAAACAGGT CTCTTTG TNFRSF5 (Accession NM_152854.1) is another GAM588 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM588 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM593 A A HTR2A ACAGCAAGTCTTTGT CAAAGCT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is a GAM593 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM593 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM593 is therefore inhibition of HTR2A, a GAM593 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A has been established by previous studies. Serotonin (5-hydroxytryptamine; 5- HT) is a neurotransmitter that occupies a uniquely important place in neurobiology because of its role in many physiologic processes such as sleep, appetite, thermoregulation, pain perception, hormone secretion, and sexual behavior. Abnormality of the serotonergic system has been implicated in a number of human diseases such as mental depression, migraine, epilepsy, obsessive-compulsive behavior, and affective disorder. Like other neurotransmitters, 5- HT is released into the synaptic junction and exerts its effect on specific receptors on the postsynaptic membranes. Based on differential radioligand binding affinities, at least 6 types of 5- HT receptors have been identified: 5- HT- 1A, - 1B, - 1C, - 1D, - 2, and - 3 (Peroutka, 1988). The deduced amino acid sequences of the human, mouse, and rat 5- HT2 receptors are highly conserved; all 3 share a 90% sequence identity (Chen et al. 1992). Kato et al. (1996) presented evidence for genomic imprinting of the HTR2 gene. They demonstrated that the HTR2 gene was expressed only from the maternal allele.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Holmes, C.; Arranz, M. J.; Powell, J. F.; Collier, D. A.; Lovestone, S. : 5- HT- 2A and 5- HT- 2C receptor polymorphisms and psychopathology in late onset Alzheimer's disease. Hum. Molec. Genet. 7: 1507- 1509, 1998. ; and

Hsieh, C.- L.; Bowcock, A. M.; Farrer, L. A.; Hebert, J. M.; Huang, K. N.; Cavalli- Sforza, L. L.; Julius, D.; Francke, U. : The serotonin receptor subtype 2 locus HTR2 is on human chromo.

Further studies establishing the function and utilities of HTR2A are found in John Hopkins OMIM database record ID 182135, and in cited publications listed in Table 9, hereby incorporated herein.

GAM593 VLDLR ACAGCAAGTCTTTGT CAAAGCT Very Low Density Lipoprotein Receptor (VLDLR, Accession NM_003383.1) is another GAM593 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM593 RNA are set A A

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM593 is therefore inhibition of VLDLR, a GAM593 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR has been established by previous studies. A specific isoform of apolipoprotein E (OMIM Ref. No. 107741), encoded by the APOE4 allele, is associated with the accelerated rate of disease expression of sporadic Alzheimer disease (AD) and late- onset familial AD. Okuizumi et al. (1995) noted that, in patients who carry the APOE4 allele, an earlier age of onset has also been demonstrated in patients who also have mutations in the amyloid precursor protein gene (OMIM Ref. No. 104760) involving codon 717 (104760.0002) and codons 670 and 671 (104760.0008). On the other hand, the presence of the APOE4 allele makes no difference in familial AD patients with APP692 (104760.0005) or APP693 mutations, nor does it make a difference in chromosome 14- linked familial AD patients (OMIM Ref. No. 104311). Hypothesizing that receptors for APOE- containing lipoproteins act as a potential risk factor for AD, Okuizumi et al. (1995) performed an association study using a polymorphic triplet (CGG) repeat in the VLDLR gene. The frequency of the 5- repeat allele was significantly higher in all Japanese sporadic AD patients (P less than 0.02) than in Japanese controls. Moreover, the odds ratio was significantly increased in the AD patients homozygous for the 5- repeat allele; OR = 2.1, 95% confidence interval = 1.1- 4.2. Multiple logistic regression analysis showed that the relative risk conferred by the presence of 2 copies of the 5- repeat allele and at least 1 copy of the APOE4 allele is 8.7; 95% CI = 2.9- 25.8. Okuizumi et al. (1995) concluded that VLDLR is a susceptibility gene for AD. Animal model experiments lend further support to the function of VLDLR. Layering of neurons in the cerebral cortex and cerebellum requires reelin (RELN; 600514), an extracellular matrix protein, and mammalian disabled (DAB1; 603448), a cytosolic protein that activates tyrosine kinases. By targeted disruption experiments in mice, Trommsdorff et al. (1999) showed that 2 cell surface receptors, VLDLR and apolipoprotein E receptor- 2 (APOER2; 602600), are also required. Both receptors bound Dab1 on their cytoplasmic tails and were expressed in cortical and cerebellar layers adjacent to layers expressing Reln. Dab1 expression was upregulated in knockout mice lacking both the Vldlr and Apoer2 genes. Inversion of cortical layers, absence of cerebellar foliation, and the migration of Purkinje cells in these animals precisely mimicked the phenotype of mice lacking Reln or Dab1. These findings established novel signaling functions for the LDL receptor gene family and suggested that VLDLR and APOER2 participate in transmitting the extracellular RELN signal to intracellular signaling processes initiated by

DAB1.

It is appreciated that the abovementioned animal model for VLDLR is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Okuizumi, K.; Onodera, O.; Namba, Y.; Ikeda, K.; Yamamoto, T.; Seki, K.; Ueki, A.; Nanko, S.; Tanaka, H.; Takahashi, H.; Oyanagi, K.; Mizusawa, H.; Kanazawa, I.; Tsuji, S. : Genetic association of the very low density lipoprotein (VLDL) receptor gene with sporadic Alzheimer's disease. Nature Genet. 11: 207- 209, 1995. ; and

Trommsdorff, M.; Gotthardt, M.; Hiesberger, T.; Shelton, J.; Stockinger, W.; Nimpf, J.; Hammer, R. E.; Richardson, J. A.; Herz, J. : Reeler/Disabled- like disruption of neuronal migration.

Further studies establishing the function and utilities of VLDLR are found in John Hopkins OMIM database record ID 192977, and in cited publications listed in Table 9, hereby incorporated herein.

GAM604 APBA1 GTGGCATTGGTGGTG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GCATTGG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM604 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM604 is therefore inhibition of APBA1, a GAM604 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM604 CRAT GTGGCATTGGTGGTG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is A A

GCATTGG another GAM604 target gene. CRAT BINDING SITE1 and CRAT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CRAT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE1 and CRAT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM604 is therefore inhibition of CRAT, a GAM604 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM604 CTNND2 GTGGCATTGGTGGTG GCATTGG Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM604 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM604 is therefore inhibition of CTNND2, a GAM604 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM604 DHCR24 GTGGCATTGGTGGTG GCATTGG 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM604 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM604 is therefore inhibition of DHCR24, a GAM604 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM604	IL1B	GTGGCATTGGTGGTG GCATTGG	Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another GAM604 target gene. IL1B BINDING SITE1 and IL1B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL1B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE1 and IL1B BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM604 is therefore inhibition of IL1B, a GAM604 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B has been established by previous studies. Interleukin- 1, produced mainly by blood monocytes, mediates the panoply of host reactions collectively known as acute phase response. It is identical to endogenous pyrogen. The multiple biologic activities that define IL1 are properties of a 15- to 18- kD protein that is derived from a 30- to 35- kD precursor. El- Omar et al. (2000) reported that interleukin- 1 gene cluster polymorphisms suspected of enhancing production of interleukin- 1- beta are associated with an increased risk of both hypochlorhydria induced by Helicobacter pylori and gastric cancer. Two of these polymorphisms are in near- complete linkage disequilibrium, and 1 is a TATA- box polymorphism that markedly affects DNA- protein interactions in vitro. The association with disease may be explained by the biologic properties of interleukin- 1- beta, which is an important proinflammatory cytokine and a powerful inhibitor of gastric acid secretion. Host genetic factors that affect interleukin- 1- beta may determine why some individuals infected with H. pylori develop gastric cancer while others do not. IL1- beta is upregulated in the presence of H. pylori and is important in initiating and amplifying the inflammatory response to this infection. Three diallelic polymorphisms in IL1B have been reported, all representing C- to- T base transitions, at positions - 511, - 31, and 3954 basepairs from the transcriptional start site. To determine whether these polymorphisms are important with respect to different outcomes of H. pylori infections, El- Omar et al. (2000) studied their effects on gastric physiology in healthy subjects. Carriers of the ILB - 31T allele (147720.0001) had an age- adjusted odds ratio of 9.1 (95% confidence interval, 2.2- 37) for low acid secretion, and there was little difference between homozygous and heterozygous carriers. The IL1B 3954 genotype was not associated with the risk of hypochlorhydria. Carriers of IL1B - 31T had an increased gastric cancer risk at an odds ratio of 1.9 (95% confidence interval, 1.5- 2.6), with no significant difference

between homozygotes and heterozygotes Hamajima et al. (2001) determined that the C- to- T transition at position - 31, creating a TATA box, is associated with vulnerability to persistent H. pylori infection, and that the susceptibility is modified by smoking Animal model experiments lend further support to the function of IL1B. Mature IL1- beta levels are a sensitive and specific indicator of caspase- 1 (OMIM Ref. No. 147678) activation. Ona et al. (1999) studied the effect of inhibition of caspase- 1 on the progression of Huntington disease (OMIM Ref. No. 143100) in the mouse model developed by Mangiarini et al. (1996), which they called R6/2 mice. Ona et al. (1999) crossed R6/2 mice with a well- characterized transgenic mouse strain expressing a dominant- negative mutant of caspase- 1 in the brain (NSE M17Z). Double mutant mice showed extended survival and delayed appearance of neuronal inclusions, neurotransmitter receptor alterations, and onset of symptoms, indicating that caspase- 1 is important in the pathogenesis of Huntington disease. Mature IL1- beta levels in R6/2 mice were elevated to 268% of those in wildtype controls. This increase was significantly inhibited in the R6/2- NSE M17Z mice. IL1- beta levels in the brains of human patients also exhibited significant increases, to 213% of those in normal controls

It is appreciated that the abovementioned animal model for IL1B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

El- Omar, E. M.; Carrington, M.; Chow, W.- H.; McColl, K. E. L.; Bream, J. H.; Young, H. A.; Herrera, J.; Lissowska, J.; Yuan, C.- C.; Rothman, N.; Lanyon, G.; Martin, M.; Fraumeni, J. F. Jr.; Rabkin, C. S. : Interleukin- 1 polymorphisms associated with increased risk of gastric cancer. Nature 404: 398- 402, 2000. Note: Erratum: Nature 412: 99 only, 2001. ; and

Ona, V. O.; Li, M.; Vonsattel, J. P. G.; Andrews, L. J.; Khan, S. Q.; Chung, W. M.; Frey, A. S.; Menon, A. S.; Li, X.- J.; Stieg, P. E.; Yuan, J.; Penney, J. B.; Young, A. B.; Cha, J.- H.

Further studies establishing the function and utilities of IL1B are found in John Hopkins OMIM database record ID 147720, and in cited publications listed in Table 9, hereby incorporated herein.

GAM604	MAPT	GTGGCATTGGTGGTG GCATTGG	Microtubule- associated Protein Tau (MAPT, Accession NM_016841.1) is another GAM604 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE	A	A

III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM604 is therefore inhibition of MAPT, a GAM604 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM604 NCKAP1 GTGGCATTGGTGGTG NCKAP1 (Accession NM_013436.2) is another GAM604 target gene. A A

GCATTGG NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM604 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM604 PRND GTGGCATTGGTGGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GCATTGG another GAM604 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM604 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM604 is therefore inhibition of PRND, a GAM604 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM604 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM640 ACE GGCGTGATCTTGGCT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

CACCACA (ACE, Accession NM_152831.1) is a GAM640 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM640 is therefore inhibition of ACE, a GAM640 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM640 HTR2A GGCGTGATCTTGGCT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
CACCACA NM_000621.1) is another GAM640 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM640 is therefore inhibition of HTR2A, a GAM640 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM640 MAPT GGCGTGATCTTGGCT Microtubule- associated Protein Tau (MAPT, Accession A A
CACCACA NM_173727.1) is another GAM640 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM640 is therefore inhibition of MAPT, a GAM640 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM640 A A MTNR1A CACCACA GGCGTGATCTTGGCT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM640 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM640 is therefore inhibition of MTNR1A, a GAM640 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM640 B A IAPP TCAAGCGATTCTCAT GCCTTAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM640 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM640 is therefore inhibition of IAPP, a GAM640 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM667 A A MAPT TGTAGGTGGTTGAGA GAATGAA Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is a GAM667 target gene. MAPT BINDING SITE1 and MAPT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 and MAPT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM667 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM667 is therefore inhibition of MAPT, a GAM667 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM667 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM667 MME TGTAGGTGGTTGAGA GAATGAA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM667 target gene. MME BINDING SITE1 through MME BINDING SITE4 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 through MME BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM667 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM667 is therefore inhibition of MME, a GAM667 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM667 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM674 APLP2 TGAGATCATCGTTAC AAGCAGC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM674 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM674 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM674 is therefore inhibition of APLP2, a GAM674 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 has been established by previous studies. Yan et al. (1990) cloned a cDNA that encoded a human sperm membrane protein identified by a monoclonal antibody raised against this protein and designated YWK- II. They found that the deduced polypeptide contains a segment with high homology to the transmembrane- cytoplasmic domains of the A4 amyloid protein (APP;

104760) found in brain plaques of Alzheimer disease patients. Rather than the lys- lys- lys sequence found in the A4 protein, an arg- lys- arg sequence was found at the probable membrane- cytoplasmic junction that may represent a unique property of sperm membrane proteins. The human amyloid precursor- like protein APLP2 is a highly conserved homolog of a sequence- specific DNA- binding mouse protein with an important function in the cell cycle. The mouse amyloid precursor- like protein Aplp1 has 42% sequence identity to mouse App; the human homolog of APLP1 (OMIM Ref. No. 104775) maps to 19q11- q13.2 (Wasco et al. 1993). By study of somatic cell hybrids segregating human chromosomes, von der Kammer et al. (1994) mapped the APLP2 gene to chromosome 11; by fluorescence in situ hybridization, the assignment was confirmed and further localized to 11q23- q25. By FISH, Leach et al. (1999) mapped the gene to 11q24.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Wasco, W.; Brook, J. D.; Tanzi, R. E. : The amyloid precursor-like protein (APLP) gene maps to the long arm of human chromosome 19. Genomics 15: 237- 239, 1993. ; and

Yan, Y. C.; Bai, Y.; Wang, L.; Miao, S.; Koide, S. S. : Characterization of cDNA encoding a human sperm membrane protein related to A4 amyloid protein. Proc. Nat. Acad. Sci. 87: 2405-240.

Further studies establishing the function and utilities of APLP2 are found in John Hopkins OMIM database record ID 104776, and in cited publications listed in Table 9, hereby incorporated herein.

GAM674 FHL2 TGAGATCATCGTTAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AAGCAGC another GAM674 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM674 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM674 is therefore inhibition of FHL2, a GAM674 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM689 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM689 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM689 is therefore inhibition of APPBP2, a GAM689 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM689 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM689 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM689 is therefore inhibition of BACE2, a GAM689 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM689 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM689 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM689 is therefore inhibition of FHL2, a GAM689 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM689 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM689 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM689 is therefore inhibition of IGF1, a GAM689 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM689 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM689 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM689 is therefore inhibition of MME, a GAM689 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM689 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM689 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA A A

encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM689 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM689 is therefore inhibition of PRND, a GAM689 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM744 A A AGTAGCC BACE AAAATGCTTACAGGC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) is a GAM744 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM744 is therefore inhibition of BACE, a GAM744 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM744 A A AGTAGCC CAV2 AAAATGCTTACAGGC Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM744 target gene. CAV2 BINDING SITE1 through CAV2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 through CAV2 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM744 is therefore inhibition of CAV2, a GAM744 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM750 A A BACE AGGGGTA TTCTCATTGGCCCAC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM750 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM750 is therefore inhibition of BACE, a GAM750 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM760 A A GFAP AACAGCA AGTCAGACGTTTGGC GFAP (Accession NM_002055.2) is a GAM760 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM760 is therefore inhibition of GFAP. Accordingly, utilities of GAM760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM760 A A HD AACAGCA AGTCAGACGTTTGGC HD (Accession NM_002111.3) is another GAM760 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM760 is therefore inhibition of HD. Accordingly, utilities of GAM760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with HD.

GAM760 A A SNCA AGTCAGACGTTTGGC AACAGCA SNCA (Accession NM_007308.1) is another GAM760 target gene. SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM760 is therefore inhibition of SNCA. Accordingly, utilities of GAM760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM760 A A TFCP2 AGTCAGACGTTTGGC AACAGCA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM760 target gene. TFCP2 BINDING SITE1 and TFCP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TFCP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE1 and TFCP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM760 is therefore inhibition of TFCP2, a GAM760 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 has been established by previous studies. Lambert et al. (2000) reported an association between a noncoding polymorphism (G- A) in the 3- prime untranslated region of TFCP2 and sporadic Alzheimer disease (AD5; 602096) in French and British populations and a similar trend in a North American population. The combined analysis of the 3 independent populations suggested a protective effect of the A allele (OR = 0.58, 95% CI 0.44- 0.75). The A allele demonstrated reduced binding to nuclear protein(s) from a neuroblastoma cell line, and absence of the A allele was associated with lower gene expression in lymphocytes from AD cases compared with controls. The authors suggested that polymorphic variation in TFCP2 may be important for the pathogenesis of AD, particularly since the gene product interacts with proteins such as GSK3B (OMIM Ref. No. 605004), Fe65 (OMIM Ref. No. 602709), and certain factors involved in the inflammatory response. Swendeman et al. (1994) characterized the genomic structure, chromosome location, promoter, and expression pattern of CP2, a 66- kD cellular transcription factor that interacts with the alpha- globin (OMIM

Ref. No. 141800) promoter as well as with additional cellular and viral promoter elements. Homodimers of CP2, together with a 45- kD partner protein, form the so- called stage selector protein complex (Jane et al. 1995) that binds to a proximal gamma- globin gene promoter regulatory sequence, termed the stage selector element (SSE). The SSE is thought to be involved in silencing beta globin gene (OMIM Ref. No. 141900) transcription during fetal erythropoiesis (Cunningham et al. 1995).

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Swendeman, S. L.; Spielholz, C.; Jenkins, N. A.; Gilbert, D. J.; Copeland, N. G.; Sheffery, M. : Characterization of the genomic structure, chromosomal location, promoter, and developmental expression of the alpha- globin transcription factor CP2. J. Biol. Chem. 269: 11663- 11671, 1994. ; and

Lambert, J.- C.; Goumidi, L.; Wavrant- De Vrieze, F.; Frigard, B.; Harris, J. M.; Cummings, A.; Coates, J.; Pasquier, F.; Cottel, D.; Gaillac, M.; St. Clair, D.; Mann, D. M. A.; Hardy, J.;.

Further studies establishing the function and utilities of TFCP2 are found in John Hopkins OMIM database record ID 189889, and in cited publications listed in Table 9, hereby incorporated herein.

GAM772 A APCS A GCCAGGATGAAGAGG AGGAGAA Amyloid P Component, Serum (APCS, Accession NM_001639.2) is a GAM772 target gene. APCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM772 is therefore inhibition of APCS, a GAM772 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS has been established by previous studies. Woo et al. (1987) found a genetic marker for susceptibility to amyloidosis in juvenile arthritis: an 8.8- kb RFLP band determined by a polymorphic DNA site 5- prime to the SAP gene. Homozygosity for the alternative 5.6- kb band was found in none of 28 amyloid patients. Among 19 juvenile arthritic patients without amyloidosis, the distribution of the polymorphism was the same as that in the normal group. With a RFLP

of the cloned mouse Sap gene, Whitehead et al. (1988) demonstrated that the gene maps to chromosome 1 in the same region specified by quantitative variation in Sap levels. They thought it might be significant that the same region includes CRP, SAP, and histone genes, all of which have products that interact with DNA. Animal model experiments lend further support to the function of APCS. Botto et al. (1997) generated mice with a targeted deletion of the SAP gene. Induction of reactive amyloidosis was retarded in these mice, demonstrating the participation of SAP in pathogenesis of amyloidosis in vivo and confirming that inhibition of SAP binding to amyloid fibrils is an attractive therapeutic target. Pepys et al. (2002) developed a drug that is a competitive inhibitor of SAP binding to amyloid fibrils. This palindromic compound also crosslinks and dimerizes SAP molecules, leading to their very rapid clearance by the liver and thus producing a marked depletion of circulating human SAP. Pepys et al. (2002) suggested that this mechanism of drug action potently removes SAP from human amyloid deposits in tissues and may provide a new therapeutic approach to both systemic amyloidosis and diseases associated with local amyloid, including Alzheimer disease (OMIM Ref. No. 104300) and type 2 diabetes (OMIM Ref. No. 125853).

It is appreciated that the abovementioned animal model for APCS is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Botto, M.; Hawkins, P. N.; Bickerstaff, M. C.; Herbert, J.; Bygrave, A. E.; McBride, A.; Hutchinson, W. L.; Tennent, G. A.; Walport, M. J.; Pepys, M. B. : Amyloid deposition is delayed in mice with targeted deletion of the serum amyloid P component gene. Nature Med. 3: 855- 859, 1997. ; and

Woo, P.; O'Brien, J.; Robson, M.; Ansell, B. M. : A genetic marker for systemic amyloidosis in juvenile arthritis. Lancet I: 767- 769, 1987.

Further studies establishing the function and utilities of APCS are found in John Hopkins OMIM database record ID 104770, and in cited publications listed in Table 9, hereby incorporated herein.

GAM772 ARHA GCCAGGATGAAGAGG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

AGGAGAA is another GAM772 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM772 is therefore inhibition of ARHA, a GAM772 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM772 MAPK10 GCCAGGATGAAGAGG AGGAGAA Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is another GAM772 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM772 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM772 is therefore inhibition of MAPK10, a GAM772 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM779 IGF1 TTGGTTGGTGATGAG CATTGAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM779 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM779 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM779 is therefore inhibition of IGF1, a GAM779 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM779 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM779 A A MTNR1A TTGGTTGGTGATGAG CATTGAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM779 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM779 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM779 is therefore inhibition of MTNR1A, a GAM779 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM779 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM779 A A TRPM2 TTGGTTGGTGATGAG CATTGAA TRPM2 (Accession NM_003307.1) is another GAM779 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM779 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM779 is therefore inhibition of TRPM2, a GAM779 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM779 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM785 A A MME AGAAGATCCCTGCTC TGAGTCA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is a GAM785 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM785 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM785 is therefore inhibition of MME, a GAM785 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM785 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM801 CASP3 TTGTGCTTGTACTGA CCATGTA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM801 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM801 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM801 is therefore inhibition of CASP3, a GAM801 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM801 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 has been established by previous studies. Nicholson et al. (1995) developed a potent peptide aldehyde inhibitor and showed that it prevents apoptotic events in vitro, suggesting that apopain/CPP32 is important for the initiation of apoptotic cell death.Apoptosis of human endothelial cells after growth factor deprivation is associated with rapid and dramatic upregulation of cyclin A- associated cyclin- dependent kinase- 2 (CDK2; 116953) activity. Levkau et al. (1998) showed that in apoptotic cells the carboxyl termini of the CDK inhibitors CDKN1A (OMIM Ref. No. 116899) and CDKN1B (OMIM Ref. No. 600778) are truncated by specific cleavage. The enzyme involved in this cleavage is CASP3 and/or a CASP3- like caspase. After cleavage, CDKN1A loses its nuclear localization sequence and exits the nucleus. Cleavage of CDKN1A and CDKN1B resulted in a substantial reduction in their association with nuclear cyclin- CDK2 complexes, leading to a dramatic induction of CDK2 activity. Dominant- negative CDK2, as well as a mutant CDKN1A resistant to caspase cleavage, partially suppressed apoptosis. These data suggested that CDK2 activation, through caspase- mediated cleavage of CDK inhibitors, may be instrumental in the execution of apoptosis following caspase activation. Animal model experiments lend further support to the function of CASP3. To analyze the function of CPP32 in vivo, Kuida et al. (1996) generated CPP32- deficient mice by homologous recombination. These mice, born at a frequency lower than expected by mendelian genetics, were smaller than their littermates and died at 1 to 3 weeks of age. Although their thymocytes retained normal

susceptibility to various apoptotic stimuli, brain development in CPP32- deficient mice was profoundly affected, and discernible by embryonic day 12, resulting in a variety of hypoplasias and disorganized cell deployment. These supernumerary cells were postmitotic and terminally differentiated by the postnatal stage. Pyknotic clusters at sites of major morphogenetic change during normal brain development were not observed in the mutant embryos, indicating increased apoptosis in the absence of CPP32. Thus, CPP32 was shown by Kuida et al. (1996) to play a critical role during morphogenetic cell death in the mammalian brain.

It is appreciated that the abovementioned animal model for CASP3 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Kuida, K.; Zheng, T. S.; Na, S.; Kuan, C.; Yang, D.; Karasuyama, H.; Rakio, P.; Flavell, R. A. : Decreased apoptosis in the brain and premature lethality in CPP32- deficient mice. Nature 384: 368- 372, 1996. ; and

Nicholson, D. W.; Ali, A.; Thornberry, N. A.; Vaillancourt, J. P.; Ding, C. K.; Gallant, M.; Gareau, Y.; Griffin, P. R.; Labelle, M.; Lazebnik, Y. A.; Munday, N. A.; Raju, S. M.; Smulso.

Further studies establishing the function and utilities of CASP3 are found in John Hopkins OMIM database record ID 600636, and in cited publications listed in Table 9, hereby incorporated herein.

GAM801	CTNND2	TTGTGCTTGTACTGA CCATGTA	Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM801 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM801 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM801 is therefore inhibition of CTNND2, a GAM801 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM801 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM550.

GAM801 MAPT TTGTGCTTGTACTGA CCATGTA Microtubule- associated Protein Tau (MAPT, Accession NM_005910.2) is another GAM801 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM801 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM801 is therefore inhibition of MAPT, a GAM801 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM801 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM807 NCKAP1 TAAGTGCTGCTGATT TTGGAAA NCKAP1 (Accession NM_013436.2) is a GAM807 target gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM807 RNA are set forth in Tables 6 and 7, hereby incorporated herein. NCKAP1 A A

A function of GAM807 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM807 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM821 AVP ACACAGGCCCAGAGA GGCAGTG AVP (Accession NM_000490.2) is a GAM821 target gene. AVP BINDING SITE1 and AVP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by AVP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE1 and AVP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM821 is therefore inhibition of AVP. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM821 CRAT ACACAGGCCCAGAGA GGCAGTG Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is another GAM821 target gene. CRAT BINDING SITE is a target binding A A

site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of CRAT, a GAM821 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM821 CTSB ACACAGGCCCAGAGA A A GGCAGTG CTSB (Accession NM_001908.2) is another GAM821 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of CTSB. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM821 MAPT ACACAGGCCCAGAGA A A GGCAGTG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM821 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of MAPT, a GAM821 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM821 NCSTN ACACAGGCCCAGAGA NCSTN (Accession NM_015331.1) is another GAM821 target gene. A A

GGCAGTG NCSTN BINDING SITE1 and NCSTN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCSTN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE1 and NCSTN BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of NCSTN, a GAM821 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM821 S100B ACACAGGCCCAGAGA S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

GGCAGTG NM_006272.1) is another GAM821 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of S100B, a GAM821 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM821 SLC17A7 ACACAGGCCCAGAGA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

GGCAGTG NM_020309.1) is another GAM821 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of SLC17A7, a GAM821 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM821 SNCB ACACAGGCCCAGAGA GGCAGTG A A Synuclein, Beta (SNCB, Accession NM_003085.2) is another target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM821 is therefore inhibition of SNCB, a GAM821 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM828 APPBP2 ACACATCTAATGGCT GTGCTGA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM828 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM828 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM828 is therefore inhibition of APPBP2, a GAM828 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM828 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM828 BLMH ACACATCTAATGGCT GTGCTGA A A Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another GAM828 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM828 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM828 is therefore inhibition of BLMH, a GAM828 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM828 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH has been established by previous studies. Using PCR- SSCP, Bromme et al. (1996) and Montoya et al. (1997) found a 1450A- G polymorphism of the BMH gene that resulted in an ile443- to- val (I443V) conserved amino acid substitution in the carboxy terminus of the protein (602403.0001). BMH is suspected of being the unknown beta secretase that cleaves off the amyloid beta fragment from the amyloid precursor protein (APP; 104760) associated with Alzheimer disease (AD). In pooled AD cases and controls, the frequency of the 1450A and 1450G alleles were statistically indistinguishable. The G/G homozygote genotype distribution, however, was significantly different between AD cases (12.7%) and controls (6.6%); (P less than 0.001). Significant differences were not seen in the A/A homozygote and A/G heterozygote genotype distributions. Further studies by Montoya et al. (1998) indicated that the frequency of the G/G homozygote was significantly higher in AD cases than in controls only in the non- APOE4 (see OMIM Ref. No. 107741) group (15.9% in cases vs 4.7% in controls). The odds ratio for developing AD with BMH G/G genotype in the absence of an APOE4 allele was 3.81; in the presence of an APOE4 allele, the odds ratio was 0.98. Farrer et al. (1998) were unable to confirm this association in a sample of 621 Caucasian Alzheimer patients drawn from 4 North American university-based research centers. Susceptibility to bleomycin- induced chromatid breaks in cultured peripheral blood lymphocytes may reflect the way a person deals with carcinogenic challenges (Hsu et al. 1989). This susceptibility, also referred to as mutagen sensitivity, has been found to be increased in patients with environmentally related cancers, including cancers of the head and neck, lung, and colon. In combination with carcinogenic exposure, this susceptibility can greatly influence cancer risk. Cloos et al. (1999) determined the number of bleomycin- induced breaks per cell for 135 healthy volunteers without cancer. These individuals were from 53 different pedigrees and included 25 monozygotic twin pairs, 14 pairs of dizygotics, and 14 families selected on the basis of a first- degree relative who was successfully treated for head and neck cancer and who had no sign of recurrence for at least 1 year. Results showed no evidence for the influence of a shared family environment on bleomycin- induced chromatid breaks. On the other hand, genetic influences were statistically significant and

accounted for 75% of the total variance.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Bromme, D.; Rossi, A. B.; Smeekens, S. P.; Anderson, D. C.; Payan, D. G. : Human bleomycin hydrolase: molecular cloning, sequencing, functional expression, and enzymatic characterization. Biochemistry 35: 6706- 6714, 1996. ; and

Hsu, T. C.; Johnston, D. A.; Cherry, L. M.; Ramkissoon, D.; Schantz, S. P.; Jessup, J. M.; Winn, R. J.; Shirley, L.; Furlong, C. : Sensitivity to genotoxic effects of bleomycin in human.

Further studies establishing the function and utilities of BLMH are found in John Hopkins OMIM database record ID 602403, and in cited publications listed in Table 9, hereby incorporated herein.

GAM828	MAPT	TCAGTTGATAGCAGA TGCTGTT	Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM828 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM828 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM828 is therefore inhibition of MAPT, a GAM828 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM828 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM834	ACE	GGCAGGATCATAGCT CACTGCA	Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM834 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM834 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

A function of GAM834 is therefore inhibition of ACE, a GAM834 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with

Alzheimer. Accordingly, utilities of GAM834 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM834 HTR2A GGCAGGATCATAGCT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
CACTGCA NM_000621.1) is another GAM834 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM834 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM834 is therefore inhibition of HTR2A, a GAM834 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM834 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM840 APPBP2 TTGCACTCCAGCCTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGTAACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM840 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM840 is therefore inhibition of APPBP2, a GAM840 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM840 FHL2 TTGCACTCCAGCCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGTAACA another GAM840 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM840 is therefore inhibition of FHL2, a GAM840 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM840 IGF1 TTGCACTCCAGCCTG GGTAACA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM840 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM840 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM840 is therefore inhibition of IGF1, a GAM840 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM840 PRND TTGCACTCCAGCCTG GGTAACA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM840 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM840 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM840 is therefore inhibition of PRND, a GAM840 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM842 NGB GCTGAGACCACCCTT Neuroglobin (NGB, Accession NM_021257.2) is a GAM842 target A A

GCCTGCC gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM842 is therefore inhibition of NGB, a GAM842 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM842 TRPM2 GCTGAGACCACCCTT TRPM2 (Accession NM_003307.1) is another GAM842 target gene. A A

GCCTGCC TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of TRPM2, a GAM842 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM842 APBB2 GGCTGGGCATGGTGG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A

CTCACGC 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM842 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of APBB2, a GAM842 target gene which Interacts with beta- amyloid

precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM842 AVP GGCTGGGCATGGTGG AVP (Accession NM_000490.2) is another GAM842 target gene. AVP B A

CTCACGC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of AVP. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM842 CTSB GGCTGGGCATGGTGG CTSB (Accession NM_147783.1) is another GAM842 target gene. B A

CTCACGC CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of CTSB. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM842 GFAP GGCTGGGCATGGTGG GFAP (Accession NM_002055.2) is another GAM842 target gene. B A

CTCACGC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of GFAP. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM842 IGF1 GGCTGGGCATGGTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession B A

CTCACGC NM_000618.2) is another GAM842 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of IGF1, a GAM842 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM842 PRND GGCTGGGCATGGTGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

CTCACGC another GAM842 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of PRND, a GAM842 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM842 TNF GGCTGGGCATGGTGG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, B A

CTCACGC Accession NM_000594.2) is another GAM842 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM842 is therefore inhibition of TNF, a GAM842 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM846 FOS TGCTTTAGTTCTTCT A A GAAGTGT V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is a GAM846 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM846 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM846 is therefore inhibition of FOS, a GAM846 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM846 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS has been established by previous studies. Muller et al. (1983) reported that the level of the c- fos gene transcripts is 100- fold greater in human term fetal membranes than in other normal human tissues and cells. These levels of c- fos expression in human amniotic and chorionic cells are close to that of v- fos expression that results in the induction of osteosarcomas in mice and transformation of fibroblasts in vitro. The human c- fms gene (OMIM Ref. No. 164770) is expressed at high levels in term placenta and trophoblastic cells. Muller et al. (1983) suggested that the physiologic role of the proteins encoded by the FOS and FMS genes may be related to these embryo- derived cells whose primary functions are protection and nourishment of the human fetus. Using the technique of in situ hybridization, Dony and Gruss (1987) demonstrated that stage-specific expression of the FOS gene in mouse embryos is restricted to the perichondrial growth regions of the cartilaginous skeleton. The possibility of a defect in FOS in a skeletal dysplasia is raised by these findings Animal model experiments lend further support to the function of FOS. Stable expression of c- fos in mice has been demonstrated in developing bones and teeth, hematopoietic cells, germ cells, and the central nervous system. The gene product is thought to have an important role in signal transduction, cell proliferation, and differentiation. Wang et al. (1991) demonstrated that overexpression of the gene in transgenic and chimeric mice specifically affects bone, cartilage, and hematopoietic cell development. Wang et al. (1992) studied the effects of lack of c-fos by gene targeting in embryonic stem cells. They reported that mice heterozygous for lack of the gene appeared normal, although females exhibited a distorted transmission frequency. All homozygous fos - /- mice were growth- retarded, developed osteopetrosis with deficiencies in bone remodeling and tooth eruption, and had altered hematopoiesis. Johnson et al. (1992) found similar results.

Homozygous mutants showed reduced placental and fetal weights and significant loss of viability at birth. However, approximately 40% of the homozygous mutants survived and grew at normal rates until severe osteopetrosis, characterized by foreshortening of the long bones, ossification of the marrow space, and absence of tooth eruption, began to develop at approximately 11 days. Among other abnormalities, these mice showed delayed or absent gametogenesis, lymphopenia, and altered behavior. Despite these defects, many lived as long as their wildtype or heterozygous littermates (currently 7 months).

It is appreciated that the abovementioned animal model for FOS is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Dony, C.; Gruss, P. : Proto- oncogene c- fos expression in growth regions of fetal bone and mesodermal web tissue. Nature 328: 711- 714, 1987. ; and

Wang, Z.- Q.; Grigoriadis, A. E.; Mohle- Steinlein, U.; Wagner, E. F. : A novel target cell for c- fos- induced oncogenesis: development of chondrogenic tumours in embryonic stem cell chime.

Further studies establishing the function and utilities of FOS are found in John Hopkins OMIM database record ID 164810, and in cited publications listed in Table 9, hereby incorporated herein.

GAM869 A NGB A ACCTGGCCTGTAGGC AAGTCTT Neuroglobin (NGB, Accession NM_021257.2) is a GAM869 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM869 is therefore inhibition of NGB, a GAM869 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM869 NOTCH1 ACCTGGCCTGTAGGC Notch (Drosophila) Homolog 1 (translocation- associated) A A

AAGTCTT (NOTCH1, Accession NM_017617.2) is another GAM869 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM869 is therefore inhibition of NOTCH1, a GAM869 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 has been established by previous studies. Cytogenetic studies have shown that chromosome 7 band q34- q35, which contains the gene for the beta T- cell receptor (OMIM Ref. No. 186930), is a common site for translocation in T- cell neoplasms. In a translocation t(7;9)(q34;q34.3) found in a case of acute T- cell lymphoblastic leukemia, Ellisen et al. (1991) found that the locus on chromosome 9 contains a gene highly homologous to the Drosophila gene 'Notch.' Transcripts of the human gene, for which they proposed the name TAN1 (an acronym for translocation- associated Notch homolog), and its murine counterpart were demonstrated in many normal human fetal and adult mouse tissues but were most abundant in lymphoid tissues. In t(7;9)(q34;q34.3) translocations from 3 cases of acute T- cell lymphoblastic leukemia, Ellisen et al. (1991) found breakpoints within 100 bp of an intron in TAN1, resulting in truncation of TAN1 transcripts. They interpreted the observations to indicate that TAN1 is important for normal lymphocyte function and that alterations in TAN1 play a role in the pathogenesis of some T- cell neoplasms. Milner et al. (1994) found that at least 1 Notch homolog is expressed in human bone marrow CD34 cells, a population enriched for hematopoietic precursors. On the basis of these findings, they suggested that members of the Notch family, including TAN1, may be involved in mediating cell- fate decisions during hematopoiesis. Animal model experiments lend further support to the function of NOTCH1. Huppert et al. (2000) mutated valine at position 1744 of the mouse Notch1 gene to glycine. This position is the site for proteolytic cleavage and is critical for Notch1 intracellular processing in tissue- culture cells. Huppert et al. (2000) generated homozygous animals carrying 2 germline mutations and compared these with mice who have 2 null alleles for Notch1 (Conlon et al. 1995). At embryonic day 8.5 to 10.5, homozygous embryos were detected at the expected mendelian frequency. Similar to the null alleles, embryo absorption was detected between embryonic day 10 and 12, and no homozygous embryos were recovered past embryonic day 12. These

results suggested that efficient Notch processing is necessary for the early embryonic developmental aspects of Notch activity. RT- PCR and immunoprecipitation showed comparable amounts of Notch mRNA and protein, respectively, in the processing- deficient embryos and their heterozygous and wildtype littermates. The phenotypes associated with the single point mutation resembled the null Notch1 phenotype, but with slightly reduced penetrance.

It is appreciated that the abovementioned animal model for NOTCH1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Ellisen, L. W.; Bird, J.; West, D. C.; Soreng, A. L.; Reynolds, T. C.; Smith, S. D.; Sklar, J. : TAN- 1, the human homolog of the Drosophila Notch gene, is broken by chromosomal translocations in T lymphoblastic neoplasms. Cell 66: 649- 661, 1991. ; and

Huppert, S. S.; Le, A.; Schroeter, E. H.; Mumm, J. S.; Saxena, M. T.; Milner, L. A.; Kopan, R. : Embryonic lethality in mice homozygous for a processing- deficient allele of Notch1. Natu.

Further studies establishing the function and utilities of NOTCH1 are found in John Hopkins OMIM database record ID 190198, and in cited publications listed in Table 9, hereby incorporated herein.

GAM869 A A SNCG ACCTGGCCTGTAGGC AAGTCTT SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM869 target gene. SNCG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM869 is therefore inhibition of SNCG, a GAM869 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG has been established by previous studies. The synuclein gene family comprises genes that are highly conserved between species. Lavedan et al. (1998) identified and characterized a novel member of the human synuclein gene family, gamma- synuclein (SNCG). The SNCG gene contains 5 exons and encodes a 127- amino acid protein that is

highly homologous to alpha- synuclein (SNCA; 163890) and beta-synuclein (SNCB; 602569). Northern blot analysis showed that the gene is principally expressed in the brain, particularly in the substantia nigra. Through a survey of an EST database, Lavedan et al. (1998) found that the SNCG gene may also be overexpressed in ovarian tumors. Ji et al. (1997) used a high- throughput direct-differential cDNA sequencing approach to identify genes differentially expressed in normal breast as compared with breast cancer. Of many putative differentially expressed genes, a breast cancer- specific gene, BCSG1, which was expressed in high abundance in a breast cancer cDNA library but scarcely at all in a normal breast cDNA library, was identified as a putative breast cancer marker. In situ hybridization analysis demonstrated stage- specific BCSG1 expression as follows: BCSG1 was undetectable in normal or benign breast lesions, showing partial expression in ductal carcinoma in situ, but was expressed at an extremely high level in advanced infiltrating breast cancer. The predicted amino acid sequence of the BCSG1 gene product had a significant homology to the nonamyloid beta protein fragment of Alzheimer disease amyloid protein (OMIM Ref. No. 163890). BCSG1 overexpression may indicate breast cancer malignant progression from benign or in situ carcinoma.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Ji, H.; Liu, Y. E.; Jia, T.; Wang, M.; Liu, J.; Xiao, G.; Joseph, B. K.; Rosen, C.; Shi, Y. E. : Identification of a breast cancer- specific gene, BCSG1, by direct differential cDNA sequencing. Cancer Res. 57: 759- 764, 1997. ; and

Lavedan, C.; Buchholtz, S.; Auburger, G.; Albin, R. L.; Athanassiadou, A.; Blancato, J.; Burguera, J. A.; Ferrell, R. E.; Kostic, V.; Leroy, E.; Leube, B.; Mota- Vieira, L.; and 9 others.

Further studies establishing the function and utilities of SNCG are found in John Hopkins OMIM database record ID 602998, and in cited publications listed in Table 9, hereby incorporated herein.

GAM892	BACE2	TATCTCTTGCCTTGA CCTCCTA	Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is a GAM892 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

A function of GAM892 is therefore inhibition of BACE2, a

GAM892 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM892 A A PSEN1 TATCTCTTGCCTTGA CCTCCTA PSEN1 (Accession NM_000021.2) is another GAM892 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM892 is therefore inhibition of PSEN1. Accordingly, utilities of GAM892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM933 A A IL1A TTAGGGCAGGCATGA GAGAACT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a GAM933 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM933 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM933 is therefore inhibition of IL1A, a GAM933 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM933 A A TNFSF5 TTAGGGCAGGCATGA GAGAACT TNFSF5 (Accession NM_000074.1) is another GAM933 target gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM933 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM933 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM965 SNCA AAGGTAGATAAAGGC SNCA (Accession NM_000345.2) is a GAM965 target gene. SNCA A A
TTCACGT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM965 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM965 is therefore inhibition of SNCA. Accordingly, utilities of GAM965 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM973 APPBP2 TATTGCTAAGAATTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
AGGTAGT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM973 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM973 is therefore inhibition of APPBP2, a GAM973 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM973 IGF1 TATTGCTAAGAATTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
AGGTAGT NM_000618.2) is another GAM973 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM973 is therefore inhibition of IGF1, a GAM973 target gene which are structurally and functionally

related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM973 A A AGGTAGT NPY TATTGCTAAGAATTC Neuropeptide Y (NPY, Accession NM_000905.2) is another GAM973 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM973 is therefore inhibition of NPY, a GAM973 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM999 A A AACATTT FOS AGCTGCCAGTTGAAG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is a GAM999 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM999 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM999 is therefore inhibition of FOS, a GAM999 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM999 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM1017 A A GTTGACA FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM1017 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1017 is therefore inhibition of FHL2, a GAM1017 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1017 IGF1 ACTGCACTCCAGCCT GTTGACA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1017 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1017 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1017 is therefore inhibition of IGF1, a GAM1017 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1017 PRND ACTGCACTCCAGCCT GTTGACA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM1017 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1017 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1017 is therefore inhibition of PRND, a GAM1017 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1032 CHAT CTAGACTGAAGCTCC Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a A A
TTGAGGA GAM1032 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1032 is therefore inhibition of CHAT, a GAM1032 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1032 CTSK CTAGACTGAAGCTCC CTSK (Accession NM_000396.2) is another GAM1032 target gene. A A
TTGAGGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1032 is therefore inhibition of CTSK. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM1032 MPO CTAGACTGAAGCTCC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM1032 A A
TTGAGGA target gene. MPO BINDING SITE1 and MPO BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE1 and MPO BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1032 is therefore inhibition of MPO, a GAM1032 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MPO.The function of MPO has been established by previous studies. Weil et al. (1988) found that the MPO gene was translocated to chromosome 15 in all cases of acute promyelocytic leukemia (subtype M3), which is consistently associated with the chromosomal translocation t(15;17)(q22;q11.2). In 2 of 4 cases examined by genomic blot analysis, rearrangement of the MPO gene was detected in leukemia cells. Weil et al. (1988) also suggested that MPO may be pivotal in the pathogenesis of APL. According to HGM10, the MPO gene is located at a distance from the breakpoint in APL, and the gene itself is probably usually not rearranged in APL. Myeloperoxidase has been detected in activated microglial macrophages and within amyloid plaques in the central nervous system. Using statistical analysis, Reynolds et al. (2000) examined the relationship between APOE (OMIM Ref. No. 107741) and MPO polymorphisms in the risk of Alzheimer disease (AD; 104300) in a genetically homogeneous Finnish population. They found that the presence of the MPO A allele in conjunction with APOE E4 significantly increased the risk of AD in men, but not in women (odds ratio for men with both alleles = 11.4 vs APOE E4 alone = 3.0). Reynolds et al. (2000) also found that estrogen receptor-alpha (OMIM Ref. No. 133430) binds to the MPO A promoter, which may explain the gender differences.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Reynolds, W. F.; Hiltunen, M.; Pirskanen, M.; Mannermaa, A.; Helisalmi, S.; Lehtovirta, M.; Alafuzoff, I.; Soininen, H. : MPO and APOE epsilon- 4 polymorphisms interact to increase risk for AD in Finnish males. Neurology 55: 1284- 1290, 2000. ; and

Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Lemons, R. S.; Swanson, M. S.; Carrino, J. J.; Diaz, M. O.; Le Beau, M. M. : Translocation and rearrangement of myeloperoxida.

Further studies establishing the function and utilities of MPO are found in John Hopkins OMIM database record ID 606989, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1032 3	SERPINA TTGAGGA	CTAGACTGAAGCTCC	Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 antiprotei	A	A

(SERPINA3, Accession NM_001085.2) is another GAM1032 target gene. SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINA3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1032 is therefore inhibition of SERPINA3, a GAM1032 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 has been established by previous studies. Alpha- 1- antichymotrypsin is a plasma protease inhibitor synthesized in the liver. It is a single glycopeptide chain of about 68,000 daltons and belongs to the class of serine protease inhibitors. In man, the normal serum level is about one- tenth that of alpha- 1- antitrypsin (PI; 107400), with which it shares nucleic acid and protein sequence homology (Chandra et al. 1983). Both are major acute phase reactants; their concentrations in plasma increase in response to trauma, surgery, and infection. Antithrombin III, which also is structurally similar to alpha- 1- antitrypsin, shows less sequence homology to antichymotrypsin and is not an acute phase reactant. Kelsey et al. (1988) cloned and analyzed the AACT gene, partly because of the possibility that genetic variation in other protease inhibitors may influence the prognosis in AAT deficiency. They isolated the AACT gene on a series of cosmid clones, with restriction mapping of about 70 kb around the gene.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C. : Sequence homology between human alpha- 1- antichymotrypsin, alpha- 1- antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061, 1983. ; and

Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.; Corney, G.; Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli- Vergani, G.; Mowat, A. P. : Cloning of the human alpha- 1 antichym.

Further studies establishing the function and utilities of SERPINA3 are found in John Hopkins OMIM database record ID 107280, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1032 TNFRSF6 CTAGACTGAAGCTCC TNFRSF6 (Accession NM_152874.1) is another GAM1032 target gene. A A

TTGAGGA TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1032 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM1033 BACE TTTTCAATGGCTGAC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A
ACTGTCT is a GAM1033 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1033 is therefore inhibition of BACE, a GAM1033 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1087 CAV1 CAGTGGGAAAAGTTT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
GTCTCAT NM_001753.3) is a GAM1087 target gene. CAV1 BINDING SITE1 and CAV1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE1 and CAV1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1087 is therefore inhibition of CAV1, a GAM1087 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 has been established by previous studies. In addition to the role of mutations in CAV3 in limb- girdle muscular dystrophy, Engelman et al. (1998) reviewed the cell culture and biochemical findings suggesting that heritable differences in the interaction between caveolins and their partners may lead to other conditions as well. They reviewed the evidence that CAV1 is a tumor suppressor gene and a negative regulator of the Ras- p42/44 MAP kinase cascade. Loss of heterozygosity analysis implicates 7q31.1 in the pathogenesis of multiple types of cancer, including breast, ovarian, prostate, and colorectal carcinoma, as well as uterine

sarcomas and leiomyomas. Yang et al. (1998) found elevated caveolin-1 levels associated with lymph node metastasis in prostate cancer (OMIM Ref. No. 176807), raising the possibility that CAV1 may also act as an oncogene. Because the closest known gene to CAV1 is the MET protooncogene (OMIM Ref. No. 164860), however, this finding may simply reflect coamplification of CAV1 along with MET. MET was first identified and cloned as a metastasis- associated gene (Giordano et al. 1989). Animal model experiments lend further support to the function of CAV1. By targeted disruption of caveolin- 1, Drab et al. (2001) generated mice that lacked caveolae. The absence of this organelle impaired nitric oxide and calcium signaling in a cardiovascular system, causing aberrations in endothelium- dependent relaxation, contractility, and maintenance of myogenic tone. In addition, the lungs of knockout mice displayed thickening of alveolar septa caused by uncontrolled endothelial cell proliferation and fibrosis, resulting in severe physical limitations in caveolin-1- disrupted mice. Thus, Drab et al. (2001) concluded that caveolin-1 and caveolae play a fundamental role in organizing multiple signaling pathways in the cell.

It is appreciated that the abovementioned animal model for CAV1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Yang, G.; Truong, L. D.; Timme, T. L.; Ren, C.; Wheeler, T. M.; Park, S. H.; Nasu, Y.; Bangma, C. H.; Kattan, M. W.; Scardino, P. T.; Thompson, T. C. : Elevated expression of caveolin is associated with prostate and breast cancer. Clin. Cancer Res. 4: 1873- 1880, 1998. ; and

Drab, M.; Verkade, P.; Elger, M.; Kasper, M.; Lohn, M.; Lauterbach, B.; Menne, J.; Lindschau, C.; Mende, F.; Luft, F. C.; Schedl, A.; Haller, H.; Kurzchalia, T. V. : Loss of caveolae, va.

Further studies establishing the function and utilities of CAV1 are found in John Hopkins OMIM database record ID 601047, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1087 A GYPA CAGTGGGAAAAGTTT A GTCTCAT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM1087 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1087 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1087 is therefore inhibition of GYPA, a GAM1087 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1087 HD CAGTGGGAAAAGTTT HD (Accession NM_002111.3) is another GAM1087 target gene. HD A A

GTCTCAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1087 is therefore inhibition of HD. Accordingly, utilities of GAM1087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM1087 MME CAGTGGGAAAAGTTT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GTCTCAT enkephalinase, (MME, Accession NM_007287.1) is another GAM1087 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1087 is therefore inhibition of MME, a GAM1087 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1088 ADAM17 GAAGAGCTGTGTGCT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GTGATGT factor, (ADAM17, Accession NM_003183.3) is a GAM1088 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM1088 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1088 is therefore inhibition of ADAM17, a GAM1088 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1088 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1089 APBA1 GGGAGGATCCTTGCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

CAACTTA 1 (X11) (APBA1, Accession NM_001163.2) is a GAM1089 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1089 is therefore inhibition of APBA1, a GAM1089 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM1089 GLUL GGGAGGATCCTTGCT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

CAACTTA NM_002065.3) is another GAM1089 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of GLUL, a GAM1089 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM519.

GAM1089 TFCP2 GGGAGGATCCTTGCT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

CAACTTA another GAM1089 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of TFCP2, a GAM1089 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM1089 ACE GTGTGGGCAGGGCCG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 B A

TGCTCCC (ACE, Accession NM_152831.1) is another GAM1089 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of ACE, a GAM1089 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1089 BACE2 GTGTGGGCAGGGCCG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession B A

TGCTCCC NM_138992.1) is another GAM1089 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of BACE2, a GAM1089 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1089 CHAT GTGTGGGCAGGGCCG Choline Acetyltransferase (CHAT, Accession NM_020985.1) is B A

TGCTCCC another GAM1089 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of CHAT, a GAM1089 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1089 GFAP GTGTGGGCAGGGCCG GFAP (Accession NM_002055.2) is another GAM1089 target gene. B A

TGCTCCC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of GFAP. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1089 PRND GTGTGGGCAGGGCCG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

TGCTCCC another GAM1089 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of PRND, a GAM1089 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1089 TGFB1 GTGTGGGCAGGGCCG TGFB1 (Accession NM_000660.1) is another GAM1089 target gene. B A

TGCTCCC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1089 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1099 HTR2C CTGTTCAGATCTGTG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

TGCATTT NM_000868.1) is a GAM1099 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1099 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1099 is therefore inhibition of HTR2C, a GAM1099 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1099 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM1144 APBB2 TCTTGGTGCTTTTGC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TGGATGA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM1144 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM1144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1144 is therefore inhibition of APBB2, a GAM1144 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1144 APOC1 TCTTGGTGCTTTTGC Apolipoprotein C- I (APOC1, Accession NM_001645.2) is another A A

TGGATGA GAM1144 target gene. APOC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1144 is therefore inhibition of APOC1, a GAM1144 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 has been established by previous studies. Smit et al. (1988) presented a map of the apolipoprotein E- C1- C2 gene cluster on chromosome 19: 5- prime- - APOE- - 4.3 kb- - APOC1- - 6 kb- - APOC1 pseudogene- - about 22 kb- - APOC2- - 3- prime. Thus, the cluster spans approximately 48 kb. This gene order and the size of the cluster were confirmed by Myklebost and Rogne (1988) by pulsed-field gel electrophoresis mapping methods. A HpaI RFLP in the APOE-C1- C2 gene cluster on chromosome 19 is strongly associated with familial dysbetalipoproteinemia. Smit et al. (1988) showed that this RFLP site is between APOE and APOC1 and specifically that it is located 317 bp upstream of the transcription initiation site of the APOC1 gene. They constructed a detailed restriction map of the gene cluster, showing that the APOC2 gene is located 15 kb downstream of the APOC1 pseudogene. Although Trask et al. (1993) did not map the APOC1 gene directly, the mapping of the APOE and APOC2 genes to 19q13.2 by fluorescence in situ hybridization established that the APOC1 gene is also in this band. Animal model experiments lend further support to the function of APOC1. To determine the relationship between APOC1 and CETP (OMIM Ref. No. 118470), Gautier et al. (2002) crossed transgenic mice expressing human CETP with

Apoc1 null mice. The high density lipoproteins (HDLs) of these crosses contained 50% less cholesteryl esters and showed a decreased cholesteryl ester- to- triglyceride ratio. The mean apparent diameter of LDLs from these mice was also significantly reduced. In vitro, purified Apoc1 inhibited cholesteryl ester exchange when added to either total plasma or to reconstituted HDL- free mixtures. Gautier et al. (2002) concluded that APOC1 is a specific inhibitor of CETP.

It is appreciated that the abovementioned animal model for APOC1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Gautier, T.; Masson, D.; Jong, M. C.; Duverneuil, L.; Le Guern, N.; Deckert, V.; Pais de Barros, J.- P.; Dumont, L.; Bataille, A.; Zak, Z.; Jiang, X.- C.; Tall, A. R.; Havekes, L. M.; Lagrost, L. : Apolipoprotein CI deficiency markedly augments plasma lipoprotein changes mediated by human cholesteryl ester transfer protein (CETP) in CETP transgenic/ApoCI- knocked out mice. J. Biol. Chem. 277: 31354- 31363, 2002. ; and

Smit, M.; van der Kooij- Meijs, E.; Woudt, L. P.; Havekes, L. M.; Frants, R. R. : Exact localization of the familial dysbetalipoproteinemia associated HpaI restriction site in the promo.

Further studies establishing the function and utilities of APOC1 are found in John Hopkins OMIM database record ID 107710, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1144 CHAT TCTTGGTGCTTTTGC Choline Acetyltransferase (CHAT, Accession NM_020986.1) is A A TGGATGA another GAM1144 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1144 is therefore inhibition of CHAT, a GAM1144 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1144	CLU	TCTTGGTGCTTTTGC TGGATGA	Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is another GAM1144 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM1144 is therefore inhibition of CLU, a GAM1144 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU has been established by previous studies. Sulfated glycoprotein- 2 (SGP- 2) is the major secreted product of Sertoli cells and is thought to play a critical role in spermatogenesis. Murphy et al. (1988) described a novel serum protein, SP- 40,40, using a series of monoclonal antibodies directed to the immune deposit- containing glomerular basement membranes of a patient with membranous glomerulonephritis. The protein was shown to be a normal constituent of human blood. It consists of two 40- kD chains, alpha and beta, covalently joined by disulfide bonds. They established that SP- 40,40 is a member of the human complement system by directly demonstrating its presence within the S- protein- containing soluble variant of the C5b- 9 complex, SC5b- 9. SP- 40,40 is also called complement lysis inhibitor. It acts as a control mechanism of the complement cascade; specifically, it prevents the binding of a C5b- C7 complex to the membrane of the target cell and in this way inhibits complement- mediated cytolysis . Animal model experiments lend further support to the function of CLU. Following neonatal hypoxic- ischemic brain injury in mice (a model of cerebral palsy), there is evidence of apoptotic changes such as activation of neuronal caspase- 3 (OMIM Ref. No. 600636), as well as an accumulation of clusterin in dying neurons. Han et al. (2001) generated mice deficient in clusterin by targeted disruption. Clusterin - /- mice had 50% less brain injury following neonatal hypoxia- ischemia. The absence of clusterin had no effect on caspase- 3 activation, and clusterin accumulation and caspase- 3 activation did not colocalize to the same cells. Studies with cultured cortical neurons demonstrated that exogenous purified astrocyte- secreted clusterin exacerbated oxygen/glucose- deprivation- induced necrotic death. Han et al. (2001) concluded that clusterin may be a therapeutic target to modulate noncaspase- dependent neuronal death following acute brain injury

It is appreciated that the abovementioned animal model for CLU is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Murphy, B. F.; Kirszbaum, L.; Walker, I. D.; d'Apice, A. J. F. : SP- 40,40, a newly identified normal human serum protein found in the SC5b- 9 complex of complement and in the immune deposits in glomerulonephritis. J. Clin. Invest. 81: 1858- 1864, 1988. ; and

Han, B. H.; DeMattos, R. B.; Dugan, L. L.; Kim- Han, J. S.; Brendza, R. P.; Fryer, J. D.; Kierson, M.; Cirrito, J.; Quick, K.; Harmony, J. A. K.; Aronow, B. J.; Holtzman, D. M. : Cluster.

Further studies establishing the function and utilities of CLU are found in John Hopkins OMIM database record ID 185430, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1163 ACE CTGCATGGAGGTGGT CTATGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM1163 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1163 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1163 is therefore inhibition of ACE, a GAM1163 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1191 ACHE CTGGGCGTGTGAGGC GGCTGTG Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM1191 target gene. ACHE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated A A

herein.

A function of GAM1191 is therefore inhibition of ACHE, a GAM1191 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE has been established by previous studies. Coates and Simpson (1972) concluded that 3 phenotypic variants of acetylcholinesterase (EC 3.1.1.7) result from 2 codominant alleles at a single locus. Rotundo et al. (1988) showed that all the forms of acetylcholinesterase observed in avian nerves and muscle are encoded by a single autosomal gene. Differences in assembly and localization of the multiple synaptic forms of acetylcholinesterase are thought to arise through posttranscriptional events. Lapidot- Lifson et al. (1989) referred to the cloning of the gene for acetylcholinesterase. They used these clones to study the coamplification of acetylcholinesterase and pseudocholinesterase (butyrylcholinesterase; BCHE; 177400). Their coamplification in certain leukemias and in disorders of platelet formation suggest that the 2 loci may be linked. (The pseudocholinesterase gene is located at 3q25.2.) Whereas pseudocholinesterase is a soluble plasma enzyme presumed to be produced by the liver but also present in muscle and brain, acetylcholinesterase or 'true' cholinesterase is involved in the signal transmission at neuromuscular junctions and is also intensely expressed in the human central nervous system and the erythrocyte membrane. That such was the case was demonstrated by Getman et al. (1992). By chromosomal in situ suppression hybridization analysis, they showed that a single gene is located at 7q22 and confirmed the results by PCR analysis of genomic DNA from a human/hamster somatic cell hybrid containing a single human chromosome 7. Thus the gene maps to the same region that is frequently the site of nonrandom deletion in leukemias of myeloid cell precursors known to express acetylcholinesterase during normal differentiation. Animal model experiments lend further support to the function of ACHE. Feng et al. (1999) generated ColQ (OMIM Ref. No. 603033) - /- mice to study the roles played by ColQ and AChE in synapses and elsewhere.

It is appreciated that the abovementioned animal model for ACHE is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Lapidot- Lifson, Y.; Prody, C. A.; Ginzberg, D.; Meytes, D.; Zakut, H.; Soreq, H. : Coamplification of human acetylcholinesterase

and butyrylcholinesterase genes in blood cells: correlation with various leukemias and abnormal megakaryocytopoiesis. Proc. Nat. Acad. Sci. 86: 4715- 4719, 1989. ; and

Feng, G.; Krejci, E.; Molgo, J.; Cunningham, J. M.; Massoulie, J.; Sanes, J. R. : Genetic analysis of collagen Q: roles in acetylcholinesterase and butyrylcholinesterase assembly and in.

Further studies establishing the function and utilities of ACHE are found in John Hopkins OMIM database record ID 100740, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1191 FHL2 CTGGGCGTGTGAGGC A A GGCTGTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM1191 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1191 is therefore inhibition of FHL2, a GAM1191 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1191 MME CTGGGCGTGTGAGGC A A GGCTGTG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM1191 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1191 is therefore inhibition of MME, a GAM1191 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1191 PSEN1 CTGGGCGTGTGAGGC A A PSEN1 (Accession NM_007318.1) is another GAM1191 target gene.

GGCTGTG PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1191 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1191 SERPINA CTGGGCGTGTGAGGC Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 A A
3 GGCTGTG antiprotei (SERPINA3, Accession NM_001085.2) is another GAM1191 target gene. SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINA3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1191 is therefore inhibition of SERPINA3, a GAM1191 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM1191 SNCB CTGGGCGTGTGAGGC Synuclein, Beta (SNCB, Accession NM_003085.2) is another A A
GGCTGTG GAM1191 target gene. SNCB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1191 is therefore inhibition of SNCB, a GAM1191 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM1193 ACE CACCCAGGCTGGAGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GCAGTGG (ACE, Accession NM_152831.1) is a GAM1193 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1193 is therefore inhibition of ACE, a GAM1193 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1193 ADAM17 CACCCAGGCTGGAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
GCAGTGG factor, (ADAM17, Accession NM_021832.1) is another GAM1193 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1193 is therefore inhibition of ADAM17, a GAM1193 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1193 FLNB CACCCAGGCTGGAGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GCAGTGG NM_001457.1) is another GAM1193 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1193 is therefore inhibition of FLNB, a GAM1193 target gene which Filamin B, beta; binds actin,

interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB has been established by previous studies. The platelet GpIb complex (see OMIM Ref. No. 138720) mediates the adherence of platelets at the site of vascular injury through the binding of GpIb- alpha (OMIM Ref. No. 231200) to subendothelial von Willebrand factor (VWF; 193400). In platelets, the GpIb complex is tightly bound to the actin cytoskeleton via an interaction of GpIb- alpha with ABP280 (filamin A; 300017). Using a yeast 2- hybrid screen with the cytoplasmic tail of GpIb- alpha as bait, Takafuta et al. (1998) isolated partial cDNAs encoding a novel filamin homolog that they designated beta- filamin. They used the partial cDNAs to screen a placenta library and recovered additional cDNAs corresponding to the entire beta- filamin coding region. Like ABP280, the predicted 2,602- amino acid protein contains an N- terminal actin- binding domain, a backbone of 24 tandem repeats, and 2 hinge regions. Excluding the unique first hinge region of beta- filamin, the sequences of beta- filamin and ABP280 are 70% identical. Antibodies against beta- filamin detected a 280- kD protein on Western blots of human umbilical vein endothelial cell (HUVEC) extracts and stained normal human endothelial cells in culture and in situ. Using antigen- capture ELISA, Takafuta et al. (1998) found that beta- filamin associates with GpIb- alpha in both platelets and HUVEC extracts. They determined that the GpIb- alpha- binding domain in beta- filamin is in repeats 17- 20, a region that corresponds to the GpIb- alpha- binding domain in ABP280. Northern blot analysis revealed that beta- filamin is expressed as 2 approximately 9.5- kb mRNAs in many adult tissues. The 2 different transcripts appear to result from use of alternative polyadenylation signals. Takafuta et al. (1998) concluded that beta- filamin is a new member of the filamin family that may have significance for GpIb- alpha function in endothelial cells and platelets. Independently, Xu et al. (1998) isolated cDNAs encoding beta- filamin, which they referred to as ABP278. These authors also identified alternatively spliced mRNAs encoding ABP276, a beta- filamin isoform missing the first hinge region. RT- PCR analysis indicated that the 2 isoforms were expressed at different relative levels in various human tissues. The addition of thyroid- stimulating hormone (TSH; OMIM Ref. No. 188530) to cultured thyroid follicular cells induces rapid and profound disruption of actin microfilaments. Using serum from a Graves disease (OMIM Ref. No. 275000) patient, Leedman et al. (1993) identified a thyroid cDNA encoding TABP (truncated actin- binding protein), a predicted 195- amino acid protein with homology to the C terminus of ABP280. Both Xu et al. (1998) and Takafuta et al. (1998) considered TABP to be a truncated form of beta- filamin. Mutations in the presenilin genes PS1 (OMIM Ref. No. 104311) and PS2 (OMIM Ref. No. 600759) account for approximately 50% of early- onset familial Alzheimer disease (AD; 104300). Zhang et al. (1998)

identified beta- filamin as filamin homolog 1 (FH1), a filamin-related protein that interacts with the loop regions of PS1 and PS2. A monoclonal antibody recognizing both ABP280 and FH1 bound to blood vessels and astrocytes in the normal brain. In the brains of AD patients, Zhang et al. (1998) observed staining also in neurofibrillary tangles, neuropil threads, and dystrophic neurites within some senile plaques. The authors stated that detection of these presenilin- interacting proteins in these brain structures suggests that ABP280 and FH1 may be involved in the development of AD and that interactions between presenilins and ABP280/FH1 may be functionally significant. Takafuta et al. (1998) noted that the FH1 sequence is identical to the C- terminal 291 amino acids of beta-filamin except for 2 residues, making it very likely that FH1 represents the C- terminal region of beta- filamin. By analysis of somatic cell hybrids, Zhang et al. (1998) mapped the FH1 gene to chromosome 3. Takafuta et al. (1998) refined the map position to 3p21.1- p14.3 based on inclusion of a previously mapped STS within the beta- filamin sequence. By FISH, Brocker et al. (1999) assigned the FLNB gene to 3p14.3. Chakarova et al. (2000) mapped FLNB to 3p14 by radiation hybrid analysis.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Brocker, F.; Bardenheuer, W.; Vieten, L.; Julicher, K.; Werner, N.; Marquitan, G.; Michael, D.; Opalka, B.; Schutte, J. : Assignment of human filamin gene FLNB to human chromosome band 3p14.3 and identification of YACs containing the complete FLNB transcribed region. Cytogenet. Cell Genet. 85: 267- 268, 1999. ; and

Chakarova, C.; Wehnert, M. S.; Uhl, K.; Sakthivel, S.; Vosberg, H.- P.; van der Ven, P. F. M.; Furst, D. O. : Genomic structure and fine mapping of the two human filamin gene paralogues.

Further studies establishing the function and utilities of FLNB are found in John Hopkins OMIM database record ID 603381, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1193 A A FPRL1 GCAGTGG CACCCAGGCTGGAGT FPRL1 (Accession NM_001462.1) is another GAM1193 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1193 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1193 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1193 IAPP CACCCAGGCTGGAGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A GCAGTGG another GAM1193 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1193 is therefore inhibition of IAPP, a GAM1193 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1193 TGFB1 CACCCAGGCTGGAGT TGFB1 (Accession NM_000660.1) is another GAM1193 target gene. A A GCAGTGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1193 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1197 MPO TGTCAGTTTTTTAAA Myeloperoxidase (MPO, Accession NM_000250.1) is a GAM1197 A A TACTCAG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1197 is therefore inhibition of MPO, a GAM1197 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM1197	SOD2	TGTCAGTTTTTTAAA TACTCAG	Superoxide Dismutase 2, Mitochondrial (SOD2, Accession NM_000636.1) is another GAM1197 target gene. SOD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SOD2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM1197 is therefore inhibition of SOD2, a GAM1197 target gene which is intramitochondrial free radical scavenging enzyme. When he has polymorphism in signal peptides he could couse diseases of distribution and therefore is associated with Alzheimer. Accordingly, utilities of GAM1197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SOD2.The function of SOD2 has been established by previous studies. Rosenblum et al. (1996) emphasized the importance of polymorphism in signal peptides that target organelle- specific proteins to their subcellular sites of action. They discovered a polymorphism when they cloned the SOD2 gene from cell lines of normal individuals and patients with genetic diseases of premature aging. The polymorphism consisted of a single nucleotide change in the region of the DNA that encodes the signal sequence such that either an alanine or a valine was present (147460.0001). Rosenblum et al. (1996) suggested that such signal sequence polymorphism could result in diseases of distribution, where essential proteins are not properly targeted, thereby leading to absolute or relative deficiencies of critical enzymes within specific cellular compartments. They suggested that progeria (OMIM Ref. No. 176670) and related syndromes may be diseases of distribution. Hiroi et al. (1999) found an increased frequency for the SOD2- VV genotype (homozygosity for the valine (V) allele vs the alanine allele) in Japanese with nonfamilial idiopathic cardiomyopathy (IDC) and suggested that this polymorphism may collaborate with the DRP1*1401 allele of the HLA- DRB1 gene (OMIM Ref. No. 142857) in controlling the susceptibility to nonfamilial IDC

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Hiroi, S.; Harada, H.; Nishi, H.; Satoh, M.; Nagai, R.; Kimura, A. : Polymorphisms in the SOD2 and HLA- DRB1 genes are associated with nonfamilial idiopathic dilated cardiomyopathy in Japanese. Biochem. Biophys. Res. Commun. 261: 332- 339, 1999. ; and

Rosenblum, J. S.; Gilula, N. B.; Lerner, R. A. : On signal sequence polymorphisms and diseases of distribution. Proc. Nat. Acad. Sci. 93: 4471- 4473, 1996.

Further studies establishing the function and utilities of SOD2 are found in John Hopkins OMIM database record ID 147460, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1216 ADAMTS5 TACAGGCAGGCACAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

AGGCAGT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM1216 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1216 is therefore inhibition of ADAMTS5, a GAM1216 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 has been established by previous studies. Proteolysis of the extracellular matrix plays a critical role in establishing tissue architecture during development and in tissue degradation in diseases such as cancer, arthritis, Alzheimer disease, and a variety of inflammatory conditions. The proteolytic enzymes responsible include members of diverse protease families and they may work in concert or in cascades to degrade or process molecules. Two groups of zinc metalloproteinases in particular, ADAMs and MMPs (e.g. 600754), appear broadly relevant to extracellular proteolysis. Most ADAM family members are quite similar in domain organization, bearing, from amino to carboxyl termini, a signal peptide, a proregion, a zinc metalloprotease catalytic domain with the typical reprolysin signature motif, a disintegrin domain, a cysteine- rich domain, an EGF- like domain, and, in many cases, a membrane- spanning region and a cytoplasmic domain with signaling potential. Members of the ADAMTS family differ substantially from the prototypic ADAM structure in that they lack the EGF- like domain, do not have a canonical disintegrin sequence, and possess modules with similar thrombospondin type 1 repeats. By searching an EST database using the protein sequences of human ADAMTS1 to ADAMTS4 and a C. elegans ADAMTS as queries, Hurskainen et al. (1999) identified ADAMTS5, ADAMTS6 (OMIM Ref. No. 605008), and ADAMTS7 (OMIM Ref. No. 605009). They determined a partial human ADAMTS5 cDNA sequence that lacked 5- prime coding sequence. The predicted partial ADAMTS5 protein has the domain structure

characteristic of ADAMTSs, beginning with a partial metalloproteinase domain. Northern blot analysis of several human tissues detected an approximately 10- kb ADAMTS5 transcript that was expressed at a low level in placenta and at barely detectable levels in a number of other tissues. Northern blot analysis showed that mouse Adamts5 was specifically expressed in a 7- day mouse embryo, and at low or undetectable levels thereafter. In situ hybridization of an 8.5- day mouse embryo showed uniform Adamts5 expression throughout the embryo. In addition, Adamts5 expression was found in trophoblastic cells lining the uterine cavity, in the developing placenta, and in the decidual reaction within the uterus. In a 10.5- day mouse embryo, Adamts5 expression was widespread, but at a lower level than in the 8.5- day embryo. Expression was found in mesenchyme and somites, as well as in the neural tube and developing hindgut. Abbaszade et al. (1999) demonstrated that recombinant ADAMTS5 expressed in insect cells cleaves aggrecan at the glu373- ala374 site, with the cleavage pattern and inhibitor profile indistinguishable from that observed with native aggrecanase. Northern blot analysis of several human tissues showed highest ADAMTS5 expression in placenta, with much lower expression in heart and brain. Major transcripts of 12.4, 10.7, 8.6, and 6.6 kb were detected. Real time PCR of a number of normal human tissues detected ADAMTS5 expression in placenta, cervix, uterus, bladder, and esophagus. Expression was also found in rib cartilage, chondroblastoma, and fibrous tissue and joint capsule samples from an arthritic patient.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Abbaszade, I.; Liu, R.- Q.; Yang, F.; Rosenfeld, S. A.; Ross, O. H.; Link, J. R.; Ellis, D. M.; Tortorella, M. D.; Pratta, M. A.; Hollis, J. M.; Wynn, R.; Duke, J. L.; and 15 others : Cloning and characterization of ADAMTS11, an aggrecanase from the ADAMTS family. J. Biol. Chem. 274: 23443- 23450, 1999. ; and

Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S. : ADAM- TS5, ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases: general features and genomic dis.

Further studies establishing the function and utilities of ADAMTS5 are found in John Hopkins OMIM database record ID 605007, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1216 APBA2 TACAGGCAGGCACAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AGGCAGT 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM1216 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of APBA2, a GAM1216 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 has been established by previous studies. The cytoplasmic domain of the Alzheimer disease locus amyloid protein precursor (APP; 104760) binds to 4 human phosphotyrosine- binding (PTB) proteins; see APBA1 (OMIM Ref. No. 602414). By use of a yeast 2- hybrid screening of a human brain cDNA library, McLoughlin and Miller (1996) identified 3 of these proteins: the human homolog of rat Fe65 (APBB1; 602709), an Fe65- like sequence (APBB2; 602710), and an X11- like sequence (APBA2). The human X11- like sequence is 83% identical to that encoded by the X11 gene (APBA1; 602414). McLoughlin and Miller (1996) detected a phosphotyrosine- binding domain in the protein encoded by the X11- like clone. Using a radiation hybrid panel, Blanco et al. (1998) mapped the APBA2 gene to human chromosome 15, between markers WI- 5590 (10.31 cR) and D15S144 (21.7 cR). In an interspecific backcross, using an SSCP- demonstrated polymorphism, they assigned the Apba2 gene to mouse chromosome 7. The location of the flanking markers suggested that Apba2 is a further addition to a gene segment conserved between mouse chromosome 7 and human 15q.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Blanco, G.; Irving, N. G.; Brown, S. D. M.; Miller, C. C. J.; McLoughlin, D. M. : Mapping of the human and murine X11- like genes (APBA2 and Apba2), the murine Fe65 gene (Apbb1), and the human Fe65-like gene (APBB2): genes encoding phosphotyrosine- binding domain proteins that interact with the Alzheimer's disease amyloid precursor protein. Mammalian Genome 9: 473- 475, 1998. ; and

McLoughlin, D. M.; Miller, C. C. J. : The intracellular cytoplasmic domain of the Alzheimer's disease amyloid precursor protein interacts with phosphotyrosine- binding domain proteins in.

Further studies establishing the function and utilities of APBA2 are found in John Hopkins OMIM database record ID 602712, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1216 DLST TACAGGCAGGCACAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
AGGCAGT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1216 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of DLST, a GAM1216 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1216 NGB TACAGGCAGGCACAG Neuroglobin (NGB, Accession NM_021257.2) is another GAM1216 A A
AGGCAGT target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of NGB, a GAM1216 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM1216 SNCG TACAGGCAGGCACAG SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another A A
AGGCAGT GAM1216 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of

SNCG, a GAM1216 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM1216 TFCP2 TACAGGCAGGCACAG Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
AGGCAGT another GAM1216 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of TFCP2, a GAM1216 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM1216 TGFB1 TACAGGCAGGCACAG TGFB1 (Accession NM_000660.1) is another GAM1216 target gene. A A
AGGCAGT TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1216 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1217 APPBP2 TATTACATTCATTTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GATGGTT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM1217 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1217 is therefore inhibition of APPBP2, a GAM1217 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1217 IL1A TATTACATTCATTTT GATGGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM1217 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1217 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1217 is therefore inhibition of IL1A, a GAM1217 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM1221 BACE TTCCAGATGGGTAGG AATACCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) is a GAM1221 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1221 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1221 is therefore inhibition of BACE, a GAM1221 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1234 BACE2 TGTCTTCATCCAGGA ACCACAT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM1234 target gene. BACE2 BINDING SITE is a A A

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1234 is therefore inhibition of BACE2, a GAM1234 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1234 DHCR24 TGTCTTCATCCAGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A
ACCACAT NM_014762.1) is another GAM1234 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1234 is therefore inhibition of DHCR24, a GAM1234 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1234 IAPP GCTGTGGTTCTGCAT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A
GAAGACA another GAM1234 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1234 is therefore inhibition of IAPP, a GAM1234 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1234 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1234 MME GCTGTGGTTCTGCAT GAAGACA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM1234 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1234 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM1234 is therefore inhibition of MME, a GAM1234 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1238 CTSB TGCACCACTGCACTC CAGCCTG CTSB (Accession NM_147782.1) is a GAM1238 target gene. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1238 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1238 is therefore inhibition of CTSB. Accordingly, utilities of GAM1238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM1238 FHL2 TGCACCACTGCACTC CAGCCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM1238 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1238 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1238 is therefore inhibition of FHL2, a GAM1238 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM1238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1238 IGF1 TGCACCACTGCACTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CAGCCTG NM_000618.2) is another GAM1238 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1238 is therefore inhibition of IGF1, a GAM1238 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1238 PRND TGCACCACTGCACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
CAGCCTG another GAM1238 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1238 is therefore inhibition of PRND, a GAM1238 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1293 ADAMTS5 GCTGTGTTAACTGTT A Disintegrin- like and Metalloprotease (reprolysin type) with A A
CAAACTC Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM1293 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM1293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1293 is therefore inhibition of ADAMTS5, a GAM1293 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM1293 APPBP2 GCTGTGTTAACTGTT CAAACTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM1293 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1293 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1293 is therefore inhibition of APPBP2, a GAM1293 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1293 DHCR24 GCTGTGTTAACTGTT CAAACTC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM1293 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1293 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1293 is therefore inhibition of DHCR24, a GAM1293 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM44.

GAM1293 PRNP GCTGTGTTAACTGTT CAAACTC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM1293 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1293 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1293 is therefore inhibition of PRNP, a GAM1293 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM1294 DHCR24 TGGATTAGTAAAGAA GAATGAA 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM1294 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1294 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1294 is therefore inhibition of DHCR24, a GAM1294 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1294 DLST TGGATTAGTAAAGAA GAATGAA Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1294 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1294 RNA are set forth in Tables 6 and 7, hereby A A

incorporated herein.

Another function of GAM1294 is therefore inhibition of DLST, a GAM1294 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1294 PSEN1 TGGATTAGTAAAGAA PSEN1 (Accession NM_007318.1) is another GAM1294 target gene. A A

GAATGAA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1294 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1294 SLC6A4 TGGATTAGTAAAGAA Solute Carrier Family 6 (neurotransmitter transporter, A A
GAATGAA serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM1294 target gene. SLC6A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1294 is therefore inhibition of SLC6A4, a GAM1294 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 has been established by previous studies. Altered function of the serotonin neurotransmission system has been implicated in the aggressive behavior in patients with Alzheimer disease (AD; 104300). Sukonick et al. (2001) studied 137 subjects diagnosed as having possible or probable AD, 58 of whom demonstrated aggressive behavior. They found that the *L/*L genotype was significantly associated with aggression in patients with AD (odds ratio, 2.8). Similar results were obtained for *L allele frequency. Hariri et al. (2002) reported that

individuals with 1 or 2 copies of the short allele of the serotonin transporter promoter polymorphism, which has been associated with reduced serotonin expression and function and increased fear and anxiety- related behaviors, exhibited greater amygdala neuronal activity, as assessed by functional MRI, in response to fearful stimuli compared with individuals homozygous for the long allele. Each group consisted of 14 adults. Hariri et al. (2002) concluded that their results demonstrated genetically driven variation in the response of brain regions underlying human emotional behavior and suggested that differential excitability of the amygdala to emotional stimuli may contribute to the increased fear and anxiety typically associated with the short SLC6A4 allele

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Hariri, A. R.; Mattay, V. S.; Tessitore, A.; Kolachana, B.; Fera, F.; Goldman, D.; Egan, M. F.; Weinberger, D. R. : Serotonin transporter genetic variation and the response of the human amygdala. Science 297: 400- 403, 2002. ; and

Sukonick, D. L.; Pollock, B. G.; Sweet, R. A.; Mulsant, B. H.; Rosen, J.; Klunk, W. E.; Kastango, K. B.; DeKosky, S. T.; Ferrell, R. E. : The 5- HTTPR*S/*L polymorphism and aggressive behav.

Further studies establishing the function and utilities of SLC6A4 are found in John Hopkins OMIM database record ID 182138, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1295 BACE2 GAGAGAGGTAGAGGG GAGCAGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM1295 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1295 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1295 is therefore inhibition of BACE2, a GAM1295 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1295 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1295 DLST GAGAGAGGTAGAGGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGCAGA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1295 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1295 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1295 is therefore inhibition of DLST, a GAM1295 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1295 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1295 GFAP GAGAGAGGTAGAGGG GFAP (Accession NM_002055.2) is another GAM1295 target gene. A A

GAGCAGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1295 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1295 is therefore inhibition of GFAP. Accordingly, utilities of GAM1295 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1300 ADAM10 TGCTAGGCTTATTCT A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

CTTCCTC Accession NM_001110.1) is a GAM1300 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1300 is therefore inhibition of ADAM10, a GAM1300 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 has been established by previous studies. Wolfsberg et al. (1995) identified a family of proteins containing a disintegrin and metalloproteinase

(ADAM) domain. Members of this family are cell surface proteins with a unique structure possessing both potential adhesion and protease domains. Tumor necrosis factor- alpha (TNFA; 191160) is synthesized as a proinflammatory cytokine from a 233- amino acid precursor. Conversion of the membrane- bound precursor to a secreted mature protein is mediated by a protease termed TNFA convertase. Lunn et al. (1997) found that ADAM10 possesses TNFA convertase activity. TNFA is involved in a variety of diseases. To elucidate whether the ADAM10 locus maps to the same region as a disease susceptibility, Yamazaki et al. (1997) mapped the ADAM10 locus. Using a radiation hybrid mapping method, they showed that ADAM10 is located on 15q21.3- q23. Although ephrins form a high- affinity multivalent complex with their receptors present on axons, axons can be rapidly repelled rather than being bound. Hattori et al. (2000) showed that ephrin- A2 (OMIM Ref. No. 602756) forms a stable complex with the metalloproteinase Kuzbanian (OMIM Ref. No. ADAM10) involving interactions outside the cleavage region and the protease domain. Eph receptor binding triggered ephrin- A2 cleavage in a localized reaction specific to the cognate ligand. The cleavage- inhibiting mutation in ephrin- A2 delayed axon withdrawal. Hattori et al. (2000) concluded that their studies reveal mechanisms for protease recognition and control of cell surface proteins, and, for ephrin-A2, they may provide a means for efficient axon detachment and termination of signaling.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula, S. K.; Lundell, D. : Purification of ADAM 10 from bovine spleen as a TNFalpha convertase. FEBS Lett. 400: 333- 335, 1997. ; and

Hattori, M.; Osterfield, M.; Flanagan, J. G. : Regulated cleavage of a contact- mediated axon repellent. Science 289: 1360-1365, 2000.

Further studies establishing the function and utilities of ADAM10 are found in John Hopkins OMIM database record ID 602192, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1300 CHAT TGCTAGGCTTATTCT A A CTTCCTC Choline Acetyltransferase (CHAT, Accession NM_020985.1) is another GAM1300 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1300 is therefore inhibition of CHAT, a GAM1300 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1300 A A NGB CTTCCTC TGCTAGGCTTATTCT Neuroglobin (NGB, Accession NM_021257.2) is another GAM1300 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1300 is therefore inhibition of NGB, a GAM1300 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM1300 A A PSEN1 CTTCCTC TGCTAGGCTTATTCT PSEN1 (Accession NM_000021.2) is another GAM1300 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1300 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1300 A A S100B CTTCCTC TGCTAGGCTTATTCT S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is another GAM1300 target gene. S100B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1300 is therefore inhibition of S100B, a GAM1300 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM1300 SNCAIP TGCTAGGCTTATTCT CTTCCTC Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM1300 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1300 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1300 is therefore inhibition of SNCAIP, a GAM1300 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP has been established by previous studies. Parkinson disease (PD) is a neurodegenerative disease characterized by tremor, bradykinesia, rigidity, and postural instability. Postmortem examination shows loss of neurons and Lewy bodies, which are cytoplasmic eosinophilic inclusions, in the substantia nigra and other brain regions. A few families have been found to have PD on the basis of mutations, A53T (163890.0001) or A30P (163890.0002), in the gene encoding alpha-synuclein (SNCA). Alpha- synuclein is present in Lewy bodies of patients with sporadic PD, suggesting that alpha- synuclein may be involved in the pathogenesis of PD. To determine the protein-interaction partners of alpha- synuclein, Engelender et al. (1999) screened human brain libraries in the yeast 2- hybrid system. They identified a novel interacting protein they designated synphilin- 1, encoded by the gene SNCAIP. The predicted 919- amino acid synphilin-1 protein contains several protein- protein interaction domains, such as ankyrin- like repeats and a coiled- coil domain. An approximately 4- kb SNCAIP transcript was detected in many human tissues by Northern blot analysis and was particularly enriched in brain, heart, and placenta. Synphilin- 1 was present in many regions in brain, including substantia nigra. In immunoblot analyses of human brain, synphilin- 1 appeared as a single band of approximately 90 kD in several brain regions, with no differences in the level of

expression in controls, patients with PD, or patients with Alzheimer disease (OMIM Ref. No. 104300). They found that alpha- synuclein interacts in vivo with synphilin- 1 in neurons. Cotransfection of both proteins (but not control proteins) in HEK293 cells yielded cytoplasmic eosinophilic inclusions. Engelender et al. (2000) determined that the human SNCAIP gene contains 10 exons and has a highly polymorphic GT repeat within intron 5 that is suitable for linkage analysis in families with Parkinson disease. Using immunohistochemistry in human postmortem brain tissue, they found that synphilin- 1 protein, like alpha- synuclein protein, is present in neuropil.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Engelender, S.; Kaminsky, Z.; Guo, X.; Sharp, A. H.; Amaravi, R. K.; Kleiderlein, J. J.; Margolis, R. L.; Troncoso, J. C.; Lanahan, A. A.; Worley, P. F.; Dawson, V. L.; Dawson, T. M.; Ross, C. A. : Synphilin- 1 associates with alpha- synuclein and promotes the formation of cytosolic inclusions. Nature Genet. 22: 110- 114, 1999. ; and

Engelender, S.; Wanner, T.; Kleiderlein, J. J.; Wakabayashi, K.; Tsuji, S.; Takahashi, H.; Ashworth, R.; Margolis, R. L.; Ross, C. A. : Organization of the human synphilin- 1 gene, a ca.

Further studies establishing the function and utilities of SNCAIP are found in John Hopkins OMIM database record ID 603779, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1310 AVP CACTGCAACCCCCGC AVP (Accession NM_000490.2) is a GAM1310 target gene. AVP A A
CTCCCAG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1310 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1310 is therefore inhibition of AVP. Accordingly, utilities of GAM1310 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM1310 IAPP CACTGCAACCCCCGC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
CTCCCAG another GAM1310 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM1310 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1310 is therefore inhibition of IAPP, a GAM1310 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1310 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1310 NGB CACTGCAACCCCCGC Neuroglobin (NGB, Accession NM_021257.2) is another GAM1310 A A
CTCCCAG target gene. NGB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1310 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1310 is therefore inhibition of NGB, a GAM1310 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1310 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM1310 TFCP2 CACTGCAACCCCCGC Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
CTCCCAG another GAM1310 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1310 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1310 is therefore inhibition of TFCP2, a GAM1310 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1310 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM1332 DSCR1 TGAGGTAGGTGCTGA Down Syndrome Critical Region Gene 1 (DSCR1, Accession
A A
AACTGC NM_004414.3) is a GAM1332 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1332 is therefore inhibition of DSCR1, a GAM1332 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 has been established by previous studies. The study of patients with partial trisomy 21 has defined an area of approximately 3 Mb at chromosomal region 21q22 as the minimal candidate region for the Down syndrome phenotype (OMIM Ref. No. 190685). Using a novel exon cloning strategy, Fuentes et al. (1995) identified several putative exons from region 21q22.1- q22.2. One exon was used to isolate fetal brain cDNAs corresponding to a gene that the authors designated DSCR1. The predicted 171- amino acid protein contains 2 proline-rich regions, a putative DNA- binding domain, and an acidic region. Northern blot analysis revealed that the 2.2- kb DSCR1 transcript is expressed at the highest levels in fetal brain and adult heart and at lower levels in various other tissues. An additional 2- kb mRNA was detected in fetal and adult liver. Increased expression in the brains of young rats compared with adults suggested to Fuentes et al. (1995) that DSCR1 plays a role during central nervous system development. Fuentes et al. (1997) determined that DSCR1 spans nearly 45 kb and contains 7 exons, 4 of which are alternative first exons. They found tissue- specific expression patterns for the alternative transcripts. Kingsbury and Cunningham (2000) referred to the proteins encoded by the MCIP genes as calcipressins. Functional analysis showed that when expressed in yeast, DSCR1 and ZAKI4 inhibited calcineurin function. The authors proposed that increased expression of DSCR1 in trisomy- 21 individuals may contribute to the neurologic, cardiac, or immunologic defects of Down syndrome.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Fuentes, J. J.; Pritchard, M. A.; Estivill, X. : Genomic organization, alternative splicing, and expression patterns of the DSCR1 (Down syndrome candidate region 1) gene. Genomics 44: 358-361, 1997. ; and

Kingsbury, T. J.; Cunningham, K. W. : A conserved family of calcineurin regulators. Genes Dev. 14: 1595- 1604, 2000.

Further studies establishing the function and utilities of DSCR1 are found in John Hopkins OMIM database record ID 602917, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1332 FLNB TGAGGTAGGTGCTGA AACTGC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM1332 target gene. FLNB BINDING SITE1 and FLNB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLNB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE1 and FLNB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1332 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1332 is therefore inhibition of FLNB, a GAM1332 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM1332 IAPP TGAGGTAGGTGCTGA AACTGC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM1332 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1332 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1332 is therefore inhibition of IAPP, a GAM1332 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1332 IGF1 TGAGGTAGGTGCTGA AACTGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1332 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1332 is therefore inhibition of IGF1, a GAM1332 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1338 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM1338 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1338 is therefore inhibition of APPBP2, a GAM1338 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1338 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM1338 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1338 is therefore inhibition of BACE2, a GAM1338 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1338 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM1338 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1338 is therefore inhibition of FHL2, a GAM1338 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1338 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM1338 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1338 is therefore inhibition of IGF1, a GAM1338 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1338 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM1338 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

Another function of GAM1338 is therefore inhibition of MME, a GAM1338 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1338 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM1338 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM1338 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1338 is therefore inhibition of PRND, a GAM1338 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1361 APLP2 AGAAGTAGTAGTAGC AGTAGTA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM1361 target gene. APLP2 BINDING SITE1 and APLP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APLP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE1 and APLP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1361 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1361 is therefore inhibition of APLP2, a GAM1361 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM1361 HTR2A AGAAGTAGTAGTAGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

AGTAGTA NM_000621.1) is another GAM1361 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1361 is therefore inhibition of HTR2A, a GAM1361 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM1363 DSCR1 AGCTGGTGTGTAGCG Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

GGTACCT NM_004414.3) is a GAM1363 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1363 is therefore inhibition of DSCR1, a GAM1363 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM1363 PRNP AGCTGGTGTGTAGCG Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

GGTACCT Strausler- (PRNP, Accession NM_000311.1) is another GAM1363 target gene. PRNP BINDING SITE1 and PRNP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRNP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE1 and PRNP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1363 is therefore inhibition of PRNP, a GAM1363 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal

and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM1372 FHL2 CACTGCACTCCAACC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGACAA a GAM1372 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1372 is therefore inhibition of FHL2, a GAM1372 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1372 IGF1 CACTGCACTCCAACC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGACAA NM_000618.2) is another GAM1372 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1372 is therefore inhibition of IGF1, a GAM1372 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1372 PRND CACTGCACTCCAACC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGACAA another GAM1372 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1372 is therefore inhibition of PRND, a GAM1372 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1423 HD GTCAGCAAGGAGGGG HD (Accession NM_002111.3) is a GAM1423 target gene. HD BINDING A A
TGGACAA SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1423 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1423 is therefore inhibition of HD. Accordingly, utilities of GAM1423 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM1431 IGF1 CTGGGATGGAGGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ATTAGAG NM_000618.2) is a GAM1431 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1431 is therefore inhibition of IGF1, a GAM1431 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1440 BACE TCCAGTGAAACAGGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
CTCTTTG is a GAM1440 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1440 is therefore inhibition of BACE, a GAM1440 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1440 TNFRSF5 TCCAGTGAAACAGGT TNFRSF5 (Accession NM_152854.1) is another GAM1440 target gene. A A

CTCTTTG TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1440 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM1440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM1443 ADAMTS5 GGCATGTGTGAGCAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CTGCAGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM1443 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1443 is therefore inhibition of ADAMTS5, a GAM1443 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM1443 APLP2 GGCATGTGTGAGCAG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

CTGCAGG NM_001642.1) is another GAM1443 target gene. APLP2 BINDING SITE1 and APLP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APLP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE1 and APLP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of APLP2, a GAM1443 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM1443 APPBP2 GGCATGTGTGAGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CTGCAGG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM1443 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of APPBP2, a GAM1443 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1443 CNTF GGCATGTGTGAGCAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A
CTGCAGG another GAM1443 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of CNTF, a GAM1443 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM1443 HD GGCATGTGTGAGCAG HD (Accession NM_002111.3) is another GAM1443 target gene. HD A A

CTGCAGG BINDING SITE1 through HD BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 through HD BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of HD. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM1443 MAPK10 GGCATGTGTGAGCAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

CTGCAGG NM_138981.1) is another GAM1443 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of MAPK10, a GAM1443 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM1443 TRPM2 GGCATGTGTGAGCAG TRPM2 (Accession NM_003307.1) is another GAM1443 target gene. A A

CTGCAGG TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1443 is therefore inhibition of TRPM2, a GAM1443 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM1443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1447 PRND TGCTGTGCTAAAGGA AGGATTA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a GAM1447 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1447 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1447 is therefore inhibition of PRND, a GAM1447 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1456 BACE2 ATACTGAGAGAAAAA GCTTGTC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM1456 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1456 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1456 is therefore inhibition of BACE2, a GAM1456 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1456 IGF1 ATACTGAGAGAAAAA GCTTGTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1456 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1456 is therefore inhibition of IGF1, a GAM1456 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1461 BACE2 TGGGCTCGCTCTTCA GTCTCGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM1461 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1461 is therefore inhibition of BACE2, a GAM1461 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1469 APBB2 TTCTATGATTCTCTA AGTAGCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM1469 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1469 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1469 is therefore inhibition of APBB2, a GAM1469 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1469 OLR1 TTCTATGATTCTCTA AGTAGCA Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM1469 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1469 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1469 is therefore inhibition of OLR1, a GAM1469 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1469 BACE2 TCTGCTTGGACTGAT CATTGAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM1469 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1469 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM1469 is therefore inhibition of BACE2, a GAM1469 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1469 GFAP TCTGCTTGGACTGAT CATTGAA GFAP (Accession NM_002055.2) is another GAM1469 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1469 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM1469 is therefore inhibition of GFAP. Accordingly, utilities of GAM1469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1469 MAPT TCTGCTTGGACTGAT CATTGAA Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM1469 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1469 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM1469 is therefore inhibition of MAPT, a GAM1469 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM1479 GYPA GAAGGCAGTAGGTTG TATAGTT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is a GAM1479 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1479 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1479 is therefore inhibition of GYPA, a GAM1479 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1479 IGF1 GAAGGCAGTAGGTTG TATAGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1479 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1479 RNA are set A A

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1479 is therefore inhibition of IGF1, a GAM1479 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1484 IGF1 ATATTGGTGAAATGC TAGCAAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM1484 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1484 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1484 is therefore inhibition of IGF1, a GAM1484 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1484 SOD2 ATATTGGTGAAATGC TAGCAAA Superoxide Dismutase 2, Mitochondrial (SOD2, Accession NM_000636.1) is another GAM1484 target gene. SOD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SOD2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1484 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1484 is therefore inhibition of SOD2, a GAM1484 target gene which is intramitochondrial free radical scavenging enzyme. When he has polymorphism in signal peptides he could couse diseases of distribution and therefore is associated with Alzheimer. Accordingly, utilities of GAM1484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SOD2.The function of SOD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1197.

GAM1484 ACT TTTGCAGTGTTCATC Activator of CAMP- responsive Element Modulator (CR (ACT, B A

AGTATTT Accession NM_020482.3) is another GAM1484 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1484 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1484 is therefore inhibition of ACT, a GAM1484 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT has been established by previous studies. Alpha- 1- antichymotrypsin is a plasma protease inhibitor synthesized in the liver. It is a single glycopeptide chain of about 68,000 daltons and belongs to the class of serine protease inhibitors. In man, the normal serum level is about one- tenth that of alpha- 1- antitrypsin (PI; 107400), with which it shares nucleic acid and protein sequence homology (Chandra et al. 1983). Both are major acute phase reactants; their concentrations in plasma increase in response to trauma, surgery, and infection. Antithrombin III, which also is structurally similar to alpha- 1- antitrypsin, shows less sequence homology to antichymotrypsin and is not an acute phase reactant. Sefton et al. (1990) concluded that the PI- PIL gene cluster is only 220 kb away from the AACT gene and that it is oriented in the opposite direction. (PIL refers to 'PI- like' and is also referred to as 'antitrypsin- related,' or ATR (OMIM Ref. No. 107410).) The comparatively short interval between the genes came as a surprise given previous estimates of the level of genetic recombination between them. By PCR- single strand conformation polymorphism (SSCP) analysis, Tsuda et al. (1992) identified a point mutation in exon 5 of the AACT gene resulting in substitution of met by val at codon 389. The mutation, an A- to- G transition at basepair 1252, was found in heterozygous state in 6 patients; 4 of the 6 (aged 38, 43, 69, and 80 years) had occlusive cerebrovascular disease.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C. : Sequence homology between human alpha- 1- antichymotrypsin, alpha- 1- antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061, 1983. ; and

Tsuda, M.; Sei, Y.; Yamamura, M.; Yamamoto, M.; Shinohara, Y. : Detection of a new mutant alpha- 1- antichymotrypsin in patients with occlusive- cerebrovascular disease. FEBS Lett. 304: 66.

Further studies establishing the function and utilities of ACT are found in John Hopkins OMIM database record ID 107280, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1484 ADAMTS5 TTTGCAGTGTTCATC A Disintegrin- like and Metalloprotease (reprolysin type) with B A
AGTATTT Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM1484 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1484 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1484 is therefore inhibition of ADAMTS5, a GAM1484 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM1484 NCKAP1 TTTGCAGTGTTCATC NCKAP1 (Accession NM_013436.2) is another GAM1484 target gene. B A
AGTATTT NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1484 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1484 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM1484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM1490 ACHE GTGTGTGGAAATGCA Acetylcholinesterase (YT blood group) (ACHE, Accession A A
GATGACC NM_015831.1) is a GAM1490 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1490 is therefore inhibition of ACHE, a GAM1490 target gene which rapidly hydrolyzes choline released into

the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM1490 MAPT GTGTGTGGAAATGCA GATGACC Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM1490 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1490 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1490 is therefore inhibition of MAPT, a GAM1490 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM1500 ACE GGCAGTGTCATTAGC TGATTGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_000789.2) is a GAM1500 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1500 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1500 is therefore inhibition of ACE, a GAM1500 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1500 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1500 PSEN1 GGCAGTGTCATTAGC TGATTGT PSEN1 (Accession NM_007318.1) is another GAM1500 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE A A

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1500 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1500 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1500 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1502 ACT TATATGTCTGGTATT CTTGGGG Activator of CAMP- responsive Element Modulator (CR (ACT, Accession NM_020482.3) is a GAM1502 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1502 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1502 is therefore inhibition of ACT, a GAM1502 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1502 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM1502 MME TATATGTCTGGTATT CTTGGGG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM1502 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1502 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1502 is therefore inhibition of MME, a GAM1502 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1502 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1523 MAPK10 GTTTGGCACTGAATC ATATACA Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is a GAM1523 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE A A

III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1523 is therefore inhibition of MAPK10, a GAM1523 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM1523 RAGE GTTTGGCACTGAATC Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

ATATACA GAM1523 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1523 is therefore inhibition of RAGE, a GAM1523 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM1523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE has been established by previous studies. Sugaya et al. (1994) identified 3 genes located 90 to 140 kb centromeric to the tenascin- like gene (OMIM Ref. No. 600261) in the MHC class III region near the junction with class II. One of these was the gene for receptor of advanced glycosylation end products of proteins, a member of the immunoglobulin superfamily. A second was the PBX2 homeo box gene (OMIM Ref. No. 176311), and a third was the human counterpart of the mouse mammary tumor gene int- 3 (OMIM Ref. No. 164951). The PBX2 and AGER genes are immediately contiguous and are transcribed in the same direction. In addition to mapping by contiguous cosmids and YAC clones, Sugaya et al. (1994) determined the location of the AGER sequence on 6p21.3 by fluorescence in situ hybridization. Yan et al. (1996) reported that the AGER protein, called RAGE (receptor for advanced glycation end products) by them, is an important receptor for the amyloid beta peptide (OMIM Ref. No. 104760) and that expression of this receptor increases in Alzheimer disease (OMIM Ref. No. 104300). They noted that expression of RAGE is particularly increased in neurons close to deposits of amyloid beta peptide and to neurofibrillary tangles.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.; Ikemura, T. : Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a Notch homolog, human counterpart of mouse mammary tumor gene int- 3. Genomics 23: 408- 419, 1994. ; and

Yan, S. D.; Chen, X.; Fu, J.; Chen, M.; Zhu, H.; Roher, A.; Slattery, T.; Zhao, L.; Nagashima, M.; Morser, J.; Migheli, A.; Nawroth, P.; Stern, D.; Schmidt, A. M. : RAGE and amyloid- beta.

Further studies establishing the function and utilities of RAGE are found in John Hopkins OMIM database record ID 600214, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1543 APPBP2 ATTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGGTGAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM1543 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1543 is therefore inhibition of APPBP2, a GAM1543 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1543 FHL2 ATTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGTGAC another GAM1543 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1543 is therefore inhibition of FHL2, a GAM1543 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1543 IGF1 ATTGCACTCCAGCCT GGGTGAC A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1543 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1543 is therefore inhibition of IGF1, a GAM1543 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1543 PRND ATTGCACTCCAGCCT GGGTGAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM1543 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1543 is therefore inhibition of PRND, a GAM1543 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1543 TNFRSF5 ATTGCACTCCAGCCT GGGTGAC A A TNFRSF5 (Accession NM_152854.1) is another GAM1543 target gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1543 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM1543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM1550 ACE TGAGTATTCACCAGG TGCTGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM1550 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1550 is therefore inhibition of ACE, a GAM1550 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1550 ADAM17 TGAGTATTCACCAGG TGCTGGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is another GAM1550 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1550 is therefore inhibition of ADAM17, a GAM1550 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1550 CAV1 TGAGTATTCACCAGG TGCTGGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM1550 target gene. CAV1 BINDING SITE1 and CAV1 BINDING SITE2 are target binding sites found in untranslated A A

regions of mRNA encoded by CAV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE1 and CAV1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1550 is therefore inhibition of CAV1, a GAM1550 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM1550 GYPA TGAGTATTCACCAGG Glycophorin A (includes MN blood group) (GYPA, Accession A A

TGCTGGG NM_002099.2) is another GAM1550 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1550 is therefore inhibition of GYPA, a GAM1550 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1550 NOTCH1 TGAGTATTCACCAGG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGCTGGG (NOTCH1, Accession NM_017617.2) is another GAM1550 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1550 is therefore inhibition of NOTCH1, a GAM1550 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1550 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM1550 PSEN2 TGAGTATTCACCAGG A A TGCTGGG PSEN2 (Accession NM_012486.1) is another GAM1550 target gene. PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1550 is therefore inhibition of PSEN2. Accordingly, utilities of GAM1550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM1602 APPBP2 GGAGTGTAAAGAAGG A A ATGTTAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM1602 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1602 is therefore inhibition of APPBP2, a GAM1602 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1602 B2M GGAGTGTAAAGAAGG A A ATGTTAC Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another GAM1602 target gene. B2M BINDING SITE1 and B2M BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by B2M, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE1 and B2M BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1602 is therefore inhibition of B2M, a GAM1602 target gene which is the beta- chain of major

histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM1602 MAPT GGAGTGTAAAGAAGG ATGTTAC A A Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM1602 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1602 is therefore inhibition of MAPT, a GAM1602 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM1607 BACE TTAATGCTAATCGTG A A ATAGGGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM1607 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1607 is therefore inhibition of BACE, a GAM1607 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1607 FPRL1 TTAATGCTAATCGTG A A ATAGGGG FPRL1 (Accession NM_001462.1) is another GAM1607 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1607 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1607 SLC6A4 TTAATGCTAATCGTG ATAGGGG Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM1607 target gene. SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SLC6A4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1607 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1607 is therefore inhibition of SLC6A4, a GAM1607 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM1617 ACE TTGCCCAGGCTGGAG TGCAGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM1617 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1617 is therefore inhibition of ACE, a GAM1617 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1617 ADAM17 TTGCCCAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TGCAGTG factor, (ADAM17, Accession NM_003183.3) is another GAM1617 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of ADAM17, a GAM1617 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1617 CHAT TTGCCCAGGCTGGAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is A A
TGCAGTG another GAM1617 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of CHAT, a GAM1617 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1617 FLNB TTGCCCAGGCTGGAG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
TGCAGTG NM_001457.1) is another GAM1617 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of FLNB, a GAM1617 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM1617 A TGCAGTG A HTR2A TTGCCCAGGCTGGAG A 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM1617 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of HTR2A, a GAM1617 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM1617 A TGCAGTG A IAPP TTGCCCAGGCTGGAG A Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM1617 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of IAPP, a GAM1617 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1617 A TGCAGTG A NOTCH1 TTGCCCAGGCTGGAG A Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM1617 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of NOTCH1, a GAM1617 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM1617 A A TGFB1 TGCAGTG TTGCCCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM1617 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1617 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1650 A A BAX GAATATG TCCAAAAGTGGAGAG BCL2- associated X Protein (BAX, Accession NM_138764.1) is a GAM1650 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1650 is therefore inhibition of BAX, a GAM1650 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM1650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX has been established by previous studies. Oltvai et al. (1993) showed that BCL2 associates in vivo with a 21-kD program partner, BAX. BAX shows extensive amino acid homology with BCL2 and forms homodimers and heterodimers with BCL2 in vivo. When BAX predominates, programmed cell death is accelerated, and the death repressor activity of BCL2 is countered. Their findings suggested to Oltvai et al. (1993) a model in which the ratio of BCL2 to BAX determines survival or death following an apoptotic stimulus.

Studies of Bax- deficient mice indicated that the pro- apoptotic BAX molecule can function as a tumor suppressor. For that reason, Meijerink et al. (1998) examined human hematopoietic malignancies and found that approximately 21% of lines possessed mutations in BAX, perhaps most commonly in the acute lymphoblastic leukemia subset. Approximately half were nucleotide insertions or deletions within a deoxyguanosine (G8) tract, resulting in a proximal frameshift and loss of immunodetectable BAX protein. Other BAX mutants bore single amino acid substitutions within BH1 or BH3 domains, demonstrated altered patterns of protein dimerization, and had lost death- promoting activity. LeBlanc et al. (2002) demonstrated that BAX can be essential for death receptor- mediated apoptosis in cancer cells. BAX- deficient human colon carcinoma cells were resistant to death- receptor ligands, whereas BAX-expressing sister clones were sensitive. BAX was dispensable for apical death- receptor signaling events including caspase- 8 (OMIM Ref. No. 601763) activation, but crucial for mitochondrial changes and downstream caspase activation. Treatment of colon cancer cells deficient in DNA mismatch repair with the TRAIL (OMIM Ref. No. 603598) selected in vitro or in vivo for refractory subclones with BAX frameshift mutations including deletions at a novel site. Chemotherapeutic agents upregulated expression of the TRAIL receptor DR5 (OMIM Ref. No. 603612) and the BAX homolog BAK (OMIM Ref. No. 600516) in BAX - /- cells, and restored TRAIL sensitivity in vitro and in vivo. Thus, LeBlanc et al. (2002) concluded that BAX mutation in mismatch repair- deficient tumors can cause resistance to death receptor- targeted therapy, but pre- exposure to chemotherapy rescues tumor sensitivity. Animal model experiments lend further support to the function of BAX. Proapoptotic Bcl2 family members have been proposed to play a central role in regulating apoptosis, yet mice lacking Bax display limited phenotypic abnormalities. Lindsten et al. (2000) found that Bak - /- mice were developmentally normal and reproductively fit and failed to develop any age- related disorders. However, when Bak- deficient mice were mated to Bax-deficient mice to create mice lacking both genes, the majority of Bax- /- Bak- /- animals died perinatally, with fewer than 10% surviving into adulthood. Bax- /- Bak- /- mice displayed multiple developmental defects, including persistence of interdigital webs, an imperforate vaginal canal, and accumulation of excess cells within both the central nervous and hematopoietic systems. Thus, the authors concluded that Bax and Bak have overlapping roles in the regulation of apoptosis during mammalian development and tissue homeostasis.

It is appreciated that the abovementioned animal model for BAX is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the

following publications, the disclosure of which are hereby incorporated by reference:

LeBlanc, H.; Lawrence, D.; Varfolomeev, E.; Totpal, K.; Morlan, J.; Schow, P.; Fong, S.; Schwall, R.; Sinicropi, D.; Ashkenazi, A. : Tumor- cell resistance to death receptor- induced apoptosis through mutational inactivation of the proapoptotic Bcl- 2 homolog Bax. Nature Med. 8: 274- 281, 2002. ; and

Lindsten, T.; Ross, A. J.; King, A.; Zong, W.- X.; Rathmell, J. C.; Shiels, H. A.; Ulrich, E.; Waymire, K. G.; Mahar, P.; Frauwirth, K.; Chen, Y.; Wei, M.; and 9 others : The combined f.

Further studies establishing the function and utilities of BAX are found in John Hopkins OMIM database record ID 600040, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1650 IGF1 TCCAAAAGTGGAGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GAATATG NM_000618.2) is another GAM1650 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1650 is therefore inhibition of IGF1, a GAM1650 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1650 APBB2 ATTTTTCTGCATTTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A TATTGGA 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM1650 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1650 is therefore inhibition of APBB2, a GAM1650 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1650 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1650 B A SLC17A7 ATTTTTCTGCATTTG TATTGGA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM1650 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1650 is therefore inhibition of SLC17A7, a GAM1650 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM1650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM1650 B A TNFSF5 ATTTTTCTGCATTTG TATTGGA TNFSF5 (Accession NM_000074.1) is another GAM1650 target gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1650 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM1650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM1653 A A A2M TGGAGCAGAAAGGCA GGAGTCC Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a GAM1653 target gene. A2M BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1653 is therefore inhibition of A2M, a GAM1653 target gene which inhibit all four classes of proteinases

and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M has been established by previous studies. Kan et al. (1985) isolated A2M cDNA clones from a human liver cDNA library by using synthetic oligonucleotides as hybridization probes. Matthijs et al. (1992) demonstrated that the A2M gene spans approximately 48 kb and consists of 36 exons, from 21 to 229 bp in size and with consensus splice sites. Intron sizes range from 125 bp to 7.5 kb. The A2M gene is present in single copy in the haploid genome. Umans et al. (1994) found that the homologous gene in the mouse contains 36 exons, coding for a 4.8- kb cDNA. Including putative control elements in the 5- prime flanking region, the gene covers about 45 kb. The promoter region of the mouse A2m gene differed considerably from the known promoter sequences of the human and rat genes. Alpha- 2- macroglobulin, a serum pan- protease inhibitor, has been implicated in Alzheimer disease (AD; 104300) based on its ability to mediate the clearance and degradation of A-beta, the major component of amyloid beta deposits. Blacker et al. (1998) analyzed a deletion in the A2M gene at the 5- prime splice site of 'exon II' of the bait region (exon 18) and found that inheritance of the deletion, designated A2M- 2, conferred increased risk for AD (Mantel- Haenzel odds ratio = 3.56, P = 0.001). The sibship disequilibrium test (SDT) also revealed a significant association between A2M and AD. These values were comparable to those obtained for the APOE4 allele in the same sample, but in contrast to APOE4, A2M- 2 did not affect age of onset. The observed association that A2M with AD did not appear to account for the previously published linkage of AD to chromosome 12, which Blacker et al. (1998) were unable to confirm in their sample. Thus, A2M, the A2M receptor (LRP1; 107770), and the genes for 2 other LRP (low density lipoprotein- related protein) ligands, APOE (OMIM Ref. No. 107741) and APP (OMIM Ref. No. 104760), had all been genetically linked to AD, suggesting that these proteins may participate in the common neuropathogenic pathway leading to the disease. Liao et al. (1998) found an association between the val1000- to- ile polymorphism (103950.0001) and AD.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Umans, L.; Serneels, L.; Hilliker, C.; Stas, L.; Overbergh, L.; De Strooper, B.; Van Leuven, F.; Van den Berghe, H. : Molecular cloning of the mouse gene coding for alpha- 2- macroglobulin and targeting of the gene in embryonic stem cells. Genomics 22: 519-529, 1994. ; and

Liao, A.; Nitsch, R. M.; Greenberg, S. M.; Finckh, U.; Blacker, D.; Albert, M.; Rebeck, G. W.; Gomez- Isla, T.; Clatworthy, A.;

Binetti, G.; Hock, C.; Mueller- Thomsen, T.; Mann, U.; Zuch.

Further studies establishing the function and utilities of A2M are found in John Hopkins OMIM database record ID 103950, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1653 A APBB1 TGGAGCAGAAAGGCA GGAGTCC A Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM1653 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of APBB1, a GAM1653 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1653 A CHAT TGGAGCAGAAAGGCA GGAGTCC A Choline Acetyltransferase (CHAT, Accession NM_020986.1) is another GAM1653 target gene. CHAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of CHAT, a GAM1653 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1653 A DLST TGGAGCAGAAAGGCA GGAGTCC A Dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1653 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of DLST, a GAM1653 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1653 FPRL1 TGGAGCAGAAAGGCA FPRL1 (Accession NM_001462.1) is another GAM1653 target gene.
A A

GGAGTCC FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1653 HTR2C TGGAGCAGAAAGGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A

GGAGTCC NM_000868.1) is another GAM1653 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of HTR2C, a GAM1653 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM1653 MPO TGGAGCAGAAAGGCA Myeloperoxidase (MPO, Accession NM_000250.1) is another
GAM1653 A A

GGAGTCC target gene. MPO BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of MPO, a GAM1653 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM1653 PRND TGGAGCAGAAAGGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGAGTCC another GAM1653 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of PRND, a GAM1653 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1653 SLC6A4 TGGAGCAGAAAGGCA Solute Carrier Family 6 (neurotransmitter transporter, A A
GGAGTCC serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM1653 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of SLC6A4, a GAM1653 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM1653 TGFB1 TGGAGCAGAAAGGCA A A GGAGTCC TGFB1 (Accession NM_000660.1) is another GAM1653 target gene. TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1653 TNFRSF5 TGGAGCAGAAAGGCA A A GGAGTCC TNFRSF5 (Accession NM_152854.1) is another GAM1653 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1653 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM1653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM1698 CRAT CTTGGCCCTGTGAGG A A CTTCACC Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is a GAM1698 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1698 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1698 is therefore inhibition of CRAT, a GAM1698 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1698 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM1698 A A DHCR24 CTTGGCCCTGTGAGG CTTCACC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM1698 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1698 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1698 is therefore inhibition of DHCR24, a GAM1698 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1698 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1698 A A MPO CTTGGCCCTGTGAGG CTTCACC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM1698 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1698 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1698 is therefore inhibition of MPO, a GAM1698 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1698 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM1698 A A SNCB CTTGGCCCTGTGAGG CTTCACC Synuclein, Beta (SNCB, Accession NM_003085.2) is another GAM1698 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1698 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1698 is therefore inhibition of SNCB, a GAM1698 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1698 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM1698 TRPM2 CTTGGCCCTGTGAGG TRPM2 (Accession NM_003307.1) is another GAM1698 target gene. A A
CTTCACC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1698 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1698 is therefore inhibition of TRPM2, a GAM1698 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM1698 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1735 APLP2 TGAGATGAACCAGGT Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
ATCTCAG NM_001642.1) is a GAM1735 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1735 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1735 is therefore inhibition of APLP2, a GAM1735 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1735 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM1735 FLNB TGAGATGAACCAGGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
ATCTCAG NM_001457.1) is another GAM1735 target gene. FLNB BINDING SITE1 and FLNB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLNB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of FLNB BINDING SITE1 and FLNB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1735 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1735 is therefore inhibition of FLNB, a GAM1735 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1735 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM1748 ARHA ACTGCACTCCAGTCT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GGGTGAC is a GAM1748 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1748 is therefore inhibition of ARHA, a GAM1748 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM1748 BACE ACTGCACTCCAGTCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

GGGTGAC is another GAM1748 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1748 is therefore inhibition of BACE, a GAM1748 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function

of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1748 FHL2 ACTGCACTCCAGTCT A A GGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM1748 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1748 is therefore inhibition of FHL2, a GAM1748 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM1748 FPRL1 ACTGCACTCCAGTCT A A GGGTGAC FPRL1 (Accession NM_001462.1) is another GAM1748 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1748 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1748 IGF1 ACTGCACTCCAGTCT A A GGGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM1748 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1748 is therefore inhibition of IGF1, a GAM1748 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer,

and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1748 PRND ACTGCACTCCAGTCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM1748 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1748 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1748 is therefore inhibition of PRND, a GAM1748 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1748 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1770 A2M TGGAGCAGAAAGGCA Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a A A
GGAGTCC GAM1770 target gene. A2M BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1770 is therefore inhibition of A2M, a GAM1770 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM1770 APBB1 TGGAGCAGAAAGGCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GGAGTCC 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM1770 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of APBB1, a GAM1770 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1770 CHAT TGGAGCAGAAAGGCA Choline Acetyltransferase (CHAT, Accession NM_020986.1) is A A

GGAGTCC another GAM1770 target gene. CHAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of CHAT, a GAM1770 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM1770 DLST TGGAGCAGAAAGGCA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GGAGTCC oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1770 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of DLST, a GAM1770 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1770 FPRL1 TGGAGCAGAAAGGCA FPRL1 (Accession NM_001462.1) is another GAM1770 target gene.
A A

GGAGTCC FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1770 HTR2C TGGAGCAGAAAGGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A

GGAGTCC NM_000868.1) is another GAM1770 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of HTR2C, a GAM1770 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM1770 MPO TGGAGCAGAAAGGCA Myeloperoxidase (MPO, Accession NM_000250.1) is another
GAM1770 A A

GGAGTCC target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of MPO, a GAM1770 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM1032.

GAM1770 PRND TGGAGCAGAAAGGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGAGTCC another GAM1770 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of PRND, a GAM1770 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1770 SLC6A4 TGGAGCAGAAAGGCA Solute Carrier Family 6 (neurotransmitter transporter, A A
GGAGTCC serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM1770 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of SLC6A4, a GAM1770 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM1770 TGFB1 TGGAGCAGAAAGGCA TGFB1 (Accession NM_000660.1) is another GAM1770 target gene. A A
GGAGTCC TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1770 TNFRSF5 TGGAGCAGAAAGGCA A A GGAGTCC TNFRSF5 (Accession NM_152854.1) is another GAM1770 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1770 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM1770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM1782 ADAM17 ATCACAGAGGCTTAA A A GTGCTGA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM1782 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1782 is therefore inhibition of ADAM17, a GAM1782 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1782 GFAP ATCACAGAGGCTTAA A A GTGCTGA GFAP (Accession NM_002055.2) is another GAM1782 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1782 is therefore inhibition of

GFAP. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1782 MME ATCACAGAGGCTTAA GTGCTGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM1782 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1782 is therefore inhibition of MME, a GAM1782 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1782 MTNR1A ATCACAGAGGCTTAA GTGCTGA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM1782 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1782 is therefore inhibition of MTNR1A, a GAM1782 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM1782 NCKAP1 ATCACAGAGGCTTAA GTGCTGA NCKAP1 (Accession NM_013436.2) is another GAM1782 target gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby A A

incorporated herein.

Another function of GAM1782 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM1782 A A PSEN1 ATCACAGAGGCTTAA GTGCTGA PSEN1 (Accession NM_007318.1) is another GAM1782 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1782 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1782 A A RAGE ATCACAGAGGCTTAA GTGCTGA Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another GAM1782 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1782 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1782 is therefore inhibition of RAGE, a GAM1782 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM1782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM1820 A A ADAM10 AGGCTGCAGTGTAGT GGCATGA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is a GAM1820 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1820 is therefore inhibition of ADAM10, a

GAM1820 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM1820 ADAM17 AGGCTGCAGTGTAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
GGCATGA factor, (ADAM17, Accession NM_003183.3) is another GAM1820 target gene. ADAM17 BINDING SITE1 through ADAM17 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADAM17, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE1 through ADAM17 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1820 is therefore inhibition of ADAM17, a GAM1820 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1820 FPRL1 AGGCTGCAGTGTAGT FPRL1 (Accession NM_001462.1) is another GAM1820 target gene. A A
GGCATGA FPRL1 BINDING SITE1 and FPRL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FPRL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE1 and FPRL1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1820 is therefore inhibition of FPRL1. Accordingly, utilities of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM1820 HADH2 AGGCTGCAGTGTAGT Hydroxyacyl- Coenzyme A Dehydrogenase, Type II (HADH2, A A
GGCATGA Accession NM_004493.1) is another GAM1820 target gene. HADH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HADH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HADH2 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1820 is therefore inhibition of HADH2, a GAM1820 target gene which catalyzes the reversible oxidation of L- 3- hydroxyacyl- CoAs to form 3- ketoacyl- CoAs and binds intracellular amyloid- beta. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HADH2.The function of HADH2 has been established by previous studies. Amyloid- beta (OMIM Ref. No. 104760) is a neurotoxic peptide that is implicated in the pathogenesis of Alzheimer disease (AD; 104300). Yan et al. (1997) demonstrated that amyloid- beta binds an intracellular polypeptide, which they designated ERAB. They used the yeast 2- hybrid system to screen human brain and HeLa- cell cDNA libraries for encoded proteins capable of binding to a fusion protein containing amyloid- beta peptide. The full- length cDNA sequence they identified encodes a predicted 262- amino acid polypeptide (GenBank U96132). Sequence comparisons indicated that ERAB most resembles the family of short- chain alcohol dehydrogenases, including hydroxysteroid dehydrogenases (see OMIM Ref. No. 109684). The authors showed that ERAB is expressed in normal tissues but is overexpressed in neurons affected in AD. ERAB immunoprecipitates with amyloid- beta, and when cell cultures are exposed to amyloid- beta, ERAB inside the cell is rapidly redistributed to the plasma membrane. Yan et al. (1997) also found that the toxic effect of amyloid- beta on these cells is prevented by blocking ERAB with an anti- ERAB antibody fragment and is enhanced by overexpression of ERAB. The authors concluded that, by interacting with intracellular amyloid- beta, ERAB may contribute to the neuronal dysfunction associated with Alzheimer disease. In a note added in proof, Yan et al. (1997) noted that a human gene identical to ERAB and mapped to the X chromosome had been entered in GenBank by O. P. Zuchenko and colleagues (unpublished). Furthermore, Furuta et al. (1997) reported cloning a bovine cDNA that is the homolog of human ERAB. He et al. (1998) independently cloned a novel L- 3- hydroxyacyl- CoA dehydrogenase from human brain. They found the enzyme to be a homotetramer with a molecular mass of 108 kD. Its subunit consists of 261 amino acid residues and has structural features characteristic of short- chain dehydrogenases. He et al. (1998) found that the amino acid sequence of this human brain enzyme was identical to that of ERAB, which mediates neurotoxicity in Alzheimer disease. The purification of human brain short- chain L- 3- hydroxyacyl- CoA dehydrogenase made it possible to characterize the structural and catalytic properties of ERAB. This NAD( )- dependent dehydrogenase catalyzes the reversible oxidation of L- 3- hydroxyacyl- CoAs to form 3- ketoacyl- CoAs, but it does not act on the D- isomers. The human short- chain L- 3- hydroxyacyl- CoA dehydrogenase gene is organized into 6 exons and 5 introns and spans approximately 4 kb. The amino- terminal NAD- binding region of the

hydrogenase is encoded by the first 3 exons, whereas the other exons code for the carboxy- terminal substrate- binding regions harboring putative catalytic residues.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Yan, S. D.; Fu, J.; Soto, C.; Chen, X.; Zhu, H.; Al- Mohanna, F.; Collison, K.; Zhu, A.; Stern, E.; Saido, T.; Tohyama, M.; Ogawa, S.; Roher, A.; Stern, D. : An intracellular protein that binds amyloid- beta peptide and mediates neurotoxicity in Alzheimer's disease. Nature 389: 689- 695, 1997. ; and

He, X.- Y.; Schulz, H.; Yang, S.- Y. : A human brain L- 3- hydroxyacyl- coenzyme A dehydrogenase is identical to an amyloid beta- peptide- binding protein involved in Alzheimer's disease. J. Bi.

Further studies establishing the function and utilities of HADH2 are found in John Hopkins OMIM database record ID 300256, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1820 NCKAP1 AGGCTGCAGTGTAGT NCKAP1 (Accession NM_013436.2) is another GAM1820 target gene. A A

GGCATGA NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1820 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM1820 PRND AGGCTGCAGTGTAGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGCATGA another GAM1820 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1820 is therefore inhibition of PRND, a GAM1820 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM1820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1835 DSCR1 TCAACTATGATTACC AAAGCAG Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM1835 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1835 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1835 is therefore inhibition of DSCR1, a GAM1835 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM1860 NOTCH1 TTAAAGTCACCATTT GTGGGTT Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is a GAM1860 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1860 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1860 is therefore inhibition of NOTCH1, a GAM1860 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1860 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM1863 BACE TGCTAGGTTTTTTCC TTTCCCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM1863 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide A A

sequence of GAM1863 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1863 is therefore inhibition of BACE, a GAM1863 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1863 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1863 GYPA TGCTAGGTTTTTTCC Glycophorin A (includes MN blood group) (GYPA, Accession A A TTTCCCC NM_002099.2) is another GAM1863 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1863 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1863 is therefore inhibition of GYPA, a GAM1863 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1863 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1864 IGF1 TCGAGTTGATGCTAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A AATGGGT NM_000618.2) is a GAM1864 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1864 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1864 is therefore inhibition of IGF1, a GAM1864 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1864 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1887 BACE TTCTCATTGGCCCAC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

AGGGGTA is a GAM1887 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1887 is therefore inhibition of BACE, a GAM1887 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1896 DHCR24 TTCCTCTGCCACGTC 24- dehydrocholesterol Reductase (DHCR24, Accession A A
TTTCCCT NM_014762.1) is a GAM1896 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1896 is therefore inhibition of DHCR24, a GAM1896 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1896 DLST TTCCTCTGCCACGTC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
TTTCCCT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1896 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1896 is therefore inhibition of DLST, a GAM1896 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1896 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1896 MAPK10 TTCCTCTGCCACGTC Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
TTTCCCT NM_002753.2) is another GAM1896 target gene. MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPK10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1896 is therefore inhibition of MAPK10, a GAM1896 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM1896 MAPT TTCCTCTGCCACGTC Microtubule- associated Protein Tau (MAPT, Accession A A
TTTCCCT NM_005910.2) is another GAM1896 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1896 is therefore inhibition of MAPT, a GAM1896 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM1896 PSEN1 TTCCTCTGCCACGTC PSEN1 (Accession NM_007319.1) is another GAM1896 target gene. A A
TTTCCCT PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA

encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1896 is therefore inhibition of PSEN1. Accordingly, utilities of GAM1896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM1914 TNF TTCTACTAGTGGTTG ATGGCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is a GAM1914 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1914 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1914 is therefore inhibition of TNF, a GAM1914 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM1914 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1937 ACE TGAGTATTCACCAGG TGCTGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM1937 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM1937 is therefore inhibition of ACE, a GAM1937 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1937 ADAM17 TGAGTATTCACCAGG TGCTGGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is another GAM1937 target A A

gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1937 is therefore inhibition of ADAM17, a GAM1937 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1937 CAV1 TGAGTATTCACCAGG TGCTGGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM1937 target gene. CAV1 BINDING SITE1 and CAV1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE1 and CAV1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1937 is therefore inhibition of CAV1, a GAM1937 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM1937 GYPA TGAGTATTCACCAGG TGCTGGG Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM1937 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM1937 is therefore inhibition of GYPA, a GAM1937 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1937 NOTCH1 TGAGTATTCACCAGG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGCTGGG (NOTCH1, Accession NM_017617.2) is another GAM1937 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1937 is therefore inhibition of NOTCH1, a GAM1937 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM1937 PSEN2 TGAGTATTCACCAGG PSEN2 (Accession NM_012486.1) is another GAM1937 target gene. A A

TGCTGGG PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1937 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1937 is therefore inhibition of PSEN2. Accordingly, utilities of GAM1937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM1942 BCHE AGCAAGATGGTAGCA BCHE (Accession NM_000055.1) is a GAM1942 target gene. BCHE A A

TTGGAGA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1942 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1942 is therefore inhibition of BCHE. Accordingly, utilities of GAM1942 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM1942 HD AGCAAGATGGTAGCA HD (Accession NM_002111.3) is another GAM1942 target gene. HD A A

TTGGAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1942 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1942 is therefore inhibition of HD. Accordingly, utilities of GAM1942 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM1942 MME AGCAAGATGGTAGCA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TTGGAGA enkephalinase, (MME, Accession NM_000902.2) is another GAM1942 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1942 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1942 is therefore inhibition of MME, a GAM1942 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1942 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1942 PRNP AGCAAGATGGTAGCA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

TTGGAGA Strausler- (PRNP, Accession NM_000311.1) is another GAM1942 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1942 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1942 is therefore inhibition of PRNP, a GAM1942 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1942 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM1961 ADAM17 CAAAGTGCTGAGATT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

ACAGGCA factor, (ADAM17, Accession NM_003183.3) is a GAM1961 target gene. ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADAM17, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1961 is therefore inhibition of ADAM17, a GAM1961 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM1961 GFAP CAAAGTGCTGAGATT GFAP (Accession NM_002055.2) is another GAM1961 target gene. A A

ACAGGCA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of GFAP. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1961 HTR2A CAAAGTGCTGAGATT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

ACAGGCA NM_000621.1) is another GAM1961 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of HTR2A, a GAM1961 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM1961 HTR2C CAAAGTGCTGAGATT A A ACAGGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM1961 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of HTR2C, a GAM1961 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM1961 IAPP CAAAGTGCTGAGATT A A ACAGGCA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM1961 target gene. IAPP BINDING SITE1 through IAPP BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 through IAPP BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of IAPP, a GAM1961 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM1961 MTNR1A CAAAGTGCTGAGATT A A Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is

ACAGGCA another GAM1961 target gene. MTNR1A BINDING SITE1 through MTNR1A BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 through MTNR1A BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of MTNR1A, a GAM1961 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM1961 TGFB1 CAAAGTGCTGAGATT TGFB1 (Accession NM_000660.1) is another GAM1961 target gene.
A A

ACAGGCA TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1961 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1975 IGF1 TTCCAAGCCTTCCCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGATCA NM_000618.2) is a GAM1975 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1975 is therefore inhibition of IGF1, a GAM1975 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1975 CLU TGGTGGGGAGAGGCT Clusterin (complement lysis inhibitor, SP- 40,40, sulfated B A
TGGGAAG glycoprotein (CLU, Accession NM_001831.1) is another GAM1975 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of CLU, a GAM1975 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM1975 DHCR24 TGGTGGGGAGAGGCT 24- dehydrocholesterol Reductase (DHCR24, Accession B A
TGGGAAG NM_014762.1) is another GAM1975 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of DHCR24, a GAM1975 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM1975 LRP1 TGGTGGGGAGAGGCT Low Density Lipoprotein- related Protein 1 (alpha- 2- B A
TGGGAAG macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM1975 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of LRP1, a GAM1975 target gene which is a recycling lipoprotein

receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 has been established by previous studies. Herz et al. (1988) cloned a cDNA for the low density lipoprotein receptor- related protein (LRP) by virtue of its close homology to the LDL receptor (OMIM Ref. No. 606945). Kristensen et al. (1990) and Strickland et al. (1990) demonstrated that LRP is identical to the alpha- 2- macroglobulin (A2M; 103950) receptor (A2MR). Like the mannose- 6- phosphate receptor (OMIM Ref. No. 147280), the A2MR/LRP molecule is probably bifunctional The heat- shock protein gp96 (TRA1; 191175) is an intracellular protein capable of chaperoning exogenous antigens from tumors or virus- infected cells to antigen- presenting cells for presentation through major histocompatibility complex (MHC) class I rather than class II molecules, thereby eliciting CD8 (OMIM Ref. No. 186910)- positive T- cell responses. Using a mouse system, Binder et al. (2000) determined that the receptor for gp96 is CD91 (A2MR) and that A2M, a protein found in blood, inhibits gp96 binding to CD91. They proposed that CD91 acts as a sensor for necrotic cell death in tissues, leading to proinflammatory immune responses

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Strickland, D. K.; Ashcom, J. D.; Williams, S.; Burgess, W. H.; Migliorini, M.; Argraves, W. S. : Sequence identity between the alpha- 2- macroglobulin receptor and low density lipoprotein receptor- related protein suggests that this molecule is a multifunctional receptor. J. Biol. Chem. 265: 17401- 17404, 1990. ; and

Binder, R. J.; Han, D. K.; Srivastava, P. K. : CD91: a receptor for heat shock protein gp96. Nature Immun. 1: 151- 155, 2000.

Further studies establishing the function and utilities of LRP1 are found in John Hopkins OMIM database record ID 107770, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1975 MAPT TGGTGGGGAGAGGCT TGGGAAG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM1975 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM1975 is therefore inhibition of MAPT, a GAM1975 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM1975 OLR1 TGGTGGGGAGAGGCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 B A TGGGAAG (OLR1, Accession NM_002543.1) is another GAM1975 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of OLR1, a GAM1975 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM1975 TGFB1 TGGTGGGGAGAGGCT TGFB1 (Accession NM_000660.1) is another GAM1975 target gene. B A TGGGAAG TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of TGFB1. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM1975 TNF TGGTGGGGAGAGGCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, B A TGGGAAG Accession NM_000594.2) is another GAM1975 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1975 is therefore inhibition of TNF, a GAM1975 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM1975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1976 ABCD1 CTGGCTCCCTCTCTT ABCD1 (Accession NM_000033.2) is a GAM1976 target gene. ABCD1 A A

CTCTCCC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1976 is therefore inhibition of ABCD1. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM1976 BACE CTGGCTCCCTCTCTT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

CTCTCCC is another GAM1976 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of BACE, a GAM1976 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM1976 CRH CTGGCTCCCTCTCTT Corticotropin Releasing Hormone (CRH, Accession NM_000756.1) is A A

CTCTCCC another GAM1976 target gene. CRH BINDING SITE1 through CRH BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CRH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRH BINDING SITE1 through CRH BINDING SITE3,

and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of CRH, a GAM1976 target gene which regulates the release of corticotropin from pituitary gland. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRH.The function of CRH has been established by previous studies. Response to stress in mammals requires an intact hypothalamic- pituitary- adrenal axis. The proximal part of the response is mediated by secretion of corticotropin- releasing hormone (CRH) by the paraventricular nucleus of the hypothalamus. CRH is a 41- amino acid peptide derived by enzymatic cleavage from a 191- amino acid preprohormone. Shibahara et al. (1983) cloned and sequenced the human CRH gene. Arbiser et al. (1988) assigned the gene for CRH to 8q13 by somatic cell hybrid and in situ hybridization studies. The absence of secondary hybridization strongly suggested that hypothalamic and placental CRH are transcribed from the same gene. Kellogg et al. (1989) corroborated the assignment to 8q13 by in situ hybridization. Knapp et al. (1993) showed that the homologous gene is located on mouse chromosome 3 Sebaceous glands may be involved in a pathway conceptually similar to that of the hypothalamic- pituitary- adrenal (HPA) axis. CRH is the most proximal element of the HPA axis, and it acts as a central coordinator for neuroendocrine and behavioral responses to stress. To examine the probability of an HPA equivalent pathway in sebaceous glands, Zouboulis et al. (2002) investigated the expression of CRH, CRH- binding protein, CRHBP (OMIM Ref. No. 122559), and CRH receptors (CRHR1, 122561 and CRHR2, 602034) in sebocytes in vitro and their regulation by CRH and several other hormones. CRHR1 was the predominant type, being twice as abundant as CRHR2. CRH was biologically active on human sebocytes; it induced biphasic increase in synthesis of sebaceous lipids, although it did not affect cell viability, cell proliferation, or IL1B (OMIM Ref. No. 147720)- induced IL8 (OMIM Ref. No. 146930) release. Zouboulis et al. (2002) interpreted these and other findings as indicating that CRH may be an autocrine hormone for human sebocytes that exerts homeostatic lipogenic activity, whereas testosterone and growth hormone induced CRH negative feedback. The findings implicated CRH in the clinical development of acne, seborrhea, androgenetic alopecia, skin aging, xerosis, and other skin disorders associated with alterations in lipid formation of sebaceous origin Animal model experiments lend further support to the function of CRH. In adult male rhesus macaques, Habib et al. (2000) evaluated the effects of a lipophilic nonpeptide antagonist to CRH type 1 receptor, antalarmin, on the behavioral, neuroendocrine, and autonomic components of the stress response. After oral administration, significant antalarmin concentrations were detected in the systemic circulation and the

cerebrospinal fluid. The monkeys were exposed to an intense social stressor, namely, placement of 2 unfamiliar males in adjacent cages separated only by a transparent Plexiglas screen. Antalarmin significantly inhibited a repertoire of behaviors associated with anxiety and fear, such as body tremors, grimacing, teeth gnashing, urination, and defecation. In contrast, antalarmin increased exploratory and sexual behaviors that are normally suppressed during stress. Moreover, antalarmin significantly diminished the increases in cerebrospinal fluid CRH as well as the pituitary- adrenal, sympathetic, and adrenal medullary responses to stress. Habib et al. (2000) suggested that a CRH type 1 receptor antagonist may be of therapeutic value in human psychiatric, reproductive, and cardiovascular disorders associated with CRH system hyperactivity.

It is appreciated that the abovementioned animal model for CRH is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Knapp, L. T.; Keegan, C. E.; Seasholtz, A. F.; Camper, S. A. : Corticotropin- releasing hormone (Crh) maps to mouse chromosome 3. Mammalian Genome 4: 615- 617, 1993. ; and

Habib, K. E.; Weld, K. P.; Rice, K. C.; Pushkas, J.; Champoux, M.; Listwak, S.; Webster, E. L.; Atkinson, A. J.; Schulkin, J.; Contoreggi, C.; Chrousos, G. P.; McCann, S. M.; Suomi, S. J.

Further studies establishing the function and utilities of CRH are found in John Hopkins OMIM database record ID 122560, and in cited publications listed in Table 9, hereby incorporated herein.

GAM1976	DLST	CTGGCTCCCTCTCTT CTCTCCC	Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM1976 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM1976 is therefore inhibition of DLST, a GAM1976 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM1976 FLNB CTGGCTCCCTCTCTT A A CTCTCCC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM1976 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of FLNB, a GAM1976 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM1976 GFAP CTGGCTCCCTCTCTT A A CTCTCCC GFAP (Accession NM_002055.2) is another GAM1976 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of GFAP. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM1976 GLUL CTGGCTCCCTCTCTT A A CTCTCCC Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM1976 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of GLUL, a GAM1976 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM1976 HD CTGGCTCCCTCTCTT HD (Accession NM_002111.3) is another GAM1976 target gene. HD A A

CTCTCCC BINDING SITE1 through HD BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 through HD BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of HD. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM1976 LRP1 CTGGCTCCCTCTCTT Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

CTCTCCC macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM1976 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of LRP1, a GAM1976 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM1976 MPO CTGGCTCCCTCTCTT Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM1976 A A

CTCTCCC target gene. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of MPO, a GAM1976 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM1976 A A CTCTCCC NGB CTGGCTCCCTCTCTT Neuroglobin (NGB, Accession NM_021257.2) is another GAM1976 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of NGB, a GAM1976 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM1976 A A CTCTCCC PSEN2 CTGGCTCCCTCTCTT PSEN2 (Accession NM_000447.1) is another GAM1976 target gene. PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of PSEN2. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM1976 A A CTCTCCC SLC6A4 CTGGCTCCCTCTCTT Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM1976 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of

SLC6A4, a GAM1976 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM1976 TFCP2 CTGGCTCCCTCTCTT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
CTCTCCC another GAM1976 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of TFCP2, a GAM1976 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM1976 THOP1 CTGGCTCCCTCTCTT Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is A A
CTCTCCC another GAM1976 target gene. THOP1 BINDING SITE1 and THOP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by THOP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE1 and THOP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM1976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1976 is therefore inhibition of THOP1, a GAM1976 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM1997 LRP1 ACTCAGAGCCATTCC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
GCTCAGG macroglobulin recep (LRP1, Accession NM_002332.1) is a GAM1997

target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1997 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM1997 is therefore inhibition of LRP1, a GAM1997 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM1997 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM1997 IGF1 AGCGGAGACCTGAGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession B A

TATGAGT NM_000618.2) is another GAM1997 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM1997 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM1997 is therefore inhibition of IGF1, a GAM1997 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM1997 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2010 FHL2 CATTGCACTCCACCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TAGGCAA a GAM2010 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2010 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2010 is therefore inhibition of FHL2, a GAM2010 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2010 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2010 HD CATTGCACTCCACCC HD (Accession NM_002111.3) is another GAM2010 target gene. HD A A

TAGGCAA BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2010 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2010 is therefore inhibition of HD. Accordingly, utilities of GAM2010 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2010 IGF1 CATTGCACTCCACCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TAGGCAA NM_000618.2) is another GAM2010 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2010 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2010 is therefore inhibition of IGF1, a GAM2010 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2010 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2010 PRND CATTGCACTCCACCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TAGGCAA another GAM2010 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2010 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2010 is therefore inhibition of

PRND, a GAM2010 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2010 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2014 ABCD1 GCTTCTCCTGTCCCC ABCD1 (Accession NM_000033.2) is a GAM2014 target gene. ABCD1 A A

TCCCTAC BINDING SITE1 and ABCD1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ABCD1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE1 and ABCD1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2014 is therefore inhibition of ABCD1. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM2014 APBB1 GCTTCTCCTGTCCCC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TCCCTAC 1 (Fe65) (APBB1, Accession NM_001164.2) is another GAM2014 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of APBB1, a GAM2014 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2014 AVP GCTTCTCCTGTCCCC AVP (Accession NM_000490.2) is another GAM2014 target gene. AVP A A

TCCCTAC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of AVP. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM2014 A TCCCTAC BLMH GCTTCTCCTGTCCCC A Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another GAM2014 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of BLMH, a GAM2014 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM2014 A TCCCTAC DHCR24 GCTTCTCCTGTCCCC A 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM2014 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of DHCR24, a GAM2014 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2014 A TCCCTAC GLUL GCTTCTCCTGTCCCC A Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM2014 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of GLUL, a GAM2014 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM2014 LRP1 GCTTCTCCTGTCCCC TCCCTAC A A Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM2014 target gene. LRP1 BINDING SITE1 and LRP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LRP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 and LRP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of LRP1, a GAM2014 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM2014 NCKAP1 GCTTCTCCTGTCCCC TCCCTAC A A NCKAP1 (Accession NM_013436.2) is another GAM2014 target gene. NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM2014 NGB GCTTCTCCTGTCCCC TCCCTAC A A Neuroglobin (NGB, Accession NM_021257.2) is another GAM2014 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of NGB, a GAM2014 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2014 OGDH GCTTCTCCTGTCCCC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

TCCCTAC NM_002541.1) is another GAM2014 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2014 is therefore inhibition of OGDH, a GAM2014 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH has been established by previous studies. In 3 males born to first-cousin Algerian parents and presenting with hypotonia, metabolic acidosis, and hyperlactatemia immediately after birth, Bonnefont et al. (1992) described a 'new' inborn error of the tricarboxylic acid cycle, alpha- ketoglutarate dehydrogenase deficiency. Neurologic deterioration resulted in death at about 30 months of age. Low molar ratios of ketone bodies in plasma of neonates with congenital lactic acidosis were proposed as an indicator of dysfunction of the tricarboxylic acid cycle. The parents of the 3 sibs were related as first cousins. Kohlschutter et al. (1982) reported a case of partial alpha- ketoglutarate dehydrogenase deficiency in 2 sibs of a consanguineous Tunisian family. In addition to genetic defects of the tricarboxylic acid cycle, other mechanisms for recessively inherited congenital lactic acidosis include inborn errors of pyruvate metabolism and inborn errors of oxidative phosphorylation. Guffon et al. (1993) described 2 new familial cases of 2-ketoglutarate dehydrogenase deficiency: a sister and brother born of consanguineous Portuguese parents. Axial hypotonia with no head control as late as age 4 years was described in both. Metabolic acidosis with acute episodes of acidotic decompensation and

sometimes hypoglycemia occurred during infections. The sister died suddenly after a general anesthesia. The alpha- ketoglutarate dehydrogenase complex is a multienzyme complex consisting of 3 protein subunits, alpha- ketoglutarate dehydrogenase (E1k, or oxoglutarate dehydrogenase; OGDH; EC 1.2.4.2), dihydrolipoyl succinyltransferase (E2k, or DLST; 126063), and dihydrolipoyl dehydrogenase (E3; 246900). The complex catalyzes a key reaction in the Krebs tricarboxylic acid cycle. The DLST gene maps to 14q24.3 and the E3 gene maps to chromosome 7. Koike et al. (1992) cloned the E1k gene, which codes for the alpha- ketoglutarate dehydrogenase subunit. Using 2 human/rodent somatic cell hybrid panels, Szabo et al. (1994) mapped the OGDH gene to 7p13- p11.2. A second related sequence, possibly a pseudogene, was identified and mapped to chromosome 10. Szabo et al. (1994) pointed to a possible significance to the finding of a reduction in the activity of this complex in Alzheimer disease brain and cultured skin fibroblasts from Alzheimer disease patients.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Guffon, N.; Lopez- Mediavilla, C.; Dumoulin, R.; Mousson, B.; Godinot, C.; Carrier, H.; Collombet, J. M.; Divry, P.; Mathieu, M.; Guibaud, P. : 2- Ketoglutarate dehydrogenase deficiency, a rare cause of primary hyperlactataemia: report of a new case. J. Inherit. Metab. Dis. 16: 821- 830, 1993. ; and

Szabo, P.; Cai, X.; Ali, G.; Blass, J. P. : Localization of the gene (OGDH) coding for the E1k component of the alpha- ketoglutarate dehydrogenase complex to chromosome 7p13- p11.2. Genomi.

Further studies establishing the function and utilities of OGDH are found in John Hopkins OMIM database record ID 203740, and in cited publications listed in Table 9, hereby incorporated herein.

GAM2014	PIN1	GCTTCTCCTGTCCCC TCCCTAC	Protein (peptidyl- prolyl cis/trans isomerase) NIMA- interacting 1 (PIN1, Accession NM_006221.1) is another GAM2014 target gene. PIN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM2014 is therefore inhibition of PIN1, a GAM2014 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with PIN1.The function of PIN1 has been established by previous studies. In the frog, Pin1 is implicated in the regulation of cell cycle progression and required for the DNA replication checkpoint. By fluorescence microscopy, Winkler et al. (2000) observed that nuclear extracts from Xenopus eggs depleted of Pin1 inappropriately transited from the G2 to the M phase of the cell cycle in the presence of a DNA replication inhibitor. Immunoblot analysis revealed that inappropriate transition was accompanied by hyperphosphorylation of CDC25 (see OMIM Ref. No. CDC25A, 116947), activation of CDC2 (OMIM Ref. No. 116940)/cyclin B (OMIM Ref. No. 123836), and mitotic phosphoproteins. Addition of recombinant wildtype, but not mutant, Pin1 reversed the defect in replication checkpoint function. Liou et al. (2002) demonstrated that loss of Pin1 function in mouse causes phenotypes resembling cyclin D1 (OMIM Ref. No. 168461) null phenotypes. Their findings confirmed that Pin1 positively regulates cyclin D1 function at the transcriptional level and also through posttranslational stabilization. The results provided genetic evidence for an essential role of Pin1 in maintaining cell proliferation and regulating cyclin D1 function

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Liou, Y.- C.; Ryo, A.; Huang, H.- K.; Lu, P.- J.; Bronson, R.; Fujimori, F.; Uchida, T.; Hunter, T.; Lu, K. P. : Loss of Pin1 function in the mouse causes phenotypes resembling cyclin D1- null phenotypes. Proc. Nat. Acad. Sci. 99: 1335- 1340, 2002. ; and

Lu, K. P.; Hanes, S. D.; Hunter, T. : A human peptidyl- prolyl isomerase essential for regulation of mitosis. Nature 380: 544- 547, 1996.

Further studies establishing the function and utilities of PIN1 are found in John Hopkins OMIM database record ID 601052, and in cited publications listed in Table 9, hereby incorporated herein.

GAM2022 ABCD1 GTTGGGTGTGAGGGG ABCD1 (Accession NM_000033.2) is a GAM2022 target gene. ABCD1 A A

GGTCCCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2022 is therefore inhibition of ABCD1. Accordingly, utilities of GAM2022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM2022 MAPT GTTGGGTGTGAGGGG Microtubule- associated Protein Tau (MAPT, Accession A A

GGTCCCA NM_173727.1) is another GAM2022 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2022 is therefore inhibition of MAPT, a GAM2022 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2027 BACE CATGGTACTGCCACA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

GAAGAGT is a GAM2027 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2027 is therefore inhibition of BACE, a GAM2027 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2027 GSK3B CATGGTACTGCCACA Glycogen Synthase Kinase 3 Beta (GSK3B, Accession NM_002093.2) A A

GAAGAGT is another GAM2027 target gene. GSK3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GSK3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSK3B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2027 is therefore inhibition of GSK3B, a GAM2027 target gene which b subunit of glycogen synthase kinase 3 which phosphorylates regulatory proteins. and therefore is

associated with Alzheimer. Accordingly, utilities of GAM2027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSK3B.The function of GSK3B has been established by previous studies. Frame et al. (2001) demonstrated that the insulin- induced inhibition of GSK3 and its unique substrate specificity are explained by the existence of a phosphate- binding site in which arg96 is critical. Mutation of arg96 abolished the phosphorylation of 'primed' glycogen synthase as well as inhibition by protein kinase B (OMIM Ref. No. 605213)-mediated phosphorylation of ser9. Hence, the phosphorylated N terminus acts as a pseudosubstrate, occupying the same phosphate-binding site used by primed substrates. This mutation did not affect phosphorylation of 'nonprimed' substrates in the Wnt- signaling pathway (axin, 603816 and beta- catenin, 116806), suggesting novel approaches to design more selective GSK3 inhibitors for the treatment of diabetes. Animal model experiments lend further support to the function of GSK3B. Hoeflich et al. (2000) generated mice deficient in Gsk3b by targeted disruption. Although Gsk3b /- male and female mice were healthy and fertile, they did not give rise to live Gsk3b - /- progeny. Embryonic lethality occurred between embryonic days 13.5 and 14.5 due to severe liver degeneration, a phenotype consistent with excessive tumor necrosis factor (TNF; 191160) toxicity, as observed in mice lacking genes involved in the activation of transcription factor NFKB (see OMIM Ref. No. 164011). Gsk3b- deficient embryos were rescued by inhibition of TNF using anti- TNF- alpha antibody. Fibroblasts from Gsk3b- deficient embryos were hypersensitive to TNF- alpha and showed reduced NFKB function. Lithium treatment, which inhibits GSK3, sensitized wildtype fibroblasts to TNF and inhibited transactivation of NFKB. The early steps leading to NFKB activation were unaffected by the loss of Gsk3b, indicating that NFKB is regulated by GSK3B at the level of the transcriptional complex. Thus, GSK3B facilitates NFKB function. Ali et al. (2001) noted that loss of Gsk3b is not compensated by Gsk3a (OMIM Ref. No. 606784) and that NFKB activation is the only known differentiator between the 2 enzymes.

It is appreciated that the abovementioned animal model for GSK3B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Frame, S.; Cohen, P.; Biondi, R. M. : A common phosphate binding site explains the unique substrate specificity of GSK3 and its inactivation by phosphorylation. Molec. Cell 7: 1321- 1327, 2001. ; and

Hoeflich, K. P.; Luo, J.; Rubie, E. A.; Tsao, M.- S.; Jin, O.; Woodgett, J. R. : Requirement for glycogen synthase kinase- 3- beta in cell survival and NF- kappa- B activation. Nature 406: 8.

Further studies establishing the function and utilities of GSK3B are found in John Hopkins OMIM database record ID 605004, and in cited publications listed in Table 9, hereby incorporated herein.

GAM2027 HD CATGGTACTGCCACA HD (Accession NM_002111.3) is another GAM2027 target gene. HD A A

GAAGAGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2027 is therefore inhibition of HD. Accordingly, utilities of GAM2027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2027 IGF1 CATGGTACTGCCACA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAAGAGT NM_000618.2) is another GAM2027 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2027 is therefore inhibition of IGF1, a GAM2027 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2033 APLP2 TCAAGCTCATTCCTC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

TAACCTC NM_001642.1) is a GAM2033 target gene. APLP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2033 is therefore inhibition of APLP2, a

GAM2033 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM2033 HD TCAAGCTCATTCCTC HD (Accession NM_002111.3) is another GAM2033 target gene. HD A A

TAACCTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2033 is therefore inhibition of HD. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2051 ACE GAACAGCTCCAGTCT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

ACAGCCC (ACE, Accession NM_152831.1) is a GAM2051 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2051 is therefore inhibition of ACE, a GAM2051 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM2051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2051 DSCR1 GAACAGCTCCAGTCT Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

ACAGCCC NM_004414.3) is another GAM2051 target gene. DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DSCR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2051 is therefore inhibition of DSCR1, a GAM2051 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2051 HD GAACAGCTCCAGTCT HD (Accession NM_002111.3) is another GAM2051 target gene. HD A A

ACAGCCC BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2051 is therefore inhibition of HD. Accordingly, utilities of GAM2051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2051 PRNP GAACAGCTCCAGTCT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

ACAGCCC Strausler- (PRNP, Accession NM_000311.1) is another GAM2051 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2051 is therefore inhibition of PRNP, a GAM2051 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM2051 TNFSF5 GAACAGCTCCAGTCT TNFSF5 (Accession NM_000074.1) is another GAM2051 target gene. A A

ACAGCCC TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM2051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2051 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM2051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM2058 ADAMTS5 TGAAAGAGATGTGGT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GTGTGAA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM2058 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2058 is therefore inhibition of ADAMTS5, a GAM2058 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2058 MTNR1A TGAAAGAGATGTGGT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

GTGTGAA another GAM2058 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2058 is therefore inhibition of MTNR1A, a GAM2058 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM2062 APPBP2 CCCAGGAGGCGGAGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TTGCAGT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM2062 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2062 is therefore inhibition of APPBP2, a GAM2062 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2062 AVP CCCAGGAGGCGGAGG AVP (Accession NM_000490.2) is another GAM2062 target gene.
AVP A A

TTGCAGT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2062 is therefore inhibition of AVP. Accordingly, utilities of GAM2062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM2062 HTR2A CCCAGGAGGCGGAGG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession
A A

TTGCAGT NM_000621.1) is another GAM2062 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2062 is therefore inhibition of HTR2A, a GAM2062 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM2062 IGF1 CCCAGGAGGCGGAGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TTGCAGT NM_000618.2) is another GAM2062 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2062 is therefore inhibition of IGF1, a GAM2062 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2062 PRND CCCAGGAGGCGGAGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TTGCAGT another GAM2062 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2062 is therefore inhibition of PRND, a GAM2062 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2098 ACE TTGAGCACAGTTTGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GGAGTGT (ACE, Accession NM_152831.1) is a GAM2098 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2098 is therefore inhibition of ACE, a GAM2098 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with

Alzheimer. Accordingly, utilities of GAM2098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2098 FPRL1 TTGAGCACAGTTTGA FPRL1 (Accession NM_001462.1) is another GAM2098 target gene. A A

GGAGTGT FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2098 is therefore inhibition of FPRL1. Accordingly, utilities of GAM2098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM2098 IL1A TTGAGCACAGTTTGA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

GGAGTGT GAM2098 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2098 is therefore inhibition of IL1A, a GAM2098 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2098 PRND TTGAGCACAGTTTGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGAGTGT another GAM2098 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2098 is therefore inhibition of PRND, a GAM2098 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2171 HD BINDING A A GGCAATATTCCAGGA TAGGCTG HD (Accession NM_002111.3) is a GAM2171 target gene. HD BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2171 is therefore inhibition of HD. Accordingly, utilities of GAM2171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2171 HTR2C A A GGCAATATTCCAGGA TAGGCTG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM2171 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2171 is therefore inhibition of HTR2C, a GAM2171 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM2221 CTSK A A TCCAAAGACTCAACA GTTAGAC CTSK (Accession NM_000396.2) is a GAM2221 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2221 is therefore inhibition of CTSK. Accordingly, utilities of GAM2221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM2223 A ATGTGGC A OGDH TCTTAGATTGAGAAG A Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is a GAM2223 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2223 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2223 is therefore inhibition of OGDH, a GAM2223 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM2233 A TCTAAGA A HD GGACTGCAGTCACAC HD (Accession NM_002111.3) is a GAM2233 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2233 is therefore inhibition of HD. Accordingly, utilities of GAM2233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2233 A TCTAAGA A PRND GGACTGCAGTCACAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM2233 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2233 is therefore inhibition of PRND, a GAM2233 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM2233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2233 B A NGB GCCAGTG TCTTTCTACACCTCT Neuroglobin (NGB, Accession NM_021257.2) is another GAM2233 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2233 is therefore inhibition of NGB, a GAM2233 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2233 A OGDH GCCAGTG TCTTTCTACACCTCT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM2233 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2233 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B

Another function of GAM2233 is therefore inhibition of OGDH, a GAM2233 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM2251 A DSCR1 AAATGGT GATTCCTCCTCTTTA Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM2251 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure A

complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2251 is therefore inhibition of DSCR1, a GAM2251 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2251 IGF1 GATTCCTCCTCTTTA AAATGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM2251 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2251 is therefore inhibition of IGF1, a GAM2251 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2251 SNCA GATTCCTCCTCTTTA AAATGGT SNCA (Accession NM_000345.2) is another GAM2251 target gene. SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2251 is therefore inhibition of SNCA. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM2251 TGFB1 GATTCCTCCTCTTTA AAATGGT TGFB1 (Accession NM_000660.1) is another GAM2251 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2251 is therefore inhibition of TGFB1. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM2251 HD ACCCACCCTCTGTGA HD (Accession NM_002111.3) is another GAM2251 target gene. HD B A

GGAGGAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2251 is therefore inhibition of HD. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2251 MAPK10 ACCCACCCTCTGTGA Mitogen- activated Protein Kinase 10 (MAPK10, Accession B A

GGAGGAT NM_138980.1) is another GAM2251 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2251 is therefore inhibition of MAPK10, a GAM2251 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM2260 APPBP2 GGGCATGATGATGGC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

ACTAGCG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM2260 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2260 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM2260 is therefore inhibition of APPBP2, a GAM2260 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2260 HTR2C GGGCATGATGATGGC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
ACTAGCG NM_000868.1) is another GAM2260 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2260 is therefore inhibition of HTR2C, a GAM2260 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM2260 PRND GGGCATGATGATGGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
ACTAGCG another GAM2260 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2260 is therefore inhibition of PRND, a GAM2260 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2262 IGF1 TGAGGTAGGATGATT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCTAGCT NM_000618.2) is a GAM2262 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2262 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2262 is therefore inhibition of IGF1, a GAM2262 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2262 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2263 A HTR2C TTATCCTAAATGTGT TTTGAAG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is a GAM2263 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2263 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2263 is therefore inhibition of HTR2C, a GAM2263 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2263 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM2263 B PSEN1 AATTTAGAATCGTTT CTGATAG PSEN1 (Accession NM_000021.2) is another GAM2263 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2263 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2263 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2263 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM2270 ACT ATCACATTGCCAGTG Activator of CAMP- responsive Element Modulator (CR (ACT, A
A
ATTACCC Accession NM_020482.3) is a GAM2270 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2270 is therefore inhibition of ACT, a GAM2270 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM2270 APBA2 ATCACATTGCCAGTG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A
A
ATTACCC 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM2270 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2270 is therefore inhibition of APBA2, a GAM2270 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2270 DSCR1 ATCACATTGCCAGTG Down Syndrome Critical Region Gene 1 (DSCR1, Accession A
A
ATTACCC NM_004414.3) is another GAM2270 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2270 is therefore inhibition of

DSCR1, a GAM2270 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2270 HD ATCACATTGCCAGTG HD (Accession NM_002111.3) is another GAM2270 target gene. HD A A

ATTACCC BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2270 is therefore inhibition of HD. Accordingly, utilities of GAM2270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2270 PLAU ATCACATTGCCAGTG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

ATTACCC is another GAM2270 target gene. PLAU BINDING SITE1 and PLAU BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PLAU, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE1 and PLAU BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2270 is therefore inhibition of PLAU, a GAM2270 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM2270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM2272 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM2272 target gene. HD BINDING A A

ACTTGT SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2272 is therefore inhibition of HD. Accordingly, utilities of GAM2272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2272 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
ACTTGT NM_000868.1) is another GAM2272 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2272 is therefore inhibition of HTR2C, a GAM2272 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM2272 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ACTTGT NM_000618.2) is another GAM2272 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2272 is therefore inhibition of IGF1, a GAM2272 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2272 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_012486.1) is another GAM2272 target gene. A A
ACTTGT PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2272 is therefore inhibition of PSEN2. Accordingly, utilities of GAM2272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM2272 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152877.1) is another GAM2272 target gene. A A
ACTTGT TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2272 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM2272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM2290 GLUL TGTTATTTTGTCCAA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GAGAGAG NM_002065.3) is a GAM2290 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2290 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2290 is therefore inhibition of GLUL, a GAM2290 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2290 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM2290 IGF1 TGTTATTTTGTCCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GAGAGAG NM_000618.2) is another GAM2290 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2290 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2290 is therefore inhibition of IGF1, a GAM2290 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2290 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2300 APBA2 TTAGCAGTTGTGAGA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
CCCTAGA 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM2300 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2300 is therefore inhibition of APBA2, a GAM2300 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2300 PSEN1 TTAGCAGTTGTGAGA PSEN1 (Accession NM_000021.2) is another GAM2300 target gene. A A
CCCTAGA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2300 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM2300 APPBP2 TTTGGGGTCTCCCCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding B A
GCATGCA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM2300 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM2300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2300 is therefore inhibition of APPBP2, a GAM2300 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2300 DSCR1 TTTGGGGTCTCCCCA Down Syndrome Critical Region Gene 1 (DSCR1, Accession B A

GCATGCA NM_004414.3) is another GAM2300 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2300 is therefore inhibition of DSCR1, a GAM2300 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2306 ADAMTS5 TGGGTTAGTGGTTGA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

ATAGTTT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM2306 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2306 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2306 is therefore inhibition of ADAMTS5, a GAM2306 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2306 TNF TGGGTTAGTGGTTGA ATAGTTT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM2306 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2306 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2306 is therefore inhibition of TNF, a GAM2306 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM2306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2309 ACHE AGTTCCATGGAAAAC AACAAAG Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM2309 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2309 is therefore inhibition of ACHE, a GAM2309 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM2309 IAPP AGTTCCATGGAAAAC AACAAAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM2309 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2309 is therefore inhibition of

IAPP, a GAM2309 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2309 AVP CCCCACCCCAGTGGA AVP (Accession NM_000490.2) is another GAM2309 target gene. AVP B A

GCTCACC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2309 is therefore inhibition of AVP. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM2309 BACE2 CCCCACCCCAGTGGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession B A

GCTCACC NM_138992.1) is another GAM2309 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2309 is therefore inhibition of BACE2, a GAM2309 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2309 MAPT CCCCACCCCAGTGGA Microtubule- associated Protein Tau (MAPT, Accession B A

GCTCACC NM_016835.1) is another GAM2309 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2309 is therefore inhibition of MAPT, a GAM2309 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2309 B A MPO CCCCACCCCAGTGGAGCTCACC Myeloperoxidase (MPO, Accession NM_000250.1) is another target gene. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2309 is therefore inhibition of MPO, a GAM2309 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM2350 A A AGER CCTGCCCATCCTGCCTCCACCA Advanced Glycosylation End Product- specific Receptor (AGER, Accession NM_172197.1) is a GAM2350 target gene. AGER BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AGER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2350 is therefore inhibition of AGER, a GAM2350 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AGER.The function of AGER has been established by previous studies. Sugaya et al. (1994) identified 3 genes located 90 to 140 kb centromeric to the tenascin-like gene (OMIM Ref. No. 600261) in the MHC class III region near the junction with class II. One of these was the gene for receptor

of advanced glycosylation end products of proteins, a member of the immunoglobulin superfamily. A second was the PBX2 homeo box gene (OMIM Ref. No. 176311), and a third was the human counterpart of the mouse mammary tumor gene int- 3 (OMIM Ref. No. 164951). The PBX2 and AGER genes are immediately contiguous and are transcribed in the same direction. In addition to mapping by contiguous cosmids and YAC clones, Sugaya et al. (1994) determined the location of the AGER sequence on 6p21.3 by fluorescence in situ hybridization. The receptor for advanced glycation end products (RAGE), a multiligand member of the immunoglobulin superfamily of cell surface molecules, interacts with distinct molecules implicated in homeostasis, development, and inflammation, and certain diseases such as diabetes (see OMIM Ref. No. 125853, 222100) and Alzheimer disease. Engagement of RAGE by a ligand triggers activation of key cell signaling pathways, such as p21(ras) (see OMIM Ref. No. 139150), MAP kinases (see OMIM Ref. No. 176948), NF- kappa- B (see OMIM Ref. No. 164011), and cdc42 (OMIM Ref. No. 602590)/rac (OMIM Ref. No. 602048), thereby reprogramming cellular properties. RAGE is a central cell surface receptor for amphoterin (HMG1; 163905), a polypeptide linked to outgrowth of cultured cortical neurons derived from developing brain. Indeed, the colocalization of RAGE and amphoterin at the leading edge of advancing neurites indicated their potential contribution to cellular migration, and in pathologies such as tumor invasion. Taguchi et al. (2000) demonstrated that blockade of RAGE-amphoterin decreased growth and metastases of both implanted tumors and tumors developing spontaneously in susceptible mice. Inhibition of the RAGE- amphoterin interaction suppressed activation of p44 (OMIM Ref. No. 601795)/p42 (OMIM Ref. No. 603441), p38 (OMIM Ref. No. 600289), and SAP/JNK (OMIM Ref. No. 601158) MAP kinases, molecular effector mechanisms importantly linked to tumor proliferation, invasion, and expression of matrix metalloproteinases.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.; Ikemura, T. : Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a Notch homolog, human counterpart of mouse mammary tumor gene int- 3. Genomics 23: 408- 419, 1994. ; and

Taguchi, A.; Blood, D. C.; del Toro, G.; Canet, A.; Lee, D. C.; Qu, W.; Tanji, N.; Lu, Y.; Lalla, E.; Fu, C.; Hofmann, M. A.; Kislinger, T.; Ingram, M.; Lu, A.; Tanaka, H.; Hori, O.; Oga.

Further studies establishing the function and utilities of AGER are found in John Hopkins OMIM database record ID 600214, and in

cited publications listed in Table 9, hereby incorporated herein.

GAM2350 APBA1 CCTGCCCATCCTGCC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
TCCACCA 1 (X11) (APBA1, Accession NM_001163.2) is another GAM2350 target gene. APBA1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of APBA1, a GAM2350 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM2350 MAPT CCTGCCCATCCTGCC Microtubule- associated Protein Tau (MAPT, Accession A A
TCCACCA NM_173727.1) is another GAM2350 target gene. MAPT BINDING SITE1 and MAPT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 and MAPT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of MAPT, a GAM2350 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2350 PSEN1 CCTGCCCATCCTGCC PSEN1 (Accession NM_007318.1) is another GAM2350 target gene. A A
TCCACCA PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM2350 A TFCP2 A CCTGCCCATCCTGCC TCCACCA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM2350 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of TFCP2, a GAM2350 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM2350 A TGFB1 A CCTGCCCATCCTGCC TCCACCA TGFB1 (Accession NM_000660.1) is another GAM2350 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of TGFB1. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM2350 B DSCR1 A CCTGGGGGCCACTTT GCACAGG Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is another GAM2350 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of DSCR1, a GAM2350 target gene which inhibits calcineurin- dependent

transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2350 NOTCH1 CCTGGGGGCCACTTT Notch (Drosophila) Homolog 1 (translocation- associated) B A

GCACAGG (NOTCH1, Accession NM_017617.2) is another GAM2350 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of NOTCH1, a GAM2350 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM2350 SERPINA CCTGGGGGCCACTTT Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 B A 3 GCACAGG antiprotei (SERPINA3, Accession NM_001085.2) is another GAM2350 target gene. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2350 is therefore inhibition of SERPINA3, a GAM2350 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM2384 APBB2 AATCTTCACTAAAAT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGACAAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM2384 target gene. APBB2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2384 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2384 is therefore inhibition of APBB2, a GAM2384 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2384 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2384 APBB2 CGTGTTCAGTATGGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A

GGGAGAT 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM2384 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2384 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2384 is therefore inhibition of APBB2, a GAM2384 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2384 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2391 APBA2 TTAGCAGTTGTGAGA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

CCCTAGA 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM2391 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2391 is therefore inhibition of APBA2, a GAM2391 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits

production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2391 PSEN1 TTAGCAGTTGTGAGA PSEN1 (Accession NM_000021.2) is another GAM2391 target gene. A A

CCCTAGA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2391 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM2391 APPBP2 TTTGGGGTCTCCCCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding B A

GCATGCA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM2391 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2391 is therefore inhibition of APPBP2, a GAM2391 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2391 DSCR1 TTTGGGGTCTCCCCA Down Syndrome Critical Region Gene 1 (DSCR1, Accession B A

GCATGCA NM_004414.3) is another GAM2391 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2391 is therefore inhibition of DSCR1, a GAM2391 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM2393 APPBP2 AATGAAGCCACAGAG ATTTGCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM2393 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2393 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2393 is therefore inhibition of APPBP2, a GAM2393 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2393 HD AATGAAGCCACAGAG ATTTGCT HD (Accession NM_002111.3) is another GAM2393 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2393 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2393 is therefore inhibition of HD. Accordingly, utilities of GAM2393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM2398 TNFRSF6 ATCTAGAGAGGCAGT CTGGCCA TNFRSF6 (Accession NM_152875.1) is a GAM2398 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2398 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2398 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM2398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM2398 APLP1 CTGCTGCCTTTCTCT CAGAGAT Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession NM_005166.2) is another GAM2398 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2398 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM2398 is therefore inhibition of APLP1, a GAM2398 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM2398 CHAT CTGCTGCCTTTCTCT CAGAGAT Choline Acetyltransferase (CHAT, Accession NM_020986.1) is another GAM2398 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2398 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM2398 is therefore inhibition of CHAT, a GAM2398 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM2398 FLNB CTGCTGCCTTTCTCT CAGAGAT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM2398 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2398 RNA are set B A

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2398 is therefore inhibition of FLNB, a GAM2398 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM2424 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM2424 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2424 is therefore inhibition of APPBP2, a GAM2424 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2424 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM2424 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2424 is therefore inhibition of BACE2, a GAM2424 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2424 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM2424 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2424 is therefore inhibition of FHL2, a GAM2424 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2424 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM2424 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2424 is therefore inhibition of IGF1, a GAM2424 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2424 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM2424 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2424 is therefore inhibition of MME, a GAM2424 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2424 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM2424 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM2424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2424 is therefore inhibition of PRND, a GAM2424 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2440 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAC a GAM2440 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2440 is therefore inhibition of FHL2, a GAM2440 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2440 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAC NM_000618.2) is another GAM2440 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2440 is therefore inhibition of IGF1, a GAM2440 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2440 PRND ACTGCACTCCAGCCT AA GGGTGAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM2440 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2440 is therefore inhibition of PRND, a GAM2440 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2514 CTSG CTGTCCTGTGTCAGC AA CTGAAAT Cathepsin G (CTSG, Accession NM_001911.2) is a GAM2514 target gene. CTSG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2514 is therefore inhibition of CTSG, a GAM2514 target gene which is a member of the peptidase S1 protein family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSG.The function of CTSG has been established by previous

studies. Neutrophilic polymorphonuclear leukocytes contain specialized azurophil granules whose contents, including the serine proteases cathepsin G and elastase, may participate in the killing and digestion of engulfed pathogens, and in connective tissue remodeling at sites of inflammation. Cathepsin G is a 26,000- Da protease. Using mRNA from a leukemic cell line, Salvesen et al. (1987) isolated and determined the sequence of a cDNA clone encoding CTSG Since one form of Alzheimer disease, AD3, maps to 14q24.3, the lysosomal serine protease cathepsin G, which also maps to 14q, is a candidate for the site of the mutation. A defect in the cellular processing of amyloid precursor protein in familial Alzheimer disease has been postulated. Wong et al. (1993) analyzed the nucleotide sequence of the entire open reading frame of the CTSG gene and found no abnormality in 1 clinically affected member from each of 5 large FAD pedigrees that showed significant or nearly significant lod scores with one or more markers on chromosome 14. The sequence was compared with that of his/her unaffected living parent in each case and no differences were found Animal model experiments lend further support to the function of CTSG. Using mice deficient in Ctsg and/or Ela2 (OMIM Ref. No. 130130), Reeves et al. (2002) confirmed data originally generated by Tkalcevic et al. (2000) and Belaaouaj et al. (1998) that Ctsg - /- mice resist Candida but not Staphylococcal infection, whereas the reverse is true in Ela2 - /- mice. Both organisms were more virulent in double-knockout mice. Purified neutrophils from these mice mirrored these results in vitro in spite of exhibiting normal phagocytosis, degranulation, oxidase activity, superoxide production, and myeloperoxidase (MPO; 606989) activity. Reeves et al. (2002) hypothesized that reactive oxygen species (ROS) and proteases act together since deficiencies in either lead to comparable reductions in killing efficiency. They determined that conditions in the phagocytic vacuole after activation provoke the influx of enormous concentrations of ROS compensated by a surge of K ions crossing the membrane in a pH- dependent manner. The resulting rise in ionic strength induces the release of cationic granule proteins, including Ctsg and Ela2, from the highly charged anionic sulfated proteoglycan matrix within the granules. Reeves et al. (2002) concluded that it is essential for the volume of the vacuole to be restricted for the requisite hypertonicity to develop. They proposed that disruption of the integrity of the cytoskeletal network by microbial products could offer a mechanism of virulence by inhibiting the activation of granule proteins. They also suggested that a role of MPO may be to protect proteases, notably CTSG, from oxidative damage. In a commentary, Gratzer (2002) noted that mycobacteria may evade the innate immune response by their ability to disrupt actin filaments as demonstrated by Guerin and de Chastellier (2000).

It is appreciated that the abovementioned animal model for CTSG is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the

publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Salvesen, G.; Farley, D.; Shuman, J.; Przybyla, A.; Reilly, C.; Travis, J. : Molecular cloning of human cathepsin G: structural similarity to mast cell and cytotoxic T lymphocyte proteinases. Biochemistry 26: 2289- 2293, 1987. ; and

Reeves, E. P.; Lu, H.; Jacobs, H. L.; Messina, C. G. M.; Bolsover, S.; Gabella, G.; Potma, E. O.; Warley, A.; Roes, J.; Segal, A. W. : Killing activity of neutrophils is mediated through.

Further studies establishing the function and utilities of CTSG are found in John Hopkins OMIM database record ID 116830, and in cited publications listed in Table 9, hereby incorporated herein.

GAM2514 ADAM10 GTTTTAGGCAACATA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, B A

GGAAGAC Accession NM_001110.1) is another GAM2514 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2514 is therefore inhibition of ADAM10, a GAM2514 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM2514 HD GTTTTAGGCAACATA HD (Accession NM_002111.3) is another GAM2514 target gene. HD B A

GGAAGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2514 is therefore inhibition of HD. Accordingly, utilities of GAM2514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with HD.

GAM2519 ACE ACTGCAGCTTCAGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A ACTTGTG (ACE, Accession NM_152831.1) is a GAM2519 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2519 is therefore inhibition of ACE, a GAM2519 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2519 AVP ACTGCAGCTTCAGGG AVP (Accession NM_000490.2) is another GAM2519 target gene. AVP A A ACTTGTG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2519 is therefore inhibition of AVP. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM2519 CTNND2 ACTGCAGCTTCAGGG Catenin (cadherin- associated protein), Delta 2 (neural A A ACTTGTG plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM2519 target gene. CTNND2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2519 is therefore inhibition of CTNND2, a GAM2519 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM2519 DHCR24 ACTGCAGCTTCAGGG ACTTGTG A A — 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM2519 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2519 is therefore inhibition of DHCR24, a GAM2519 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2519 IAPP ACTGCAGCTTCAGGG ACTTGTG A A — Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM2519 target gene. IAPP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2519 is therefore inhibition of IAPP, a GAM2519 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2519 PSEN2 ACTGCAGCTTCAGGG ACTTGTG A A — PSEN2 (Accession NM_000447.1) is another GAM2519 target gene. PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2519 is therefore inhibition of PSEN2. Accordingly, utilities of GAM2519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM2543 BACE TTAATGCTAATCGTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

ATAGGGG is a GAM2543 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2543 is therefore inhibition of BACE, a GAM2543 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2543 FPRL1 TTAATGCTAATCGTG FPRL1 (Accession NM_001462.1) is another GAM2543 target gene. A A

ATAGGGG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2543 is therefore inhibition of FPRL1. Accordingly, utilities of GAM2543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM2543 SLC6A4 TTAATGCTAATCGTG Solute Carrier Family 6 (neurotransmitter transporter, A A

ATAGGGG serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM2543 target gene. SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SLC6A4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2543 is therefore inhibition of SLC6A4, a GAM2543 target gene which terminates the action of

serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM2565 IGF1 ATGACACAGTGGGGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CAGTTGG NM_000618.2) is a GAM2565 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2565 is therefore inhibition of IGF1, a GAM2565 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2565 MAPT ATGACACAGTGGGGC Microtubule- associated Protein Tau (MAPT, Accession A A
CAGTTGG NM_173727.1) is another GAM2565 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2565 is therefore inhibition of MAPT, a GAM2565 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2591 NGB ACCACAGTGTCACAG Neuroglobin (NGB, Accession NM_021257.2) is a GAM2591 target A A
AGTCCAT gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2591 is therefore inhibition of NGB, a GAM2591 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2608 BACE TAAGGTGCATCTAGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A GCAGTTA is a GAM2608 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2608 is therefore inhibition of BACE, a GAM2608 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2608 CASP3 TAAGGTGCATCTAGT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A GCAGTTA Accession NM_032991.1) is another GAM2608 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2608 is therefore inhibition of CASP3, a GAM2608 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM2618 ADAM17 TGGGAAGATGCTGGC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AAGGTGC factor, (ADAM17, Accession NM_021832.1) is a GAM2618 target gene. ADAM17 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2618 is therefore inhibition of ADAM17, a GAM2618 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM2618 AGER TGGGAAGATGCTGGC Advanced Glycosylation End Product- specific Receptor (AGER, A A

AAGGTGC Accession NM_172197.1) is another GAM2618 target gene. AGER BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AGER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2618 is therefore inhibition of AGER, a GAM2618 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM2618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AGER.The function of AGER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2350.

GAM2618 IGF1 TGGGAAGATGCTGGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AAGGTGC NM_000618.2) is another GAM2618 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2618 is therefore inhibition of IGF1, a GAM2618 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2618 PSEN1 TGGGAAGATGCTGGC PSEN1 (Accession NM_007319.1) is another GAM2618 target gene. A A
AAGGTGC PSEN1 BINDING SITE1 through PSEN1 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 through PSEN1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM2618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2618 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM2624 ACT TCTGAGCCCAGGAGT Activator of CAMP- responsive Element Modulator (CR (ACT, A A
TTGAGGC Accession NM_020482.3) is a GAM2624 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2624 is therefore inhibition of ACT, a GAM2624 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM2624 CTNND2 TCTGAGCCCAGGAGT Catenin (cadherin- associated protein), Delta 2 (neural A A
TTGAGGC plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM2624 target gene. CTNND2 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of CTNND2, a GAM2624 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM2624 DLST TCTGAGCCCAGGAGT TTGAGGC Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM2624 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2624 is therefore inhibition of DLST, a GAM2624 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM2624 GFAP TCTGAGCCCAGGAGT TTGAGGC GFAP (Accession NM_002055.2) is another GAM2624 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2624 is therefore inhibition of GFAP. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM2624 IGF1 TCTGAGCCCAGGAGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTGAGGC NM_000618.2) is another GAM2624 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of IGF1, a GAM2624 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2624 OGDH TCTGAGCCCAGGAGT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

TTGAGGC NM_002541.1) is another GAM2624 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of OGDH, a GAM2624 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM2624 PRND TCTGAGCCCAGGAGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TTGAGGC another GAM2624 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of PRND, a GAM2624 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2624 TFCP2 TCTGAGCCCAGGAGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
TTGAGGC another GAM2624 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of TFCP2, a GAM2624 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM2624 APPBP2 GCACTCAAGCCTGGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding B A
TTACAGA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM2624 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of APPBP2, a GAM2624 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2624 FHL2 GCACTCAAGCCTGGG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is B A
TTACAGA another GAM2624 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of FHL2, a GAM2624 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2624 IGF1 GCACTCAAGCCTGGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession B A
TTACAGA NM_000618.2) is another GAM2624 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of IGF1, a GAM2624 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2624 PRND GCACTCAAGCCTGGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A
TTACAGA another GAM2624 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM2624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2624 is therefore inhibition of PRND, a GAM2624 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2624 include diagnosis, prevention and treatment of Alzheimer,

and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2628 DHCR24 TCCCTTTGAAGCCAG A A GTTCCAG 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM2628 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2628 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2628 is therefore inhibition of DHCR24, a GAM2628 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2628 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2628 TGFB1 TCCCTTTGAAGCCAG A A GTTCCAG TGFB1 (Accession NM_000660.1) is another GAM2628 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2628 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2628 is therefore inhibition of TGFB1. Accordingly, utilities of GAM2628 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM2631 PSEN1 TTGGTGCAAATGGCA A A TTTCCAT PSEN1 (Accession NM_007318.1) is a GAM2631 target gene. PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2631 is therefore inhibition of PSEN1. Accordingly, utilities of GAM2631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with PSEN1.

GAM2640 APPBP2 ATGCCTGTAATCCCA GCATTTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM2640 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2640 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2640 is therefore inhibition of APPBP2, a GAM2640 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2640 IGF1 ATGCCTGTAATCCCA GCATTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM2640 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2640 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2640 is therefore inhibition of IGF1, a GAM2640 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2640 PRND ATGCCTGTAATCCCA GCATTTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM2640 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2640 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2640 is therefore inhibition of PRND, a GAM2640 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2672 FLNB TGTGACACGTTCATT CTGCAAG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM2672 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2672 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2672 is therefore inhibition of FLNB, a GAM2672 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2672 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM2732 ADAMTS5 ATCACTTTGCAGGGA TTACTAA A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM2732 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2732 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2732 is therefore inhibition of ADAMTS5, a GAM2732 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2732 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2732 APBB1 ATCACTTTGCAGGGA TTACTAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM2732 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A A

APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2732 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2732 is therefore inhibition of APBB1, a GAM2732 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2732 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2762 BLMH CACACAGTCGTGTAG Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a
GAM2762 A A
TTTTGCG target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2762 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2762 is therefore inhibition of BLMH, a GAM2762 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM2762 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM2762 CTNND2 CACACAGTCGTGTAG Catenin (cadherin- associated protein), Delta 2 (neural A A
TTTTGCG plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM2762 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2762 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2762 is therefore inhibition of CTNND2, a GAM2762 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2762 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM2762 IGF1 CACACAGTCGTGTAG TTTTGCG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM2762 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2762 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2762 is therefore inhibition of IGF1, a GAM2762 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2762 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2770 CASP3 CTGGCTAATTTTCTT GAGTTTT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is a GAM2770 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2770 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2770 is therefore inhibition of CASP3, a GAM2770 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM2770 HTR2C CTGGCTAATTTTCTT GAGTTTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM2770 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2770 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2770 is therefore inhibition of HTR2C, a GAM2770 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM2770	IDE	CTGGCTAATTTTCTT GAGTTTT	Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM2770 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM2770 is therefore inhibition of IDE, a GAM2770 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE has been established by previous studies. Insulin- degrading enzyme (EC 3.4.24.56), also known as insulysin, is a 110- kD neutral metallopeptidase that can degrade a number of peptides, including insulin (OMIM Ref. No. 176730) and beta- amyloid (OMIM Ref. No. 104760). Affholter et al. (1988) isolated and sequenced a cDNA coding for IDE. The deduced amino acid sequence of the enzyme contained the sequences of 13 peptides derived from the isolated protein. The cDNA transcribed in vitro yielded a synthetic RNA that in cell- free translations produced a protein that coelectrophoresed with the native proteinase and could be immunoprecipitated with monoclonal antibodies to IDE. Since the deduced sequence of this proteinase did not contain the consensus sequences for any of the known classes of proteinases (i.e. metallo, cysteine, aspartic, or serine), it may be a member of a family of proteases that are involved in intercellular peptide signaling. It did show homology to an Escherichia coli proteinase (called protease III), which also cleaves insulin and is present in the periplasmic space; thus, they may be members of the same family of proteases. et al. (1998) determined that the extracellular thiol metalloprotease capable of degrading amyloid- beta protein identified by Qiu et al. (1997) is the same as IDE. By Western blot analysis, they found a full- length 110- kD IDE band in the CSF of normal individuals and of patients with Alzheimer disease or non- Alzheimer dementia. They found no difference in IDE levels of the normal and patient populations. By biochemical analysis of IDE purified from the medium of a mouse microglial cell line, they determined that IDE could degrade both

endogenous and synthetic amyloid- beta protein and that it could catalyze the oligomerization of this protein. Through a series of inhibitor studies, in vitro translation, and biochemical assays of rat IDE expressed by transfected human kidney cells, Edbauer et al. (2002) determined that IDE may be the protease responsible for the clearance of the cytoplasmic fragment of the amyloid- beta precursor protein (APP) following liberation of the amyloid- beta protein. Affholter et al. (1990) mapped the IDE gene to human chromosome 10 and mouse chromosome 19 by hybridization of cDNA probes to human-rodent or mouse- hamster somatic cell hybrids, respectively. By a combination of somatic cell hybrid analysis and in situ hybridization, Espinosa et al. (1991) localized the IDE gene to 10q23- q25. The mapping of the IDE gene to chromosome 10q23- q25 made it a candidate gene for the Alzheimer disease- 6 locus (AD6; 605526). Abraham et al. (2001) analyzed all of the coding exons, untranslated regions, and 1,000 bp of 5- prime flanking sequence of IDE by means of denaturing HPLC and sequencing. They detected 8 single nucleotide polymorphisms (SNPs), of which 3 were found at lower than 5% frequency. None of them changed the amino acid sequence. Abraham et al. (2001) found no significant association between any individual SNP and late- onset AD or with any haplotypes. They concluded that IDE does not make a substantial contribution to the etiology of late- onset AD and therefore cannot account for the linkage between late- onset AD and 10q. Animal model experiments lend further support to the function of IDE. Genetic analysis of the diabetic GK rat has revealed several diabetes susceptibility loci (see OMIM Ref. No. 125853). Fakhrai- Rad et al. (2000) mapped one such locus, NIDDM1B, to a 1- cM region by genetic and pathophysiologic characterization of new congenic substrains for the locus. The IDE gene was also mapped to this 1- cM region, and 2 amino acid substitutions (H18R and A890V) were identified in the GK allele which reduced insulin- degrading activity by 31% in transfected cells. However, when the H18R and A890V variants were studied separately, no effects were observed, suggesting a synergistic effect of the 2 variants on insulin degradation. No effect on insulin degradation was observed in cell lysates, suggesting that the effect may be coupled to receptor- mediated internalization of insulin. Congenic rats with the IDE GK allele displayed postprandial hyperglycemia, reduced lipogenesis in fat cells, blunted insulin- stimulated glucose transmembrane uptake, and reduced insulin degradation in isolated muscle. Analysis of additional rat strains demonstrated that the dysfunctional IDE allele was unique to GK rats. The authors concluded that IDE plays an important role in the diabetic phenotype in GK rats.

It is appreciated that the abovementioned animal model for IDE is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Fakhrai- Rad, H.; Nikoshkov, A.; Kamel, A.; Fernstrom, M.; Zierath, J. R.; Norgren, S.; Luthman, H.; Galli, J. : Insulin-degrading enzyme identified as a candidate diabetes susceptibility gene in GK rats. Hum. Molec. Genet. 9: 2149- 2158, 2000. ; and

Edbauer, D.; Willem, M.; Lammich, S.; Steiner, H.; Haass, C. : Insulin- degrading enzyme rapidly removes the beta- amyloid precursor protein intracellular domain (AICD). J. Biol. Chem. 27.

Further studies establishing the function and utilities of IDE are found in John Hopkins OMIM database record ID 146680, and in cited publications listed in Table 9, hereby incorporated herein.

GAM2770	IGF1	CTGGCTAATTTTCTT GAGTTTT	Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM2770 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM2770 is therefore inhibition of IGF1, a GAM2770 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2780	SNCAIP	TGAGTGACAGAGCAA CACTCTG	Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is a GAM2780 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2780 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

A function of GAM2780 is therefore inhibition of SNCAIP, a GAM2780 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2780 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM1300.

GAM2799 ACE TTGCCCAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TGCAGTG (ACE, Accession NM_152831.1) is a GAM2799 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2799 is therefore inhibition of ACE, a GAM2799 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2799 ADAM17 TTGCCCAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TGCAGTG factor, (ADAM17, Accession NM_003183.3) is another GAM2799 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of ADAM17, a GAM2799 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM2799 CHAT TTGCCCAGGCTGGAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is A A
TGCAGTG another GAM2799 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of CHAT, a GAM2799 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM2799 FLNB TTGCCCAGGCTGGAG TGCAGTG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM2799 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2799 is therefore inhibition of FLNB, a GAM2799 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM2799 HTR2A TTGCCCAGGCTGGAG TGCAGTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM2799 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2799 is therefore inhibition of HTR2A, a GAM2799 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM2799 IAPP TTGCCCAGGCTGGAG TGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM2799 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, A A

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of IAPP, a GAM2799 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2799 NOTCH1 TTGCCCAGGCTGGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGCAGTG (NOTCH1, Accession NM_017617.2) is another GAM2799 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of NOTCH1, a GAM2799 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM2799 TGFB1 TTGCCCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM2799 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of TGFB1. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM2799 ADAM17 CACTGCAACCTCCAC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis B A

CTCCTGG factor, (ADAM17, Accession NM_003183.3) is another GAM2799 target gene. ADAM17 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of ADAM17, a GAM2799 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM2799 IAPP CACTGCAACCTCCAC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A
CTCCTGG another GAM2799 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of IAPP, a GAM2799 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2799 OGDH CACTGCAACCTCCAC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession B A
CTCCTGG NM_002541.1) is another GAM2799 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2799 is therefore inhibition of OGDH, a GAM2799 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2799 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM2807 CTSK AATCTCCATTTGTAA CTSK (Accession NM_000396.2) is a GAM2807 target gene. CTSK A A
ATGTGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2807 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2807 is therefore inhibition of CTSK. Accordingly, utilities of GAM2807 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM2808 NCKAP1 TAAGTGCTGCTGATT NCKAP1 (Accession NM_013436.2) is a GAM2808 target gene. NCKAP1 A A
TTGGAAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2808 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2808 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM2808 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM2817 MME TGATTGTATGATATA Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TGAGTTT enkephalinase, (MME, Accession NM_007287.1) is a GAM2817 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2817 is therefore inhibition of MME, a GAM2817 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2839 NGB GGGTCTCAAATGAGG Neuroglobin (NGB, Accession NM_021257.2) is a GAM2839 target A A

GACATTT gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2839 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2839 is therefore inhibition of NGB, a GAM2839 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2839 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2839 CHAT ACATTTCCAATGTTT Choline Acetyltransferase (CHAT, Accession NM_020986.1) is B A

GGGGACA another GAM2839 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2839 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2839 is therefore inhibition of CHAT, a GAM2839 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2839 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM2846 APBB2 TATTAGTTGATTCCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AGGGACC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM2846 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2846 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2846 is therefore inhibition of APBB2, a GAM2846 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM2846 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2868 APLP2 TGGAATGGCTGAAGA A A CTGTGAA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM2868 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2868 is therefore inhibition of APLP2, a GAM2868 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM2868 FLNB TGGAATGGCTGAAGA A A CTGTGAA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM2868 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2868 is therefore inhibition of FLNB, a GAM2868 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM2868 SLC17A7 TGGAATGGCTGAAGA A A CTGTGAA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM2868 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2868 RNA

are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2868 is therefore inhibition of SLC17A7, a GAM2868 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM2868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM2887 ABCD1 GGCCTGAGGTCAGCA ABCD1 (Accession NM_000033.2) is a GAM2887 target gene. ABCD1 A A

GTAGAGG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2887 is therefore inhibition of ABCD1. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM2887 APBB1 GGCCTGAGGTCAGCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GTAGAGG 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM2887 target gene. APBB1 BINDING SITE1 and APBB1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APBB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE1 and APBB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of APBB1, a GAM2887 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM2887 APLP2 GGCCTGAGGTCAGCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

GTAGAGG NM_001642.1) is another GAM2887 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of APLP2, a GAM2887 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM2887 BAX GGCCTGAGGTCAGCA BCL2- associated X Protein (BAX, Accession NM_004324.2) is A A GTAGAGG another GAM2887 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of BAX, a GAM2887 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM2887 PRND GGCCTGAGGTCAGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GTAGAGG another GAM2887 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of PRND, a GAM2887 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM44.

GAM2887 SLC17A7 GGCCTGAGGTCAGCA A A GTAGAGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM2887 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of SLC17A7, a GAM2887 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM2887 TRPM2 GGCCTGAGGTCAGCA A A GTAGAGG TRPM2 (Accession NM_003307.1) is another GAM2887 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2887 is therefore inhibition of TRPM2, a GAM2887 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM2887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM2908 CTSB CCACTGCACTCCAGC A A ACTCCAG CTSB (Accession NM_147782.1) is a GAM2908 target gene. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2908 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2908 is therefore inhibition of CTSB. Accordingly, utilities of GAM2908 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM2908 FHL2 CCACTGCACTCCAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

ACTCCAG another GAM2908 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2908 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2908 is therefore inhibition of FHL2, a GAM2908 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2908 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2908 IGF1 CCACTGCACTCCAGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTCCAG NM_000618.2) is another GAM2908 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2908 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2908 is therefore inhibition of IGF1, a GAM2908 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2908 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2911 APBA2 GACACAGGCCCAGAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AGGCAG 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM2911 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM2911 is therefore inhibition of APBA2, a GAM2911 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2911 CTSB GACACAGGCCCAGAG A A AGGCAG CTSB (Accession NM_001908.2) is another GAM2911 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2911 is therefore inhibition of CTSB. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM2911 DLST GACACAGGCCCAGAG A A AGGCAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM2911 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2911 is therefore inhibition of DLST, a GAM2911 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM2911 MAPT GACACAGGCCCAGAG A A AGGCAG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM2911 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple

transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2911 is therefore inhibition of MAPT, a GAM2911 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2911 NCSTN GACACAGGCCCAGAG NCSTN (Accession NM_015331.1) is another GAM2911 target gene. A A
AGGCAG NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2911 is therefore inhibition of NCSTN, a GAM2911 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2911 S100B GACACAGGCCCAGAG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A
AGGCAG NM_006272.1) is another GAM2911 target gene. S100B BINDING SITE1 and S100B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by S100B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE1 and S100B BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2911 is therefore inhibition of S100B, a GAM2911 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities

exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM2920 A NGB GCTGAGACCACCCTT A GCCTGCC Neuroglobin (NGB, Accession NM_021257.2) is a GAM2920 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2920 is therefore inhibition of NGB, a GAM2920 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2920 A TRPM2 GCTGAGACCACCCTT A GCCTGCC TRPM2 (Accession NM_003307.1) is another GAM2920 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of TRPM2, a GAM2920 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM2920 A APBB2 GGCTGGGCATGGTGG A CTCACGC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM2920 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of APBB2, a GAM2920 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2920 AVP GGCTGGGCATGGTGG AVP (Accession NM_000490.2) is another GAM2920 target gene.
AVP B A

CTCACGC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of AVP. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM2920 CTSB GGCTGGGCATGGTGG CTSB (Accession NM_147783.1) is another GAM2920 target gene.
B A

CTCACGC CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of CTSB. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM2920 GFAP GGCTGGGCATGGTGG GFAP (Accession NM_002055.2) is another GAM2920 target gene.
B A

CTCACGC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of GFAP. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM2920 IGF1 GGCTGGGCATGGTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession B A
CTCACGC NM_000618.2) is another GAM2920 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of IGF1, a GAM2920 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2920 PRND GGCTGGGCATGGTGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A
CTCACGC another GAM2920 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of PRND, a GAM2920 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM2920 TNF GGCTGGGCATGGTGG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, B A
CTCACGC Accession NM_000594.2) is another GAM2920 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2920 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2920 is therefore inhibition of TNF, a GAM2920 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM2920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2927 OLR1 ATAAAGCAGGTTAAC Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A AAAGCTG (OLR1, Accession NM_002543.1) is a GAM2927 target gene. OLR1 BINDING SITE1 and OLR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OLR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE1 and OLR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2927 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2927 is therefore inhibition of OLR1, a GAM2927 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2927 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2931 ADAMTS5 TGGAGAGAGCAGGTT A Disintegrin- like and Metalloprotease (reprolysin type) with A A GCTAAGA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM2931 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM2931 is therefore inhibition of ADAMTS5, a GAM2931 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM2931 CTSK TGGAGAGAGCAGGTT CTSK (Accession NM_000396.2) is another GAM2931 target gene. A A

GCTAAGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of CTSK. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM2931 IGF1 TGGAGAGAGCAGGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCTAAGA NM_000618.2) is another GAM2931 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of IGF1, a GAM2931 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM2931 IL1B TGGAGAGAGCAGGTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A

GCTAAGA GAM2931 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of IL1B, a GAM2931 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM604.

GAM2931 MAPK10 TGGAGAGAGCAGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
GCTAAGA NM_138981.1) is another GAM2931 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of MAPK10, a GAM2931 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM2931 MAPT TGGAGAGAGCAGGTT Microtubule- associated Protein Tau (MAPT, Accession A A
GCTAAGA NM_173727.1) is another GAM2931 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of MAPT, a GAM2931 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2931 TNF TGGAGAGAGCAGGTT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A
GCTAAGA Accession NM_000594.2) is another GAM2931 target gene. TNF BINDING SITE1 and TNF BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TNF, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE1 and TNF BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM2931 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

Another function of GAM2931 is therefore inhibition of TNF, a GAM2931 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM2931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM2950 BACE2 AGGCCAGAGAGGACT CTCTTTT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM2950 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM2950 is therefore inhibition of BACE2, a GAM2950 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM2950 GYPA AGGCCAGAGAGGACT CTCTTTT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM2950 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM2950 is therefore inhibition of GYPA, a GAM2950 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM2950 IL1A AGGCCAGAGAGGACT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

CTCTTTT GAM2950 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2950 is therefore inhibition of IL1A, a GAM2950 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2950 MAPT AGGCCAGAGAGGACT Microtubule- associated Protein Tau (MAPT, Accession A A
CTCTTTT NM_173727.1) is another GAM2950 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2950 is therefore inhibition of MAPT, a GAM2950 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM2950 NGB AGGCCAGAGAGGACT Neuroglobin (NGB, Accession NM_021257.2) is another GAM2950 A A
CTCTTTT target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2950 is therefore inhibition of NGB, a GAM2950 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM2950 A A NPY AGGCCAGAGAGGACT CTCTTTT Neuropeptide Y (NPY, Accession NM_000905.2) is another GAM2950 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2950 is therefore inhibition of NPY, a GAM2950 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM2950 A A TRPM2 AGGCCAGAGAGGACT CTCTTTT TRPM2 (Accession NM_003307.1) is another GAM2950 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM2950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM2950 is therefore inhibition of TRPM2, a GAM2950 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM2950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3004 A A S100B TATTTGTTTTTAATG CTGGGTG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is a GAM3004 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM3004 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3004 is therefore inhibition of S100B, a GAM3004 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3004 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM3028 ACE TTCTGGTGAATTCAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A GATGGTA (ACE, Accession NM_152831.1) is a GAM3028 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3028 is therefore inhibition of ACE, a GAM3028 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3028 ADAM17 TTCTGGTGAATTCAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A GATGGTA factor, (ADAM17, Accession NM_021832.1) is another GAM3028 target gene. ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADAM17, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3028 is therefore inhibition of ADAM17, a GAM3028 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3028 BACE2 TTCTGGTGAATTCAG GATGGTA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM3028 target gene. BACE2 BINDING SITE1 and BACE2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE1 and BACE2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3028 is therefore inhibition of BACE2, a GAM3028 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3028 IL1A TTCTGGTGAATTCAG GATGGTA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM3028 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3028 is therefore inhibition of IL1A, a GAM3028 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3028 NCKAP1 TTCTGGTGAATTCAG GATGGTA NCKAP1 (Accession NM_013436.2) is another GAM3028 target gene. A A

NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3028 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM3028 OLR1 TTCTGGTGAATTCAG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A GATGGTA (OLR1, Accession NM_002543.1) is another GAM3028 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3028 is therefore inhibition of OLR1, a GAM3028 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3057 APBA1 GGCATGATTCAGCAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A AGGAGAG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM3057 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3057 is therefore inhibition of APBA1, a GAM3057 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM3057 GFAP GGCATGATTCAGCAG GFAP (Accession NM_002055.2) is another GAM3057 target gene. A A AGGAGAG GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure

complementarity to the nucleotide sequence of GAM3057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3057 is therefore inhibition of GFAP. Accordingly, utilities of GAM3057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM3057 IGF1 GGCATGATTCAGCAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGGAGAG NM_000618.2) is another GAM3057 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3057 is therefore inhibition of IGF1, a GAM3057 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3057 THOP1 GGCATGATTCAGCAG Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is A A

AGGAGAG another GAM3057 target gene. THOP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3057 is therefore inhibition of THOP1, a GAM3057 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM3057 TRPM2 GGCATGATTCAGCAG TRPM2 (Accession NM_003307.1) is another GAM3057 target gene. A A

AGGAGAG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3057 is therefore inhibition of TRPM2, a GAM3057 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM3057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3061 DLST TTAAAGATCACTTGA CATGGAC Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is a GAM3061 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3061 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3061 is therefore inhibition of DLST, a GAM3061 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3061 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3064 PRND TTTAAGCTATAGTTC CAGGCCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a GAM3064 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3064 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3064 is therefore inhibition of PRND, a GAM3064 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3065 ACE GACATGATGTAGCAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
ATGATGG (ACE, Accession NM_152831.1) is a GAM3065 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3065 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3065 is therefore inhibition of ACE, a GAM3065 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3065 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3065 ADAMTS5 GACATGATGTAGCAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A
ATGATGG Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM3065 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3065 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3065 is therefore inhibition of ADAMTS5, a GAM3065 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3065 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM3065 APCS GACATGATGTAGCAG Amyloid P Component, Serum (APCS, Accession NM_001639.2) is A A
ATGATGG another GAM3065 target gene. APCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3065 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3065 is therefore inhibition of

APCS, a GAM3065 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3065 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM772.

GAM3065 MME GACATGATGTAGCAG ATGATGG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM3065 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3065 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3065 is therefore inhibition of MME, a GAM3065 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3065 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3065 OLR1 GACATGATGTAGCAG ATGATGG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM3065 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3065 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3065 is therefore inhibition of OLR1, a GAM3065 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3065 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3077 ACE TTACCATGTTGGCCA GGCTGGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM3077 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, A A

corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3077 is therefore inhibition of ACE, a GAM3077 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3077 ADAM17 TTACCATGTTGGCCA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
GGCTGGT factor, (ADAM17, Accession NM_003183.3) is another GAM3077 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3077 is therefore inhibition of ADAM17, a GAM3077 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3077 IAPP TTACCATGTTGGCCA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
GGCTGGT another GAM3077 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3077 is therefore inhibition of IAPP, a GAM3077 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3077 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3077 IGF1 TTACCATGTTGGCCA GGCTGGT A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3077 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3077 is therefore inhibition of IGF1, a GAM3077 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3077 TGFB1 TTACCATGTTGGCCA GGCTGGT A A TGFB1 (Accession NM_000660.1) is another GAM3077 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3077 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3081 ADAM17 CTGGGATTACAGGTG TGAACCA A A A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM3081 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3081 is therefore inhibition of ADAM17, a GAM3081 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3081 CASP3 CTGGGATTACAGGTG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A
TGAACCA Accession NM_004346.2) is another GAM3081 target gene. CASP3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3081 is therefore inhibition of CASP3, a GAM3081 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM3081 HTR2A CTGGGATTACAGGTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
TGAACCA NM_000621.1) is another GAM3081 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3081 is therefore inhibition of HTR2A, a GAM3081 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM3081 IAPP CTGGGATTACAGGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
TGAACCA another GAM3081 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3081 is therefore inhibition of IAPP, a GAM3081 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3081 MTNR1A CTGGGATTACAGGTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A
TGAACCA another GAM3081 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3081 is therefore inhibition of MTNR1A, a GAM3081 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM3081 TGFB1 CTGGGATTACAGGTG TGFB1 (Accession NM_000660.1) is another GAM3081 target gene. A A
TGAACCA TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3081 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3081 DSCR1 TGATTCATTTCTAAA Down Syndrome Critical Region Gene 1 (DSCR1, Accession B A

		CCCAGCT	NM_004414.3) is another GAM3081 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM3081 is therefore inhibition of DSCR1, a GAM3081 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.		
GAM3081	PRND	TGATTCATTTCTAAA CCCAGCT	Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM3081 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3081 RNA are set forth in Tables 6 and 7, hereby incorporated herein. Another function of GAM3081 is therefore inhibition of PRND, a GAM3081 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.	B	A
GAM3089	ACE	TTCAGCATTGCCAGT GTTTCCA	Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_000789.2) is a GAM3089 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3089 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A function of GAM3089 is therefore inhibition of ACE, a GAM3089 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its	A	A

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3089 APPBP2 TTCAGCATTGCCAGT GTTTCCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM3089 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3089 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3089 is therefore inhibition of APPBP2, a GAM3089 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3089 CHAT TTCAGCATTGCCAGT GTTTCCA Choline Acetyltransferase (CHAT, Accession NM_020549.2) is another GAM3089 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3089 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3089 is therefore inhibition of CHAT, a GAM3089 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3089 HTR2C TTCAGCATTGCCAGT GTTTCCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM3089 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3089 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3089 is therefore inhibition of HTR2C, a GAM3089 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM3091 DLST TGGGAGGCTACACGT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
TTCTCCA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM3091 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3091 is therefore inhibition of DLST, a GAM3091 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3091 HD TGGGAGGCTACACGT HD (Accession NM_002111.3) is another GAM3091 target gene. HD A A
TTCTCCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3091 is therefore inhibition of HD. Accordingly, utilities of GAM3091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM3091 MAPT TGGGAGGCTACACGT Microtubule- associated Protein Tau (MAPT, Accession A A
TTCTCCA NM_173727.1) is another GAM3091 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of

GAM3091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3091 is therefore inhibition of MAPT, a GAM3091 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM3123 PSEN2 CTTCAATGCTTGAGA PSEN2 (Accession NM_012486.1) is a GAM3123 target gene. PSEN2 A A
AGTCGTA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3123 is therefore inhibition of PSEN2. Accordingly, utilities of GAM3123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM3126 APLP2 TGAGATCATCGTTAC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
AAGCAGC NM_001642.1) is a GAM3126 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3126 is therefore inhibition of APLP2, a GAM3126 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM3126 FHL2 TGAGATCATCGTTAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
AAGCAGC another GAM3126 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3126 is therefore inhibition of FHL2, a GAM3126 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3132 NCKAP1 TAAGTGCTGCTGATT NCKAP1 (Accession NM_013436.2) is a GAM3132 target gene. NCKAP1 A A
TTGGAAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3132 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM3132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM3138 DSCR1 TGGTCTCTTGAAAGA Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A
GGCTCTT NM_004414.3) is a GAM3138 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3138 is therefore inhibition of DSCR1, a GAM3138 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM3138 IL1B TGGTCTCTTGAAAGA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A
GGCTCTT GAM3138 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3138 is therefore inhibition of IL1B, a GAM3138 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM3140 A2M TGGAGCAGAAAGGCA GGAGTCC A A

Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a GAM3140 target gene. A2M BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3140 is therefore inhibition of A2M, a GAM3140 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM3140 APBB1 TGGAGCAGAAAGGCA GGAGTCC A A

Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM3140 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of APBB1, a GAM3140 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM347.

GAM3140 CHAT TGGAGCAGAAAGGCA Choline Acetyltransferase (CHAT, Accession NM_020986.1) is A A

GGAGTCC another GAM3140 target gene. CHAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of CHAT, a GAM3140 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3140 DLST TGGAGCAGAAAGGCA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GGAGTCC oxo- glutarat (DLST, Accession NM_001933.2) is another GAM3140 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of DLST, a GAM3140 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3140 FPRL1 TGGAGCAGAAAGGCA FPRL1 (Accession NM_001462.1) is another GAM3140 target gene. A A

GGAGTCC FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of FPRL1. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM3140 A A GGAGTCC HTR2C TGGAGCAGAAAGGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM3140 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of HTR2C, a GAM3140 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM3140 A A GGAGTCC MPO TGGAGCAGAAAGGCA Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM3140 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of MPO, a GAM3140 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM3140 A A GGAGTCC PRND TGGAGCAGAAAGGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM3140 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of PRND, a GAM3140 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3140 SLC6A4 TGGAGCAGAAAGGCA GGAGTCC Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM3140 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3140 is therefore inhibition of SLC6A4, a GAM3140 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM3140 TGFB1 TGGAGCAGAAAGGCA GGAGTCC TGFB1 (Accession NM_000660.1) is another GAM3140 target gene. TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3140 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3140 TNFRSF5 TGGAGCAGAAAGGCA GGAGTCC TNFRSF5 (Accession NM_152854.1) is another GAM3140 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3140 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM3140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM3143 BACE CAGAGGATGCGGCTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

GGAACGG is a GAM3143 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3143 is therefore inhibition of BACE, a GAM3143 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3143 HD CAGAGGATGCGGCTG HD (Accession NM_002111.3) is another GAM3143 target gene. HD A A

GGAACGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3143 is therefore inhibition of HD. Accordingly, utilities of GAM3143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM3143 MPO CAGAGGATGCGGCTG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM3143 A A

GGAACGG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3143 is therefore inhibition of MPO, a GAM3143 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM3157 SNCA GTGAAGGTAGGTTTC SNCA (Accession NM_000345.2) is a GAM3157 target gene. SNCA A A

AGGTTTG BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3157 is therefore inhibition of SNCA. Accordingly, utilities of GAM3157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM3163 FOS CACTGCAATGACTGT V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

CAGAACA Accession NM_005252.2) is a GAM3163 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3163 is therefore inhibition of FOS, a GAM3163 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM3163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM3163 HTR2A CACTGCAATGACTGT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

CAGAACA NM_000621.1) is another GAM3163 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM3163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3163 is therefore inhibition of HTR2A, a GAM3163 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM3174 GLUL TTTGATGCATGTGAC Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
CTGGGAT NM_002065.3) is a GAM3174 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3174 is therefore inhibition of GLUL, a GAM3174 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM3174 TNFSF5 TTTGATGCATGTGAC TNFSF5 (Accession NM_000074.1) is another GAM3174 target gene. A A
CTGGGAT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3174 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM3174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM3183 CHAT AGTGCAGGTTCACAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a A A
GCTGGGC GAM3183 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3183 is therefore inhibition of CHAT, a GAM3183 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3183 CLU AGTGCAGGTTCACAG GCTGGGC Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is another GAM3183 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3183 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3183 is therefore inhibition of CLU, a GAM3183 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM3183 CTSB AGTGCAGGTTCACAG GCTGGGC CTSB (Accession NM_147782.1) is another GAM3183 target gene. CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3183 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3183 is therefore inhibition of CTSB. Accordingly, utilities of GAM3183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM3183 TRPM2 AGTGCAGGTTCACAG GCTGGGC TRPM2 (Accession NM_003307.1) is another GAM3183 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` A A

untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3183 is therefore inhibition of TRPM2, a GAM3183 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM3183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3190 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3190 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3190 is therefore inhibition of APPBP2, a GAM3190 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3190 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM3190 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3190 is therefore inhibition of BACE2, a GAM3190 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3190 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM3190 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3190 is therefore inhibition of FHL2, a GAM3190 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3190 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM3190 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3190 is therefore inhibition of HD. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM3190 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM3190 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3190 is therefore inhibition of IGF1, a GAM3190 target gene which are structurally and functionally

related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3190 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM3190 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM3190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3190 is therefore inhibition of PRND, a GAM3190 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3195 ADAM10 TGAGGGCAGGTGTGA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

AAATGCT Accession NM_001110.1) is a GAM3195 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3195 is therefore inhibition of ADAM10, a GAM3195 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM3195 APBB2 TGAGGGCAGGTGTGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AAATGCT 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM3195 target gene. APBB2 BINDING SITE1 and APBB2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APBB2,

corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE1 and APBB2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3195 is therefore inhibition of APBB2, a GAM3195 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3195 FPRL1 TGAGGGCAGGTGTGA A A AAATGCT FPRL1 (Accession NM_001462.1) is another GAM3195 target gene. FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3195 is therefore inhibition of FPRL1. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM3195 IGF1 TGAGGGCAGGTGTGA A A AAATGCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3195 target gene. IGF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3195 is therefore inhibition of IGF1, a GAM3195 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3195 MAPK10 TGAGGGCAGGTGTGA A A Mitogen- activated Protein Kinase 10 (MAPK10, Accession

AAATGCT NM_138981.1) is another GAM3195 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3195 is therefore inhibition of MAPK10, a GAM3195 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM3195 A A SNCA TGAGGGCAGGTGTGA AAATGCT SNCA (Accession NM_007308.1) is another GAM3195 target gene. SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3195 is therefore inhibition of SNCA. Accordingly, utilities of GAM3195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM3211 A A HTR2A TCTCATATAGCTGGG TTGCAGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is a GAM3211 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3211 is therefore inhibition of HTR2A, a GAM3211 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM593.

GAM3211 A NGB TCTCATATAGCTGGG TTGCAGC A Neuroglobin (NGB, Accession NM_021257.2) is another GAM3211 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3211 is therefore inhibition of NGB, a GAM3211 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3211 B FLNB TCACTGTTCCTTTTT GTTGAGA A Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM3211 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3211 is therefore inhibition of FLNB, a GAM3211 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM3211 B FPRL1 TCACTGTTCCTTTTT GTTGAGA A FPRL1 (Accession NM_001462.1) is another GAM3211 target gene. FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3211 is therefore inhibition of

FPRL1. Accordingly, utilities of GAM3211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM3211 IGF1 TCACTGTTCCTTTTT GTTGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3211 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3211 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM3211 is therefore inhibition of IGF1, a GAM3211 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3227 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3227 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3227 is therefore inhibition of APPBP2, a GAM3227 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3227 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM3227 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3227 is therefore inhibition of BACE2, a GAM3227 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3227 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM3227 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3227 is therefore inhibition of FHL2, a GAM3227 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3227 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM3227 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3227 is therefore inhibition of IGF1, a GAM3227 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3227 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM3227 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3227 is therefore inhibition of MME, a GAM3227 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3227 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM3227 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM3227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3227 is therefore inhibition of PRND, a GAM3227 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3236 CRYAB TTCAAGAAAGCCAAG CRYAB (Accession NM_001885.1) is a GAM3236 target gene. CRYAB A A

ATGGCTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRYAB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRYAB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3236 is therefore inhibition of CRYAB. Accordingly, utilities of GAM3236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRYAB.

GAM3236 GLUL TTCAAGAAAGCCAAG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

ATGGCTG NM_002065.3) is another GAM3236 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3236 is therefore inhibition of GLUL, a GAM3236 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM3236 NOTCH1 TTCAAGAAAGCCAAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

ATGGCTG (NOTCH1, Accession NM_017617.2) is another GAM3236 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3236 is therefore inhibition of NOTCH1, a GAM3236 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM3263 AVP TTGCCTGGAGACATT AVP (Accession NM_000490.2) is a GAM3263 target gene. AVP A A

TCTACTG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3263 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3263 is therefore inhibition of AVP. Accordingly, utilities of GAM3263 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with AVP.

GAM3263 GYPA TTGCCTGGAGACATT Glycophorin A (includes MN blood group) (GYPA, Accession A A
TCTACTG NM_002099.2) is another GAM3263 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3263 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3263 is therefore inhibition of GYPA, a GAM3263 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3263 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3266 BACE AAGCAGCCTTGGACC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
AGGAGGG is a GAM3266 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3266 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3266 is therefore inhibition of BACE, a GAM3266 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3266 IL1A AAGCAGCCTTGGACC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
AGGAGGG GAM3266 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3266 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3266 is therefore inhibition of IL1A, a GAM3266 target gene which stimulates thymocyte proliferation

by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3271 TNF TTCTACTAGTGGTTG ATGGCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is a GAM3271 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3271 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3271 is therefore inhibition of TNF, a GAM3271 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM3271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3293 APPBP2 CTCTTGAAGGAGTAT TTGTGTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3293 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3293 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3293 is therefore inhibition of APPBP2, a GAM3293 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3293 GAL AGCAAAAGCCATGCC CAGGAGA Galanin (GAL, Accession NM_015973.2) is another GAM3293 target gene. GAL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GAL BINDING SITE, B A

and secondary structure complementarity to the nucleotide sequence of GAM3293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3293 is therefore inhibition of GAL, a GAM3293 target gene which stimulates LH secretion and enhances LHRH- induced LH release from dispersed anterior pituitary cells in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GAL.The function of GAL has been established by previous studies. Galanin is a 29- amino acid peptide widely distributed in the peripheral and central nervous systems. In the brain, the highest concentrations are observed in the hypothalamus and particularly in the nerve terminals of the median eminence. Since the establishment of the neurovascular concept in the regulation of the hypothalamus- pituitary axis (Harris, 1948), it is well known that the median eminence represents a key area for neuroendocrine regulation. Hypothalamic releasing and inhibiting factors are secreted from median eminence terminals into the portal circulation to reach the adenohypophyseal cells where they exert specific actions. Lopez et al. (1991) presented evidence that galanin meets the criteria to be considered a hypothalamic-hypophysiotropic hormone. They found a possibly meaningful colocalization and cosecretion of galanin and LHRH (OMIM Ref. No. 152760). Galanin stimulates LH secretion and enhances LHRH- induced LH release from dispersed anterior pituitary cells in vitro. Galanin is important to gastrointestinal function also (Rattan, 1991). Animal model experiments lend further support to the function of GAL. The neuropeptide galanin is predominantly expressed by the lactotrophs (the prolactin- secreting cell type) in the rodent anterior pituitary and in the median eminence and paraventricular nucleus of the hypothalamus. Prolactin (PRL; 176760) and galanin colocalize in the same secretory granule, and the expression of both proteins is extremely sensitive to the estrogen status of the animal. Administration of estradiol- 17- beta induces pituitary hyperplasia followed by adenoma formation and causes a 3,000- fold increase in the galanin mRNA content of the lactotroph. To further study the role of galanin in prolactin release and lactotroph growth, Wynick et al. (1998) generated mice carrying a loss- of-function mutation of the endogenous galanin gene. There was no evidence of embryonic lethality and the mutant mice grew normally. The specific endocrine abnormalities identified related to the expression of prolactin. Pituitary prolactin message levels and protein content of adult female mutant mice were reduced by 30 to 40% compared with wildtype controls. Mutant females failed to lactate and pups died of starvation/dehydration unless fostered onto wildtype mothers. Prolactin secretion in mutant females was markedly reduced at 7 days postpartum compared with wildtype controls with an associated failure in mammary gland maturation. There was almost

complete abrogation of the proliferative response of the lactotroph to high doses of estrogen, with a failure to upregulate prolactin release and STAT5 (OMIM Ref. No. 601511) expression or to increase pituitary cell number. These data supported the hypothesis that galanin acts as a paracrine regulator of prolactin expression and as a growth factor to the lactotroph.

It is appreciated that the abovementioned animal model for GAL is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Wynick, D.; Small, C. J.; Bacon, A.; Holmes, F. E.; Norman, M.; Ormandy, C. J.; Kilic, E.; Kerr, N. C. H.; Ghatei, M.; Talamantes, F.; Bloom, S. R.; Pachnis, V. : Galanin regulates prolactin release and lactotroph proliferation. Proc. Nat. Acad. Sci. 95: 12671-12676, 1998. ; and

Lopez, F. J.; Merchenthaler, I.; Ching, M.; Wisniewski, M. G.; Negro- Vilar, A. : Galanin: a hypothalamic- hypophysiotropic hormone modulating reproductive functions. Proc. Nat. Acad. Sci.

Further studies establishing the function and utilities of GAL are found in John Hopkins OMIM database record ID 137035, and in cited publications listed in Table 9, hereby incorporated herein.

GAM3293 IGF1 AGCAAAAGCCATGCC CAGGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3293 target gene. IGF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3293 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM3293 is therefore inhibition of IGF1, a GAM3293 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3298 APP AAAGTGCTCATAGTG APP (Accession NM_000484.1) is a GAM3298 target gene. APP A A

CAGGTAG BINDING SITE1 and APP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE1 and APP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3298 is therefore inhibition of APP. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM3298 MTNR1A AAAGTGCTCATAGTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CAGGTAG another GAM3298 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of MTNR1A, a GAM3298 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM3298 PRND AAAGTGCTCATAGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CAGGTAG another GAM3298 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of PRND, a GAM3298 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3298 PSEN1 AAAGTGCTCATAGTG PSEN1 (Accession NM_000021.2) is another GAM3298 target gene.
A A

CAGGTAG PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of PSEN1. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM3298 TGFB1 AAAGTGCTCATAGTG TGFB1 (Accession NM_000660.1) is another GAM3298 target gene.
A A

CAGGTAG TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3298 TRPM2 AAAGTGCTCATAGTG TRPM2 (Accession NM_003307.1) is another GAM3298 target gene.
A A

CAGGTAG TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of TRPM2, a GAM3298 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3298 UBB AAAGTGCTCATAGTG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM3298 A
A

CAGGTAG target gene. UBB BINDING SITE1 and UBB BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by UBB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE1 and UBB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3298 is therefore inhibition of UBB, a GAM3298 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB has been established by previous studies. Ubiquitin (see OMIM Ref. No. 191320) may be evolution's most conserved protein, presumably because of its role in several important cellular processes. By in situ hybridization, Webb et al. (1990) assigned the 3- coding unit polyubiquitin gene UBB and its nonprocessed pseudogene to 17p12- p11.1. See also ubiquitin C (OMIM Ref. No. 191340). The protein deposits in neurofibrillary tangles, neuritic plaques, and neuropil threads in the cerebral cortex of patients with Alzheimer disease (AD; 104300) and Down syndrome (OMIM Ref. No. 190685) contain forms of beta- amyloid precursor protein (APP; 104760) and ubiquitin- B that are aberrant in the C terminus. These proteins are not found in young control subjects, whereas the presence of anomalous UBB in elderly control patients may indicate early stages of neurodegeneration. The 2 species of aberrant proteins were found by van Leeuwen et al. (1998) to display cellular colocalization, suggesting a common origin, operating at the transcriptional level or by posttranscriptional editing of RNA. This type of transcript mutation is likely an important factor in the widely occurring nonfamilial early- and late- onset forms of AD. The aberrant proteins were not found in patients with Parkinson disease (OMIM Ref. No. 168600). Using 2 different sensitive approaches, van Leeuwen et al. (1998) failed to find any indication of the mutation at the genomic level. The finding that frameshift mutations occur in multiple proteins within the same neuron suggested that a common denominator in the transcription- propagating events was involved. The mechanism of transcript mutation, which was a dinucleotide deletion (delta- GA, delta- GT, or delta- CT), was unclear. The frequently mutated motif in exon 9 of the APP gene, GAGAGAGA, is an extended version of the GAGAG in the vasopressin gene (OMIM Ref. No. 192340), which shows a GA deletion in vasopressin transcripts of the homozygous Brattleboro rats with diabetes insipidus. The authors commented that transcript mutations may be a widely occurring phenomenon. In principle, each transcript containing a susceptible motif, such as GAGAG, could undergo such a process. Van Leeuwen et al. (1998) stated that the process is probably not limited to postmitotic cells; however, postmitotic neurons are less capable of compensating for transcript- modifying activity and are thus particularly sensitive to the accumulation of frameshifted proteins.

Thus, during aging, single neurons may generate and accumulate abnormal proteins, consequently leading to cellular disturbances and causing degeneration. The mechanism of dinucleotide deletion at the transcript level may well underlie a number of neurodegenerative pathologies

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

van Leeuwen, F. W.; de Kleijn, D. P. V.; van den Hurk, H. H.; Neubauer, A.; Sonnemans, M. A. F.; Sluijs, J. A.; Koycu, S.; Ramdjielal, R. D. J.; Salehi, A.; Martens, G. J. M.; Grosveld, F. G.; Burbach, J. P. H.; Hol, E. M. : Frameshift mutants of beta-amyloid precursor protein and ubiquitin- B in Alzheimer's and Down patients. Science 279: 242- 247, 1998. ; and

Webb, G. C.; Baker, R. T.; Fagan, K.; Board, P. G. : Localization of the human UbB polyubiquitin gene to chromosome band 17p11.1- 17p12. Am. J. Hum. Genet. 46: 308- 315, 1990.

Further studies establishing the function and utilities of UBB are found in John Hopkins OMIM database record ID 191339, and in cited publications listed in Table 9, hereby incorporated herein.

GAM3311 A ACAGATA FOS GTGTGTGATAAGGAC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is a GAM3311 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3311 is therefore inhibition of FOS, a GAM3311 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM3311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM3311 A ACAGATA MPO GTGTGTGATAAGGAC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM3311 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence

of GAM3311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3311 is therefore inhibition of MPO, a GAM3311 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM3311 FLNB GTCTGCTGTCTACAC TACACAC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM3311 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3311 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM3311 is therefore inhibition of FLNB, a GAM3311 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM3330 BACE2 ATAACTGTGAAGAGG CAATTGT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is a GAM3330 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3330 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3330 is therefore inhibition of BACE2, a GAM3330 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3350 APPBP2 TGCAGATACATGTGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
AACTGAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3350 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3350 is therefore inhibition of APPBP2, a GAM3350 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3350 ARHA TGCAGATACATGTGT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A
AACTGAA is another GAM3350 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3350 is therefore inhibition of ARHA, a GAM3350 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM3350 DLST TGCAGATACATGTGT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
AACTGAA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM3350 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3350 is therefore inhibition of DLST, a GAM3350 target gene which catalyzes the oxidative

decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3368 HTR2A GATTTTCATAGGAGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

AGAAACC NM_000621.1) is a GAM3368 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3368 is therefore inhibition of HTR2A, a GAM3368 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM3414 IL1A TGGAGAAATTATATT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a GAM3414 A A

TTACTAA target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3414 is therefore inhibition of IL1A, a GAM3414 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3414 PLAU TGGAGAAATTATATT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

TTACTAA is another GAM3414 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3414 is therefore inhibition of PLAU, a GAM3414 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM3414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM3422 MME TCTTTTTTGGGAGAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGAGTCG enkephalinase, (MME, Accession NM_000902.2) is a GAM3422 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3422 is therefore inhibition of MME, a GAM3422 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3426 DHCR24 TCACCCAGTGTAAAC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

AGCATGA NM_014762.1) is a GAM3426 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3426 is therefore inhibition of DHCR24, a GAM3426 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3426 PLAU TCACCCAGTGTAAAC Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

AGCATGA is another GAM3426 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3426 is therefore inhibition of PLAU, a GAM3426 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM3426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM3431 APPBP2 TAATACTGCCGGGTA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

ATGATGG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3431 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3431 is therefore inhibition of APPBP2, a GAM3431 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3431 BACE TAATACTGCCGGGTA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

ATGATGG is another GAM3431 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3431 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

Another function of GAM3431 is therefore inhibition of BACE, a GAM3431 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3452 GFAP GCCTTTCCTCCAGAA GFAP (Accession NM_002055.2) is a GAM3452 target gene. GFAP A A
CTGCTCC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3452 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3452 is therefore inhibition of GFAP. Accordingly, utilities of GAM3452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM3452 OGDH GCCTTTCCTCCAGAA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
CTGCTCC NM_002541.1) is another GAM3452 target gene. OGDH BINDING SITE1 and OGDH BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 and OGDH BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3452 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3452 is therefore inhibition of OGDH, a GAM3452 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM3461 APPBP2 TATTACATTCATTTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GATGGTT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3461 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3461 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3461 is therefore inhibition of APPBP2, a GAM3461 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3461 IL1A TATTACATTCATTTT GATGGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM3461 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3461 is therefore inhibition of IL1A, a GAM3461 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3463 SNCA CACAATATAGCAAAT AGAGGGT SNCA (Accession NM_000345.2) is a GAM3463 target gene. SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3463 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3463 is therefore inhibition of SNCA. Accordingly, utilities of GAM3463 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM3479 ADAMTS5 TACAGGCAGGCACAG AGGCAGT A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM3479 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` A A

untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3479 is therefore inhibition of ADAMTS5, a GAM3479 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM3479 APBA2 TACAGGCAGGCACAG AGGCAGT A A Amyloid Beta (A4) Precursor Protein- binding, Family A, Member 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM3479 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3479 is therefore inhibition of APBA2, a GAM3479 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM3479 DLST TACAGGCAGGCACAG AGGCAGT A A Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM3479 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3479 is therefore inhibition of DLST, a GAM3479 target gene which catalyzes the oxidative

decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3479 NGB TACAGGCAGGCACAG Neuroglobin (NGB, Accession NM_021257.2) is another GAM3479 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A

AGGCAGT

Another function of GAM3479 is therefore inhibition of NGB, a GAM3479 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM3479 SNCG TACAGGCAGGCACAG SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM3479 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A

AGGCAGT

Another function of GAM3479 is therefore inhibition of SNCG, a GAM3479 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM3479 TFCP2 TACAGGCAGGCACAG Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM3479 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I,

A A

AGGCAGT

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3479 is therefore inhibition of TFCP2, a GAM3479 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM3479 TGFB1 TACAGGCAGGCACAG TGFB1 (Accession NM_000660.1) is another GAM3479 target gene. A A

AGGCAGT TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3479 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3486 OGDH TTAGTGTTCAGGCTC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

AAATGAA NM_002541.1) is a GAM3486 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3486 is therefore inhibition of OGDH, a GAM3486 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM3486 SNCA TTAGTGTTCAGGCTC SNCA (Accession NM_000345.2) is another GAM3486 target gene. A A

AAATGAA SNCA BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3486 is therefore inhibition of SNCA. Accordingly, utilities of GAM3486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM3513 ADAM17 CACTGCAAGCTCCAC CTCCCGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is a GAM3513 target gene. ADAM17 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3513 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3513 is therefore inhibition of ADAM17, a GAM3513 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3513 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3513 IAPP CACTGCAAGCTCCAC CTCCCGG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM3513 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3513 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3513 is therefore inhibition of IAPP, a GAM3513 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3513 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3535 APPBP2 TCATTGGTTGCATAA TTTGATC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM3535 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3535 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3535 is therefore inhibition of APPBP2, a GAM3535 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3593 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM3593 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3593 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3593 is therefore inhibition of APP. Accordingly, utilities of GAM3593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM3595 ADAM10 AGGCTGCAGTGTAGT GGCATGA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is a GAM3595 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3595 is therefore inhibition of ADAM10, a GAM3595 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM1300.

GAM3595 A ADAM17 AGGCTGCAGTGTAGT A A GGCATGA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is another GAM3595 target gene. ADAM17 BINDING SITE1 through ADAM17 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADAM17, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE1 through ADAM17 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3595 is therefore inhibition of ADAM17, a GAM3595 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3595 A FPRL1 AGGCTGCAGTGTAGT A A GGCATGA FPRL1 (Accession NM_001462.1) is another GAM3595 target gene. FPRL1 BINDING SITE1 and FPRL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FPRL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE1 and FPRL1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3595 is therefore inhibition of FPRL1. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM3595 A HADH2 AGGCTGCAGTGTAGT A A GGCATGA Hydroxyacyl- Coenzyme A Dehydrogenase, Type II (HADH2, Accession NM_004493.1) is another GAM3595 target gene. HADH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HADH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HADH2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3595 is therefore inhibition of HADH2, a GAM3595 target gene which catalyzes the reversible oxidation of L- 3- hydroxyacyl- CoAs to form 3- ketoacyl- CoAs and binds intracellular amyloid- beta. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HADH2.The function of HADH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1820.

GAM3595 NCKAP1 AGGCTGCAGTGTAGT NCKAP1 (Accession NM_013436.2) is another GAM3595 target gene. A A
GGCATGA NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3595 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM3595 PRND AGGCTGCAGTGTAGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGCATGA another GAM3595 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3595 is therefore inhibition of PRND, a GAM3595 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3605 ACE TTGTCAGAGGCTGGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
AGGGTGT (ACE, Accession NM_152831.1) is a GAM3605 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3605 is therefore inhibition of ACE, a

GAM3605 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3605 CTNND2 TTGTCAGAGGCTGGT AGGGTGT Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM3605 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3605 is therefore inhibition of CTNND2, a GAM3605 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM3605 DLST TTGTCAGAGGCTGGT AGGGTGT Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM3605 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3605 is therefore inhibition of DLST, a GAM3605 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3605 SNCA TTGTCAGAGGCTGGT AGGGTGT SNCA (Accession NM_000345.2) is another GAM3605 target gene. SNCA BINDING SITE is a target binding site found in the 3` A A

untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3605 is therefore inhibition of SNCA. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM3605 APLP2 GCAGCTCCCTATTCC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession B A
ATGACAG NM_001642.1) is another GAM3605 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3605 is therefore inhibition of APLP2, a GAM3605 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM3605 HD GCAGCTCCCTATTCC HD (Accession NM_002111.3) is another GAM3605 target gene. HD B A
ATGACAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3605 is therefore inhibition of HD. Accordingly, utilities of GAM3605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM3630 MAPK10 ACTGGCACAGACATC Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
TGTCAAG NM_138981.1) is a GAM3630 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and

secondary structure complementarity to the nucleotide sequence of GAM3630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3630 is therefore inhibition of MAPK10, a GAM3630 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM3630 MTNR1A ACTGGCACAGACATC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

TGTCAAG another GAM3630 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3630 is therefore inhibition of MTNR1A, a GAM3630 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM3640 ARHA GGGGGATCATTATAA Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

AAATACT is a GAM3640 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3640 is therefore inhibition of ARHA, a GAM3640 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM3640 BACE GGGGGATCATTATAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

AAATACT is another GAM3640 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3640 is therefore inhibition of BACE, a GAM3640 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3640 CASP3 GGGGGATCATTATAA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

AAATACT Accession NM_032991.1) is another GAM3640 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3640 is therefore inhibition of CASP3, a GAM3640 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM3640 CAV2 GGGGGATCATTATAA Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM3640 A A

AAATACT target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3640 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM3640 is therefore inhibition of CAV2, a GAM3640 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM3666 CNTF AGCTGAGAAAGCGAA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A GAGGTGG GAM3666 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3666 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3666 is therefore inhibition of CNTF, a GAM3666 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3666 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM3666 BACE CTACTTGTTCCTCTC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) B A ACCTCAA is another GAM3666 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3666 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3666 is therefore inhibition of BACE, a GAM3666 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3666 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3666 FPRL1 CTACTTGTTCCTCTC FPRL1 (Accession NM_001462.1) is another GAM3666 target gene. B A

ACCTCAA FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3666 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3666 is therefore inhibition of FPRL1. Accordingly, utilities of GAM3666 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM3691 BACE2 CTGGGCTCTGGTCTG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TAGGTTT NM_138991.1) is a GAM3691 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3691 is therefore inhibition of BACE2, a GAM3691 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3691 TNF CTGGGCTCTGGTCTG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

TAGGTTT Accession NM_000594.2) is another GAM3691 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3691 is therefore inhibition of TNF, a GAM3691 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM3691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3691 ABCD1 ATGACCTGCAGTCAG ABCD1 (Accession NM_000033.2) is another GAM3691 target gene. B A

GGCCCAG ABCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3691 is therefore inhibition of ABCD1. Accordingly, utilities of GAM3691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM3747 A2M TGGCACAGATCAGCA Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a A A

GAACAGG GAM3747 target gene. A2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3747 is therefore inhibition of A2M, a GAM3747 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM3747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM3747 BACE2 TGGCACAGATCAGCA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GAACAGG NM_138991.1) is another GAM3747 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3747 is therefore inhibition of BACE2, a GAM3747 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM3747 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM3747 A A DSCR1 TGGCACAGATCAGCA GAACAGG Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is another GAM3747 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3747 is therefore inhibition of DSCR1, a GAM3747 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM3747 A A OGDH TGGCACAGATCAGCA GAACAGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM3747 target gene. OGDH BINDING SITE1 and OGDH BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 and OGDH BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3747 is therefore inhibition of OGDH, a GAM3747 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM3768 A A CASP3 ATGAGAGTAGGAGTT TGGGCTC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is a GAM3768 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3768 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3768 is therefore inhibition of CASP3, a GAM3768 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM3768 IGF1 ATGAGAGTAGGAGTT TGGGCTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3768 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3768 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3768 is therefore inhibition of IGF1, a GAM3768 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3768 MAPT ATGAGAGTAGGAGTT TGGGCTC Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM3768 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3768 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3768 is therefore inhibition of MAPT, a GAM3768 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM144.

GAM3781 BCHE TTCTGTGCAGGTTAA A A
CATTTCT
BCHE (Accession NM_000055.1) is a GAM3781 target gene. BCHE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3781 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3781 is therefore inhibition of BCHE. Accordingly, utilities of GAM3781 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM3781 TNF TTCTGTGCAGGTTAA A A
CATTTCT
Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM3781 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3781 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3781 is therefore inhibition of TNF, a GAM3781 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM3781 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3788 DHCR24 TCACTTGCCTAGGGT A A
CACACAG
24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM3788 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3788 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3788 is therefore inhibition of DHCR24, a GAM3788 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3788 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM3788 IGF1 TCACTTGCCTAGGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CACACAG NM_000618.2) is another GAM3788 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3788 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3788 is therefore inhibition of IGF1, a GAM3788 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3788 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3788 PSEN2 TCACTTGCCTAGGGT PSEN2 (Accession NM_012486.1) is another GAM3788 target gene.
A A
CACACAG PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3788 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3788 is therefore inhibition of PSEN2. Accordingly, utilities of GAM3788 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM3810 ADAMTS5 TGGAGAGAAAGCGAA A Disintegrin- like and Metalloprotease (reprolysin type) with A A
GATGTAG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM3810 target gene. ADAMTS5 BINDING SITE1 and ADAMTS5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ADAMTS5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE1 and ADAMTS5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3810 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3810 is therefore inhibition of ADAMTS5, a GAM3810 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3810 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM3810 CTSK TGGAGAGAAAGCGAA A A GATGTAG CTSK (Accession NM_000396.2) is another GAM3810 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3810 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3810 is therefore inhibition of CTSK. Accordingly, utilities of GAM3810 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM3810 IGF1 TGGAGAGAAAGCGAA A A GATGTAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3810 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3810 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3810 is therefore inhibition of IGF1, a GAM3810 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3810 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3890 ACE GGTCCACAAGGGGAG A A AGCAGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM3890 target gene. ACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3890 is therefore inhibition of ACE, a

GAM3890 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3890 ADAMTS5 GGTCCACAAGGGGAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A
AGCAGGG Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM3890 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of ADAMTS5, a GAM3890 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM3890 CLU GGTCCACAAGGGGAG Clusterin (complement lysis inhibitor, SP- 40,40, sulfated A A
AGCAGGG glycoprotein (CLU, Accession NM_001831.1) is another GAM3890 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of CLU, a GAM3890 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM3890 CTSK GGTCCACAAGGGGAG CTSK (Accession NM_000396.2) is another GAM3890 target gene. A A
AGCAGGG CTSK BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of CTSK. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM3890 DLST GGTCCACAAGGGGAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

AGCAGGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM3890 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of DLST, a GAM3890 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM3890 GFAP GGTCCACAAGGGGAG GFAP (Accession NM_002055.2) is another GAM3890 target gene. A A

AGCAGGG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of GFAP. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM3890 MAPT GGTCCACAAGGGGAG Microtubule- associated Protein Tau (MAPT, Accession A A

AGCAGGG NM_173727.1) is another GAM3890 target gene. MAPT BINDING SITE1 through MAPT BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by

MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 through MAPT BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of MAPT, a GAM3890 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM3890 MT3 GGTCCACAAGGGGAG Metallothionein 3 (MT3, Accession NM_005954.1) is another A A AGCAGGG GAM3890 target gene. MT3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MT3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of MT3, a GAM3890 target gene which inhibits survival and neurite formation of cortical neurons in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MT3.The function of MT3 has been established by previous studies. Uchida et al. (1991) identified a growth inhibitory factor in human brain and purified it to homogeneity. It was found to be a 68- amino acid protein with high homology to the metallothioneins (see OMIM Ref. No. 156350). The central domain of GIFB, amino acid residues 11- 39, showed the highest homology to MT2A (OMIM Ref. No. 156360). There were, however, 3- bp and 18- bp insertions in the coding sequence for the amino- terminal and carboxy- terminal domains, respectively, in comparison with MT2A. Such insertions had, it seemed, never been observed in vertebrate metallothioneins. By Southern blot analysis of somatic cell hybrids, Tsuji et al. (1992) determined that, like the metallothioneins, GIFB is located on human chromosome 16. In contrast to metallothioneins, GIFB was found to be expressed exclusively in the nervous system. The GIFB protein produced in an E. coli expression vector system inhibited the growth of neonatal rat cortical neurons. Northern blot analysis demonstrated that expression of the GIFB mRNA is drastically decreased in brain tissue from patient's with Alzheimer disease

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Tsuji, S.; Kobayashi, H.; Uchida, Y.; Ihara, Y.; Miyatake, T. : Molecular cloning of human growth inhibitory factor cDNA and its down- regulation in Alzheimer's disease. EMBO J. 11: 4843- 4850, 1992. ; and

Uchida, Y.; Takio, K.; Titani, K.; Ihara, Y.; Tomonaga, M. : The growth inhibitory factor that is deficient in the Alzheimer's disease brain is a 68 amino acid metallothionein- like prot.

Further studies establishing the function and utilities of MT3 are found in John Hopkins OMIM database record ID 139255, and in cited publications listed in Table 9, hereby incorporated herein.

GAM3890 SLC17A7 GGTCCACAAGGGGAG A A AGCAGGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM3890 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of SLC17A7, a GAM3890 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM3890 TNF GGTCCACAAGGGGAG A A AGCAGGG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM3890 target gene. TNF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of TNF, a GAM3890 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM3890 TRPM2 GGTCCACAAGGGGAG TRPM2 (Accession NM_003307.1) is another GAM3890 target gene. A A
AGCAGGG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3890 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3890 is therefore inhibition of TRPM2, a GAM3890 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM3890 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3892 CNTF AAGTCACCTGAAAAC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A
TCAACTA GAM3892 target gene. CNTF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3892 is therefore inhibition of CNTF, a GAM3892 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM3946 ACE TTGCCCAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TGCAGTG (ACE, Accession NM_152831.1) is a GAM3946 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3946 is therefore inhibition of ACE, a GAM3946 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3946 ADAM17 TTGCCCAGGCTGGAG TGCAGTG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is another GAM3946 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3946 is therefore inhibition of ADAM17, a GAM3946 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3946 CHAT TTGCCCAGGCTGGAG TGCAGTG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is another GAM3946 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3946 is therefore inhibition of CHAT, a GAM3946 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM3946 FLNB TTGCCCAGGCTGGAG TGCAGTG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM3946 target gene. FLNB BINDING SITE is a A A

target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of FLNB, a GAM3946 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM3946 HTR2A TTGCCCAGGCTGGAG A A TGCAGTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM3946 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of HTR2A, a GAM3946 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM3946 IAPP TTGCCCAGGCTGGAG A A TGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM3946 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of IAPP, a GAM3946 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3946 NOTCH1 TTGCCCAGGCTGGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGCAGTG (NOTCH1, Accession NM_017617.2) is another GAM3946 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of NOTCH1, a GAM3946 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM3946 TGFB1 TTGCCCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM3946 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of TGFB1. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM3946 ADAM17 CACTGCAACCTCCAC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis B A

CTCCTGG factor, (ADAM17, Accession NM_003183.3) is another GAM3946 target gene. ADAM17 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3946 is therefore inhibition of

ADAM17, a GAM3946 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3946 IAPP CACTGCAACCTCCAC CTCCTGG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM3946 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM3946 is therefore inhibition of IAPP, a GAM3946 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3946 OGDH CACTGCAACCTCCAC CTCCTGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM3946 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3946 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM3946 is therefore inhibition of OGDH, a GAM3946 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM3978 GFAP TTTACAGATGGCAAA GATCTGG GFAP (Accession NM_002055.2) is a GAM3978 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of A A

Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM3978 is therefore inhibition of GFAP. Accordingly, utilities of GAM3978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM3978 IGF1 TTTACAGATGGCAAA GATCTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3978 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM3978 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3978 is therefore inhibition of IGF1, a GAM3978 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3990 ACE TTGCCTAGGCTGGAG TGCAGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM3990 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM3990 is therefore inhibition of ACE, a GAM3990 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM3990 ADAM17 TTGCCTAGGCTGGAG TGCAGTG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is another GAM3990 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` A A

untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM3990 is therefore inhibition of ADAM17, a GAM3990 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM3990 IAPP TTGCCTAGGCTGGAG TGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM3990 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3990 is therefore inhibition of IAPP, a GAM3990 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM3990 IGF1 TTGCCTAGGCTGGAG TGCAGTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM3990 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3990 is therefore inhibition of IGF1, a GAM3990 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer,

and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM3990 MAPT TTGCCTAGGCTGGAG TGCAGTG Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM3990 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3990 is therefore inhibition of MAPT, a GAM3990 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM3990 NOTCH1 TTGCCTAGGCTGGAG TGCAGTG Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM3990 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM3990 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM3990 is therefore inhibition of NOTCH1, a GAM3990 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM3990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM4008 IL1A TTAGGGCAGGCATGA GAGAACT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide GAM4008 A A

sequence of GAM4008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4008 is therefore inhibition of IL1A, a GAM4008 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM4008 TNFSF5 TTAGGGCAGGCATGA TNFSF5 (Accession NM_000074.1) is another GAM4008 target gene. A A

GAGAACT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4008 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM4008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM4011 ACHE TGTGTTGGAGCAGAG Acetylcholinesterase (YT blood group) (ACHE, Accession A A

GCAGGGG NM_015831.1) is a GAM4011 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4011 is therefore inhibition of ACHE, a GAM4011 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM4011 APBB1 TGTGTTGGAGCAGAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GCAGGGG 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM4011 target

gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of APBB1, a GAM4011 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4011 BACE2 TGTGTTGGAGCAGAG GCAGGGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM4011 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4011 is therefore inhibition of BACE2, a GAM4011 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4011 CAV1 TGTGTTGGAGCAGAG GCAGGGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM4011 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4011 is therefore inhibition of CAV1, a GAM4011 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and

therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM4011 A A CRAT TGTGTTGGAGCAGAG GCAGGGG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is another GAM4011 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of CRAT, a GAM4011 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM4011 A A GFAP TGTGTTGGAGCAGAG GCAGGGG GFAP (Accession NM_002055.2) is another GAM4011 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of GFAP. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4011 A A HTR2C TGTGTTGGAGCAGAG GCAGGGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM4011 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of

HTR2C, a GAM4011 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4011 IGF1 TGTGTTGGAGCAGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCAGGGG NM_000618.2) is another GAM4011 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of IGF1, a GAM4011 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4011 OGDH TGTGTTGGAGCAGAG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

GCAGGGG NM_002541.1) is another GAM4011 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4011 is therefore inhibition of OGDH, a GAM4011 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM4020 APBA2 ATTTGAGGAGGCTTT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

ACAGCCA 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM4020 target gene. APBA2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4020 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4020 is therefore inhibition of APBA2, a GAM4020 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4020 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM4020 A A PSEN1 ATTTGAGGAGGCTTT ACAGCCA PSEN1 (Accession NM_007319.1) is another GAM4020 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4020 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4020 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4020 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4020 B A CTSB AGCTGTGAGCCTGCC TTCCAGT CTSB (Accession NM_147783.1) is another GAM4020 target gene. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4020 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4020 is therefore inhibition of CTSB. Accordingly, utilities of GAM4020 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM4020 A PRNP AGCTGTGAGCCTGCC TTCCAGT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM4020 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4020 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4020 is therefore inhibition of PRNP, a GAM4020 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4020 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM4027 ABCD1 TTCCTGGTGGAGGCA ABCD1 (Accession NM_000033.2) is a GAM4027 target gene. ABCD1 A A
TTCGGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4027 is therefore inhibition of ABCD1. Accordingly, utilities of GAM4027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM4027 BLMH TTCCTGGTGGAGGCA Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another A A
TTCGGAG GAM4027 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4027 is therefore inhibition of BLMH, a GAM4027 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM4027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM4064 APLP2 TGGTCCAGAGGAGGA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

ATGAGGG NM_001642.1) is a GAM4064 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4064 is therefore inhibition of APLP2, a GAM4064 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM4064 BACE TGGTCCAGAGGAGGA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

ATGAGGG is another GAM4064 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of BACE, a GAM4064 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4064 DHCR24 TGGTCCAGAGGAGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A

ATGAGGG NM_014762.1) is another GAM4064 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of DHCR24, a GAM4064 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4064 A A GFAP TGGTCCAGAGGAGGA ATGAGGG GFAP (Accession NM_002055.2) is another GAM4064 target gene. GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of GFAP. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4064 A A NGB TGGTCCAGAGGAGGA ATGAGGG Neuroglobin (NGB, Accession NM_021257.2) is another GAM4064 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of NGB, a GAM4064 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM4064 A A OGDH TGGTCCAGAGGAGGA ATGAGGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM4064 target gene. OGDH BINDING SITE1 through OGDH BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 through OGDH BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of

OGDH, a GAM4064 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM4064 PSEN1 TGGTCCAGAGGAGGA A A ATGAGGG PSEN1 (Accession NM_007318.1) is another GAM4064 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4064 TRPM2 TGGTCCAGAGGAGGA A A ATGAGGG TRPM2 (Accession NM_003307.1) is another GAM4064 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4064 is therefore inhibition of TRPM2, a GAM4064 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM4064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM4074 NCKAP1 TACGCTGTGCTGTGA A A CATGGTA NCKAP1 (Accession NM_013436.2) is a GAM4074 target gene. BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4074 is therefore inhibition of NCKAP1.

Accordingly, utilities of GAM4074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM4074 A A TRPM2 CATGGTA TACGCTGTGCTGTGA TRPM2 (Accession NM_003307.1) is another GAM4074 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4074 is therefore inhibition of TRPM2, a GAM4074 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM4074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM4085 A A CTNND2 CACTCAG TGTAAACATCCCACA Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM4085 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4085 is therefore inhibition of CTNND2, a GAM4085 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM4085 A A TFCP2 CACTCAG TGTAAACATCCCACA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM4085 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4085 is therefore inhibition of TFCP2, a GAM4085 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM4130 DHCR24 GGGCCATGACAGGGA A A GATAGGC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM4130 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4130 is therefore inhibition of DHCR24, a GAM4130 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4130 MPO GGGCCATGACAGGGA A A GATAGGC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM4130 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4130 is therefore inhibition of MPO, a GAM4130 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM4130 PSEN2 GGGCCATGACAGGGA A A GATAGGC PSEN2 (Accession NM_000447.1) is another GAM4130 target gene. PSEN2 BINDING SITE is a target binding site found in the 5`

untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4130 is therefore inhibition of PSEN2. Accordingly, utilities of GAM4130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM4130 SNCB GGGCCATGACAGGGA GATAGGC Synuclein, Beta (SNCB, Accession NM_003085.2) is another GAM4130 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4130 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4130 is therefore inhibition of SNCB, a GAM4130 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM4130 TGFB1 GGGCCATGACAGGGA GATAGGC TGFB1 (Accession NM_000660.1) is another GAM4130 target gene. TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4130 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4130 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4136 ADAM17 CCAAAGTGCTAGGAT TACAGCC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM4136 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide A A

sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4136 is therefore inhibition of ADAM17, a GAM4136 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4136 CRAT CCAAAGTGCTAGGAT Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A
TACAGCC another GAM4136 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4136 is therefore inhibition of CRAT, a GAM4136 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM4136 HTR2A CCAAAGTGCTAGGAT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
TACAGCC NM_000621.1) is another GAM4136 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4136 is therefore inhibition of HTR2A, a GAM4136 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM593.

GAM4136 IAPP CCAAAGTGCTAGGAT A A TACAGCC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM4136 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4136 is therefore inhibition of IAPP, a GAM4136 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4136 MTNR1A CCAAAGTGCTAGGAT A A TACAGCC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM4136 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4136 is therefore inhibition of MTNR1A, a GAM4136 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM4136 TGFB1 CCAAAGTGCTAGGAT A A TACAGCC TGFB1 (Accession NM_000660.1) is another GAM4136 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4136 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4142 FHL2 TCTTTGATCTCTTCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGGCTT a GAM4142 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4142 is therefore inhibition of FHL2, a GAM4142 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4142 GYPA TCTTTGATCTCTTCC Glycophorin A (includes MN blood group) (GYPA, Accession A A
GGGGCTT NM_002099.2) is another GAM4142 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4142 is therefore inhibition of GYPA, a GAM4142 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4142 SLC6A4 TCTTTGATCTCTTCC Solute Carrier Family 6 (neurotransmitter transporter, A A
GGGGCTT serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM4142 target gene. SLC6A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4142 is therefore inhibition of SLC6A4, a GAM4142 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM4147 CTSK AATCTCCATTTGTAA CTSK (Accession NM_000396.2) is a GAM4147 target gene. CTSK A A

ATGTGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4147 is therefore inhibition of CTSK. Accordingly, utilities of GAM4147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM4152 ACT ATGACCAGGAATTGA Activator of CAMP- responsive Element Modulator (CR (ACT, A A

GAGACTG Accession NM_020482.3) is a GAM4152 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4152 is therefore inhibition of ACT, a GAM4152 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM4152 ADAM17 ATGACCAGGAATTGA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GAGACTG factor, (ADAM17, Accession NM_003183.3) is another GAM4152 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM4152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4152 is therefore inhibition of ADAM17, a GAM4152 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4152 PRND ATGACCAGGAATTGA AA GAGACTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM4152 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4152 is therefore inhibition of PRND, a GAM4152 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4188 CAV2 GGAAGAATGTGCTTT AA TGTTGTT Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM4188 target gene. CAV2 BINDING SITE1 and CAV2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 and CAV2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4188 is therefore inhibition of CAV2, a GAM4188 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4188 CNTF GGAAGAATGTGCTTT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

TGTTGTT another GAM4188 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4188 is therefore inhibition of CNTF, a GAM4188 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM4188 ESR2 GGAAGAATGTGCTTT Estrogen Receptor 2 (ER beta) (ESR2, Accession NM_001437.1) is A A

TGTTGTT another GAM4188 target gene. ESR2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ESR2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4188 is therefore inhibition of ESR2, a GAM4188 target gene which transcriptional activator involved in regulation of reproduction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ESR2.The function of ESR2 has been established by previous studies. Estrogen receptor- beta (ESR2) is a member of the superfamily of nuclear receptors, which can transduce extracellular signals into transcriptional responses. Mosselman et al. (1996) identified and characterized a human estrogen receptor, which they called estrogen receptor- beta. ESR- beta is homologous to the previously identified ESR- alpha (OMIM Ref. No. 133430) and has an overlapping but nonidentical tissue distribution. The DNA- binding domain of ESR- beta is 96% conserved compared to ESR, and the ligand- binding domain shows 58% conserved residues. Northern blot analysis showed that ESR- beta is expressed in human thymus, spleen, ovary, and testis. Kuiper et al. (1996) identified ESR- beta from a rat prostate cDNA library. Rat ESR- beta is expressed in rat prostate and ovary and is homologous to rat ESR (95% conserved DNA- binding domain; 55% conserved ligand- binding domain). Mosselman et al. (1996) assigned the ESR2 gene to 14q by

study of somatic cell hybrids. Tsukamoto et al. (1998) used a CA repeat at the ESR2 locus to confirm mapping to 14q by linkage to a marker in a radiation hybrid mapping panel. Using PCR and FISH, Enmark et al. (1997) mapped the ESR2 gene to 14q22- q24. Forsell et al. (2001) investigated the CA repeat in intron 5 of the ESRB gene in 336 Alzheimer disease (AD; 104300) patients and in 110 healthy age- and gender- matched controls. There was no significant difference between AD patients and controls when all alleles were compared. However, a significant difference was found when allele 5 (OMIM Ref. No. 155 bp) was studied, as this allele was seen in 13.6% of the controls but only in 8.0% of the AD patients (p of 0.014). Supporting the hypothesis that allele 5 is implicated in the prevention of AD, no AD patient homozygous for this allele was seen, in contrast to 3 homozygous controls. Forsell et al. (2001) suggested that the intronic association identified could be in linkage disequilibrium with a mutation elsewhere in the ESRB gene. Animal model experiments lend further support to the function of ESR2. Zhu et al. (2002) showed that vascular smooth muscle cells and blood vessels from ESRB- deficient mice exhibited multiple functional abnormalities. In wildtype mouse blood vessels, estrogen attenuates vasoconstriction by an ESRB- mediated increase in inducible nitric oxide synthase expression. In contrast, estrogen augments vasoconstriction in blood vessels from ESRB- deficient mice.

It is appreciated that the abovementioned animal model for ESR2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

Mosselman, S.; Polman, J.; Dijkema, R. : ER- beta: identification and characterization of a novel human estrogen receptor. FEBS Lett. 392: 49- 53, 1996. ; and

Zhu, Y.; Bian, Z.; Lu, P.; Karas, R. H.; Bao, L.; Cox, D.; Hodgin, J.; Shaul, P. W.; Thoren, P.; Smithies, O.; Gustafsson, J.- A.; Mendelsohn, M. E. : Abnormal vascular function and hype.

Further studies establishing the function and utilities of ESR2 are found in John Hopkins OMIM database record ID 601663, and in cited publications listed in Table 9, hereby incorporated herein.

GAM4188 IGF1 GGAAGAATGTGCTTT TGTTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM4188 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4188 is therefore inhibition of IGF1, a GAM4188 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4188 IL1A GGAAGAATGTGCTTT TGTTGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM4188 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4188 is therefore inhibition of IL1A, a GAM4188 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM4188 MME GGAAGAATGTGCTTT TGTTGTT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is another GAM4188 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4188 is therefore inhibition of MME, a GAM4188 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM25.

GAM4188 MTNR1A GGAAGAATGTGCTTT A A TGTTGTT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM4188 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4188 is therefore inhibition of MTNR1A, a GAM4188 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM4188 SNCAIP GGAAGAATGTGCTTT A A TGTTGTT Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM4188 target gene. SNCAIP BINDING SITE1 and SNCAIP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SNCAIP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE1 and SNCAIP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4188 is therefore inhibition of SNCAIP, a GAM4188 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM4189 ABCD1 GTCCAGTGCTCACTG ABCD1 A A CCGACAT ABCD1 (Accession NM_000033.2) is a GAM4189 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4189 is therefore inhibition of ABCD1. Accordingly, utilities of GAM4189 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM4189 DHCR24 GTCCAGTGCTCACTG 24- dehydrocholesterol Reductase (DHCR24, Accession A A
CCGACAT NM_014762.1) is another GAM4189 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4189 is therefore inhibition of DHCR24, a GAM4189 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4189 GLUL GTCCAGTGCTCACTG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
CCGACAT NM_002065.3) is another GAM4189 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4189 is therefore inhibition of GLUL, a GAM4189 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM4199 APPBP2 GGGGGATGATAGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CCAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM4199 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4199 is therefore inhibition of APPBP2, a GAM4199 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4199 MTNR1A GGGGGATGATAGCAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is
A A
CCAG another GAM4199 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4199 is therefore inhibition of MTNR1A, a GAM4199 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM4199 GFAP CCTCTCCATGTACCC GFAP (Accession NM_002055.2) is another GAM4199 target gene.
B A
ATTCCCC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4199 is therefore inhibition of GFAP. Accordingly, utilities of GAM4199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4199 PSEN1 CCTCTCCATGTACCC PSEN1 (Accession NM_007318.1) is another GAM4199 target gene.
B A
ATTCCCC PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4199 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4199 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4205 MPO TCAGGTTCCTGATTG GAGTTCT Myeloperoxidase (MPO, Accession NM_000250.1) is a target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4205 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A A A

A function of GAM4205 is therefore inhibition of MPO, a GAM4205 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM4205 OLR1 TCAGGTTCCTGATTG GAGTTCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM4205 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4205 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4205 is therefore inhibition of OLR1, a GAM4205 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4238 APBA1 AGAGATAAAGAGGTT TAGGCAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member 1 (X11) (APBA1, Accession NM_001163.2) is a GAM4238 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING A A

SITE, and secondary structure complementarity to the nucleotide sequence of GAM4238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4238 is therefore inhibition of APBA1, a GAM4238 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4238 CNTF AGAGATAAAGAGGTT TAGGCAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM4238 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4238 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4238 is therefore inhibition of CNTF, a GAM4238 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM4243 DLST AAAGGCAGACGGTGA ATGCCTT Dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo- glutarat (DLST, Accession NM_001933.2) is a GAM4243 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4243 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4243 is therefore inhibition of DLST, a GAM4243 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM240.

GAM4243 A A GFAP AAAGGCAGACGGTGA ATGCCTTT GFAP (Accession NM_002055.2) is another GAM4243 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4243 is therefore inhibition of GFAP. Accordingly, utilities of GAM4243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4243 A A GYPA AAAGGCAGACGGTGA ATGCCTTT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM4243 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4243 is therefore inhibition of GYPA, a GAM4243 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4298 A A AGER TGGCAAGGTGTGGGC TAGAGAT Advanced Glycosylation End Product- specific Receptor (AGER, Accession NM_172197.1) is a GAM4298 target gene. AGER BINDING SITE1 and AGER BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by AGER, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE1 and AGER BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4298 is therefore inhibition of AGER, a GAM4298 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM4298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with AGER.The function of AGER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2350.

GAM4298 MAPT TGGCAAGGTGTGGGC TAGAGAT Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM4298 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4298 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4298 is therefore inhibition of MAPT, a GAM4298 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4298 TRPM2 TGGCAAGGTGTGGGC TAGAGAT TRPM2 (Accession NM_003307.1) is another GAM4298 target gene. A A

TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4298 is therefore inhibition of TRPM2, a GAM4298 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM4298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM4315 ACHE TAGCACCTTCTGAAA TAACGTG Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM4315 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4315 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4315 is therefore inhibition of ACHE, a GAM4315 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM4315 SNCA TAGCACCTTCTGAAA SNCA (Accession NM_000345.2) is another GAM4315 target gene. A A

TAACGTG SNCA BINDING SITE1 and SNCA BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SNCA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE1 and SNCA BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4315 is therefore inhibition of SNCA. Accordingly, utilities of GAM4315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM4364 APPBP2 AGGGTTGTTAGTTTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TTGGTTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM4364 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4364 is therefore inhibition of APPBP2, a GAM4364 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4364 IGF1 AGGGTTGTTAGTTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TTGGTTG NM_000618.2) is another GAM4364 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING

SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4364 is therefore inhibition of IGF1, a GAM4364 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4376 APLP2 GAGGTAGAGGTTGCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
GTGAGTC NM_001642.1) is a GAM4376 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4376 is therefore inhibition of APLP2, a GAM4376 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM4376 APPBP2 GAGGTAGAGGTTGCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GTGAGTC Protein 2 (APPBP2, Accession NM_006380.2) is another GAM4376 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of APPBP2, a GAM4376 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4376 BACE GAGGTAGAGGTTGCA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

GTGAGTC is another GAM4376 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of BACE, a GAM4376 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4376 CNTF GAGGTAGAGGTTGCA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

GTGAGTC another GAM4376 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of CNTF, a GAM4376 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM4376 DLST GAGGTAGAGGTTGCA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GTGAGTC oxo- glutarat (DLST, Accession NM_001933.2) is another GAM4376 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of DLST, a GAM4376 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM4376 FHL2 GAGGTAGAGGTTGCA A A GTGAGTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM4376 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of FHL2, a GAM4376 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4376 GYPA GAGGTAGAGGTTGCA A A GTGAGTC Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM4376 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of GYPA, a GAM4376 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4376 HTR2C GAGGTAGAGGTTGCA A A GTGAGTC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM4376 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of HTR2C, a GAM4376 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4376 IGF1 GAGGTAGAGGTTGCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GTGAGTC NM_000618.2) is another GAM4376 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of IGF1, a GAM4376 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4376 MAPK10 GAGGTAGAGGTTGCA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A GTGAGTC NM_002753.2) is another GAM4376 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of MAPK10, a GAM4376 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4376 MAPT GAGGTAGAGGTTGCA GTGAGTC Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM4376 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4376 is therefore inhibition of MAPT, a GAM4376 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4376 PRND GAGGTAGAGGTTGCA GTGAGTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM4376 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4376 is therefore inhibition of PRND, a GAM4376 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4376 TNF GAGGTAGAGGTTGCA GTGAGTC Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM4376 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure A A

complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of TNF, a GAM4376 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4376 TNFRSF6 GAGGTAGAGGTTGCA GTGAGTC A A

TNFRSF6 (Accession NM_000043.3) is another GAM4376 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4376 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM4377 CAV1 CCCTGGGCTGGTGTT TGACTTG A A

Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM4377 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4377 is therefore inhibition of CAV1, a GAM4377 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM4377 DHCR24 GAGTACAAATGAAGT CTGTGGG B A

24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM4377 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4377 is therefore inhibition of DHCR24, a GAM4377 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4377 OGDH GAGTACAAATGAAGT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession B A CTGTGGG NM_002541.1) is another GAM4377 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4377 is therefore inhibition of OGDH, a GAM4377 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM4382 ACHE TGACTGGAGGAAGGG Acetylcholinesterase (YT blood group) (ACHE, Accession A A AGGTAAG NM_015831.1) is a GAM4382 target gene. ACHE BINDING SITE1 and ACHE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACHE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE1 and ACHE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4382 is therefore inhibition of ACHE, a GAM4382 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM4382 BACE TGACTGGAGGAAGGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

AGGTAAG is another GAM4382 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4382 is therefore inhibition of BACE, a GAM4382 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4382 CASP3 TGACTGGAGGAAGGG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

AGGTAAG Accession NM_032991.1) is another GAM4382 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4382 is therefore inhibition of CASP3, a GAM4382 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM4382 DHCR24 TGACTGGAGGAAGGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

AGGTAAG NM_014762.1) is another GAM4382 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4382 is therefore inhibition of DHCR24, a GAM4382 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4382 NCSTN TGACTGGAGGAAGGG NCSTN (Accession NM_015331.1) is another GAM4382 target gene. A A

AGGTAAG NCSTN BINDING SITE1 and NCSTN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCSTN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE1 and NCSTN BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4382 is therefore inhibition of NCSTN, a GAM4382 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4382 NGB TGACTGGAGGAAGGG Neuroglobin (NGB, Accession NM_021257.2) is another GAM4382 A A

AGGTAAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4382 is therefore inhibition of NGB, a GAM4382 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM281.

GAM4382 SLC6A4 TGACTGGAGGAAGGG AGGTAAG Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM4382 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4382 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4382 is therefore inhibition of SLC6A4, a GAM4382 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM4398 APBA1 ATAGAAGAGCAGTGG GGTAGAA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member 1 (X11) (APBA1, Accession NM_001163.2) is a GAM4398 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4398 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4398 is therefore inhibition of APBA1, a GAM4398 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4398 IGF1 ATAGAAGAGCAGTGG GGTAGAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM4398 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4398 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4398 is therefore inhibition of IGF1, a GAM4398 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4398 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4408 SERPINA3 TTTGGATTCCTGGTTCCTACAG Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 antiprotei (SERPINA3, Accession NM_001085.2) is a GAM4408 target gene. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4408 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4408 is therefore inhibition of SERPINA3, a GAM4408 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM4423 CASP3 AAAGGAGTTTGTGACATTGACA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM4423 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4423 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4423 is therefore inhibition of CASP3, a GAM4423 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4423 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM4423 CTSB AAAGGAGTTTGTGAC CTSB (Accession NM_147782.1) is another GAM4423 target gene. A A

ATTGACA CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4423 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4423 is therefore inhibition of CTSB. Accordingly, utilities of GAM4423 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM4426 APBB2 GAAGTTTGAAGCCTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTGTTCA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM4426 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4426 is therefore inhibition of APBB2, a GAM4426 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4426 CNTF GAAGTTTGAAGCCTG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

TTGTTCA another GAM4426 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4426 is therefore inhibition of CNTF, a GAM4426 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM175.

GAM4426 MME GAAGTTTGAAGCCTG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TTGTTCA enkephalinase, (MME, Accession NM_007288.1) is another GAM4426 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4426 is therefore inhibition of MME, a GAM4426 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4429 FLNB CGACTCTTGACCATG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GCTGGGG NM_001457.1) is a GAM4429 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4429 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4429 is therefore inhibition of FLNB, a GAM4429 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4429 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM4429 MAPT CGACTCTTGACCATG Microtubule- associated Protein Tau (MAPT, Accession A A
GCTGGGG NM_173727.1) is another GAM4429 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4429 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4429 is therefore inhibition of MAPT, a GAM4429 target gene which Microtubule- associated protein

tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4429 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4429 A A TRPM2 CGACTCTTGACCATG GCTGGGG TRPM2 (Accession NM_003307.1) is another GAM4429 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4429 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4429 is therefore inhibition of TRPM2, a GAM4429 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM4429 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM4432 A A GLUL CAGGTGCAAGTGTTA AAGGGTA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is a GAM4432 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4432 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4432 is therefore inhibition of GLUL, a GAM4432 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4432 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM4446 A A CNTF GTCGGGAGGAAAAGA AAGAAGA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a GAM4446 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4446 is therefore inhibition of CNTF, a GAM4446 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM4446 BACE TTTTTATCTTTTTCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) B A

CCAGATG is another GAM4446 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4446 is therefore inhibition of BACE, a GAM4446 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4446 CAV2 TTTTTATCTTTTTCT Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM4446 B A

CCAGATG target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4446 is therefore inhibition of CAV2, a GAM4446 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM55.

GAM4448 GLUL TCTTTGCTGGAAGGT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GCCTCCC NM_002065.3) is a GAM4448 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4448 is therefore inhibition of GLUL, a GAM4448 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM4448 PIN1 TCTTTGCTGGAAGGT Protein (peptidyl- prolyl cis/trans isomerase) NIMA- A A
GCCTCCC interacting 1 (PIN1, Accession NM_006221.1) is another GAM4448 target gene. PIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4448 is therefore inhibition of PIN1, a GAM4448 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PIN1.The function of PIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM4448 PSEN2 TCTTTGCTGGAAGGT PSEN2 (Accession NM_012486.1) is another GAM4448 target gene. A A
GCCTCCC PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4448 is therefore inhibition of

PSEN2. Accordingly, utilities of GAM4448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM4459 PSEN1 TGACAAGATACAGGG PSEN1 (Accession NM_007319.1) is a GAM4459 target gene. PSEN1 A A

TAGTGAA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4459 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4459 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4516 ADAMTS5 GGCATGATGGAGAGG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GTGGAGA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM4516 target gene. ADAMTS5 BINDING SITE1 and ADAMTS5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ADAMTS5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE1 and ADAMTS5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4516 is therefore inhibition of ADAMTS5, a GAM4516 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM4516 APLP1 GGCATGATGGAGAGG Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A

GTGGAGA NM_005166.2) is another GAM4516 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of APLP1, a GAM4516 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer.

Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM4516 APLP2 GGCATGATGGAGAGG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
GTGGAGA NM_001642.1) is another GAM4516 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of APLP2, a GAM4516 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM4516 BACE GGCATGATGGAGAGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
GTGGAGA is another GAM4516 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of BACE, a GAM4516 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4516 DHCR24 GGCATGATGGAGAGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A
GTGGAGA NM_014762.1) is another GAM4516 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of DHCR24, a GAM4516 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4516 DLST GGCATGATGGAGAGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GTGGAGA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM4516 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of DLST, a GAM4516 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM4516 GLUL GGCATGATGGAGAGG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

GTGGAGA NM_002065.3) is another GAM4516 target gene. GLUL BINDING SITE1 through GLUL BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 through GLUL BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of GLUL, a GAM4516 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM4516 HD GGCATGATGGAGAGG HD (Accession NM_002111.3) is another GAM4516 target gene. HD
A A
GTGGAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of HD. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4516 HTR2C GGCATGATGGAGAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A
GTGGAGA NM_000868.1) is another GAM4516 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of HTR2C, a GAM4516 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4516 IGF1 GGCATGATGGAGAGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GTGGAGA NM_000618.2) is another GAM4516 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of IGF1, a GAM4516 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity

and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4516 MAPT GGCATGATGGAGAGG GTGGAGA Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM4516 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4516 is therefore inhibition of MAPT, a GAM4516 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4516 MME GGCATGATGGAGAGG GTGGAGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM4516 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4516 is therefore inhibition of MME, a GAM4516 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4516 PLCD1 GGCATGATGGAGAGG GTGGAGA Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is another GAM4516 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, A A

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of PLCD1, a GAM4516 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM4516 PSEN1 GGCATGATGGAGAGG A A GTGGAGA PSEN1 (Accession NM_007319.1) is another GAM4516 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4516 SLC17A7 GGCATGATGGAGAGG A A GTGGAGA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM4516 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of SLC17A7, a GAM4516 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM4516 TNFRSF6 GGCATGATGGAGAGG A A TNFRSF6 (Accession NM_152873.1) is another GAM4516 target gene.

GTGGAGA TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM4516 TNFSF5 GGCATGATGGAGAGG TNFSF5 (Accession NM_000074.1) is another GAM4516 target gene. A A

GTGGAGA TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4516 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM4516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM4538 HTR2C GAAACTAGTGTTGGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACAAAGG NM_000868.1) is a GAM4538 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4538 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4538 is therefore inhibition of HTR2C, a GAM4538 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4538 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4538 MME GAAACTAGTGTTGGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

ACAAAGG enkephalinase, (MME, Accession NM_007288.1) is another GAM4538 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4538 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4538 is therefore inhibition of MME, a GAM4538 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4538 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4544 BACE GGTGATGCATTTAAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

AGGGCAG is a GAM4544 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4544 is therefore inhibition of BACE, a GAM4544 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4544 MAPK10 GGTGATGCATTTAAA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

AGGGCAG NM_138980.1) is another GAM4544 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4544 is therefore inhibition of MAPK10, a GAM4544 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4544 PRNP GGTGATGCATTTAAA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

AGGGCAG Strausler- (PRNP, Accession NM_000311.1) is another GAM4544 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4544 is therefore inhibition of PRNP, a GAM4544 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM4544 S100B GGTGATGCATTTAAA S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

AGGGCAG NM_006272.1) is another GAM4544 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4544 is therefore inhibition of S100B, a GAM4544 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM4544 TNFRSF6 GGTGATGCATTTAAA TNFRSF6 (Accession NM_152872.1) is another GAM4544 target gene. A A

AGGGCAG TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4544 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM4557 APPBP2 TATTACATTCATTTT GATGGTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM4557 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4557 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4557 is therefore inhibition of APPBP2, a GAM4557 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4557 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4557 IL1A TATTACATTCATTTT GATGGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM4557 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4557 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4557 is therefore inhibition of IL1A, a GAM4557 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4557 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM4561 IGF1 AGTAGACAGTGGCAA CATAGTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM4561 target gene. IGF1 BINDING SITE is a target A A

binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4561 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4561 is therefore inhibition of IGF1, a GAM4561 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4561 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4561 MME AGTAGACAGTGGCAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A CATAGTC enkephalinase, (MME, Accession NM_000902.2) is another GAM4561 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4561 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4561 is therefore inhibition of MME, a GAM4561 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4561 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4571 ADAM17 CCTGGAGTGACAGGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A GTAGCCT factor, (ADAM17, Accession NM_003183.3) is a GAM4571 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4571 is therefore inhibition of ADAM17, a GAM4571 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4571 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4571 GLUL CCTGGAGTGACAGGT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GTAGCCT NM_002065.3) is another GAM4571 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4571 is therefore inhibition of GLUL, a GAM4571 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM4571 IAPP CCTGGAGTGACAGGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
GTAGCCT another GAM4571 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4571 is therefore inhibition of IAPP, a GAM4571 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM4571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4571 PLAU CCTGGAGTGACAGGT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A
GTAGCCT is another GAM4571 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4571 is therefore inhibition of PLAU, a GAM4571 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM4571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM4571 MPO GCTGCTGCCTCAACA Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM4571 B A
TTTTAGG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4571 is therefore inhibition of MPO, a GAM4571 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM4571 NCKAP1 GCTGCTGCCTCAACA NCKAP1 (Accession NM_013436.2) is another GAM4571 target gene. B A
TTTTAGG NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4571 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM4571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM4633 BACE TCTTTTTGTTGTAGC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A
TGTATGG is a GAM4633 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4633 is therefore inhibition of BACE, a GAM4633 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4633 BCHE TCTTTTTGTTGTAGC BCHE (Accession NM_000055.1) is another GAM4633 target gene. A A

TGTATGG BCHE BINDING SITE1 and BCHE BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BCHE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE1 and BCHE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4633 is therefore inhibition of BCHE. Accordingly, utilities of GAM4633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM4633 IL1A TCTTTTTGTTGTAGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A TGTATGG GAM4633 target gene. IL1A BINDING SITE1 and IL1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE1 and IL1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4633 is therefore inhibition of IL1A, a GAM4633 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM4650 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAT a GAM4650 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4650 is therefore inhibition of FHL2, a GAM4650 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4650 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAT NM_000618.2) is another GAM4650 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4650 is therefore inhibition of IGF1, a GAM4650 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4650 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTGAT another GAM4650 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4650 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4650 is therefore inhibition of PRND, a GAM4650 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM4650 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4656 CTNND2 AAGGCACTTGCCCAG AGCTGCA Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM4656 target gene. CTNND2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4656 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4656 is therefore inhibition of CTNND2, a GAM4656 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4656 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM4656 DHCR24 AAGGCACTTGCCCAG AGCTGCA 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM4656 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4656 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4656 is therefore inhibition of DHCR24, a GAM4656 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4656 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4656 FLNB AAGGCACTTGCCCAG AGCTGCA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM4656 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4656 RNA are set A A

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4656 is therefore inhibition of FLNB, a GAM4656 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4656 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM4656 TGFB1 AAGGCACTTGCCCAG TGFB1 (Accession NM_000660.1) is another GAM4656 target gene. A A

AGCTGCA TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4656 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4656 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4656 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4671 HD ACCAGCTGCATCCTG HD (Accession NM_002111.3) is a GAM4671 target gene. HD BINDING A A

CAAACTT SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4671 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4671 is therefore inhibition of HD. Accordingly, utilities of GAM4671 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4671 HTR2C CACTTTCAGAGATGC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession B A

CCTGAGT NM_000868.1) is another GAM4671 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4671 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4671 is therefore inhibition of HTR2C, a GAM4671 target gene which activates phospholipase C and

regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4671 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4671 MAPT CACTTTCAGAGATGC CCTGAGT Microtubule- associated Protein Tau (MAPT, Accession NM_016841.1) is another GAM4671 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4671 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM4671 is therefore inhibition of MAPT, a GAM4671 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4671 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4685 ACE AGACTGGCCTCAAGC TCCCAGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM4685 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4685 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4685 is therefore inhibition of ACE, a GAM4685 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM4685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4685 HTR2A AGACTGGCCTCAAGC TCCCAGA 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM4685 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4685 is therefore inhibition of HTR2A, a GAM4685 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM4685 TGFB1 AGACTGGCCTCAAGC TGFB1 (Accession NM_000660.1) is another GAM4685 target gene. A A

TCCCAGA TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4685 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4690 ACE TCTGTCATTTTTCTC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TTTCCAT (ACE, Accession NM_152831.1) is a GAM4690 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4690 is therefore inhibition of ACE, a GAM4690 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4690 ADAMTS5 TCTGTCATTTTTCTC A Disintegrin- like and Metalloprotease (reprolysin type) with A A TTTCCAT Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM4690 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of ADAMTS5, a GAM4690 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM4690 DHCR24 TCTGTCATTTTTCTC TTTCCAT A A

24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM4690 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of DHCR24, a GAM4690 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4690 PRND TCTGTCATTTTTCTC TTTCCAT A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM4690 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of PRND, a GAM4690 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4690 PRNP TCTGTCATTTTTCTC TTTCCAT A A Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM4690 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of PRNP, a GAM4690 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM4690 SNCAIP TCTGTCATTTTTCTC TTTCCAT A A Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM4690 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of SNCAIP, a GAM4690 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM4690 TNFRSF6 TCTGTCATTTTTCTC TTTCCAT A A TNFRSF6 (Accession NM_152874.1) is another GAM4690 target gene. TNFRSF6 BINDING SITE1 through TNFRSF6 BINDING SITE4 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 through TNFRSF6 BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM4690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4690 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM4707 FHL2 CATTGCACTCCAGCC A A TAGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM4707 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4707 is therefore inhibition of FHL2, a GAM4707 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4707 HD CATTGCACTCCAGCC A A TAGGCAA HD (Accession NM_002111.3) is another GAM4707 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4707 is therefore inhibition of HD. Accordingly, utilities of GAM4707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4707 IGF1 CATTGCACTCCAGCC A A TAGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM4707 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4707 is therefore inhibition of

IGF1, a GAM4707 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4707 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TAGGCAA another GAM4707 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM4707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4707 is therefore inhibition of PRND, a GAM4707 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4709 ADAMTS5 CAGCAGTGTTGCGAA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

TCATCAC Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM4709 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4709 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4709 is therefore inhibition of ADAMTS5, a GAM4709 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4709 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM4709 TNFRSF5 CAGCAGTGTTGCGAA TNFRSF5 (Accession NM_152854.1) is another GAM4709 target gene. A A

TCATCAC TNFRSF5 BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4709 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4709 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM4709 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM4733 CAV1 TCCCCAAGCCTTGTA CCAGCGT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM4733 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4733 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4733 is therefore inhibition of CAV1, a GAM4733 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4733 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM4733 GFAP TCCCCAAGCCTTGTA CCAGCGT GFAP (Accession NM_002055.2) is another GAM4733 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4733 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4733 is therefore inhibition of GFAP. Accordingly, utilities of GAM4733 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4733 TFCP2 TCCCCAAGCCTTGTA CCAGCGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM4733 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences A A

of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4733 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4733 is therefore inhibition of TFCP2, a GAM4733 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4733 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM4738 BACE TTAATGCTAATCGTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
ATAGGGG is a GAM4738 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4738 is therefore inhibition of BACE, a GAM4738 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4738 FPRL1 TTAATGCTAATCGTG FPRL1 (Accession NM_001462.1) is another GAM4738 target gene. A A
ATAGGGG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4738 is therefore inhibition of FPRL1. Accordingly, utilities of GAM4738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM4738 SLC6A4 TTAATGCTAATCGTG Solute Carrier Family 6 (neurotransmitter transporter, A A
ATAGGGG serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM4738 target gene. SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded

by SLC6A4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE1 and SLC6A4 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4738 is therefore inhibition of SLC6A4, a GAM4738 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM4769 ACE CGCTATGTTGGCCAG GCTGGTC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM4769 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4769 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4769 is therefore inhibition of ACE, a GAM4769 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM4769 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4769 ADAM17 CGCTATGTTGGCCAG GCTGGTC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is another GAM4769 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4769 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4769 is therefore inhibition of ADAM17, a GAM4769 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM4769 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4769 HD CGCTATGTTGGCCAG HD (Accession NM_002111.3) is another GAM4769 target gene. HD A A

GCTGGTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4769 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4769 is therefore inhibition of HD. Accordingly, utilities of GAM4769 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4769 IAPP CGCTATGTTGGCCAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

GCTGGTC another GAM4769 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4769 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4769 is therefore inhibition of IAPP, a GAM4769 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM4769 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4769 TGFB1 CGCTATGTTGGCCAG TGFB1 (Accession NM_000660.1) is another GAM4769 target gene. A A

GCTGGTC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4769 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4769 is therefore inhibition of

TGFB1. Accordingly, utilities of GAM4769 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4796 ADAMTS5 TACTCATTTATGCAT TGTTTTG A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM4796 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4796 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4796 is therefore inhibition of ADAMTS5, a GAM4796 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4796 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM4796 CASP3 TACTCATTTATGCAT TGTTTTG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is another GAM4796 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4796 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4796 is therefore inhibition of CASP3, a GAM4796 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4796 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM4796 MME TACTCATTTATGCAT TGTTTTG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM4796 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4796 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4796 is therefore inhibition of MME, a GAM4796 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4796 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4800 A DHCR24 GGAAAACAAGTACCC CTGGAAC A 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM4800 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4800 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4800 is therefore inhibition of DHCR24, a GAM4800 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4800 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4800 A PSEN1 GGAAAACAAGTACCC CTGGAAC A PSEN1 (Accession NM_000021.2) is another GAM4800 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4800 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4800 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4800 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4803 A CTSG ATGGGCAAATACTGG GAGCTGG A Cathepsin G (CTSG, Accession NM_001911.2) is a GAM4803 target gene. CTSG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4803 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM4803 is therefore inhibition of CTSG, a GAM4803 target gene which is a member of the peptidase S1 protein family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4803 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSG.The function of CTSG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2514.

GAM4803 PLCD1 ATGGGCAAATACTGG GAGCTGG Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is another GAM4803 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4803 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4803 is therefore inhibition of PLCD1, a GAM4803 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM4803 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM4803 TNF ATGGGCAAATACTGG GAGCTGG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM4803 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4803 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM4803 is therefore inhibition of TNF, a GAM4803 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM4803 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4814 ADAM17 TTGCCCAGGCTAGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TGCAGTG factor, (ADAM17, Accession NM_003183.3) is a GAM4814 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4814 is therefore inhibition of ADAM17, a GAM4814 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM4814 CHAT TTGCCCAGGCTAGAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is A A

TGCAGTG another GAM4814 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of CHAT, a GAM4814 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM4814 HTR2A TTGCCCAGGCTAGAG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

TGCAGTG NM_000621.1) is another GAM4814 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of HTR2A, a GAM4814 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM4814 IAPP TTGCCCAGGCTAGAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TGCAGTG another GAM4814 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of IAPP, a GAM4814 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4814 TGFB1 TTGCCCAGGCTAGAG TGFB1 (Accession NM_000660.1) is another GAM4814 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4814 HTR2C CACTGCAACCTCTGC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession B A

CTCCTGG NM_000868.1) is another GAM4814 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of

HTR2C, a GAM4814 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4814 IAPP CACTGCAACCTCTGC CTCCTGG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM4814 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM4814 is therefore inhibition of IAPP, a GAM4814 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4814 MTNR1A CACTGCAACCTCTGC CTCCTGG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM4814 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM4814 is therefore inhibition of MTNR1A, a GAM4814 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM4814 OGDH CACTGCAACCTCTGC CTCCTGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM4814 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as B A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of OGDH, a GAM4814 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM4814 PRND CACTGCAACCTCTGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

CTCCTGG another GAM4814 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4814 is therefore inhibition of PRND, a GAM4814 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4821 MME TATGTGAGACACTGT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

CCTAGGC enkephalinase, (MME, Accession NM_007288.1) is a GAM4821 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4821 is therefore inhibition of MME, a GAM4821 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM25.

GAM4821 ACT GCCTGGCCTTCCTGT Activator of CAMP- responsive Element Modulator (CR (ACT, B A GTTTTAC Accession NM_020482.3) is another GAM4821 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4821 is therefore inhibition of ACT, a GAM4821 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM4844 MME TGATTGTATGATATA Membrane Metallo- endopeptidase (neutral endopeptidase, A A TGAGTTT enkephalinase, (MME, Accession NM_007287.1) is a GAM4844 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4844 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4844 is therefore inhibition of MME, a GAM4844 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4844 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4895 ABCD1 GCTGCTCCTGCTCTC ABCD1 (Accession NM_000033.2) is a GAM4895 target gene. ABCD1 A A CCTCTCC BINDING SITE1 and ABCD1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ABCD1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE1 and ABCD1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4895 is therefore inhibition of ABCD1. Accordingly, utilities of GAM4895 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM4895 ADAM10 GCTGCTCCTGCTCTC A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

CCTCTCC Accession NM_001110.1) is another GAM4895 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of ADAM10, a GAM4895 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM4895 APBA1 GCTGCTCCTGCTCTC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

CCTCTCC 1 (X11) (APBA1, Accession NM_001163.2) is another GAM4895 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of APBA1, a GAM4895 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4895 APBB1 GCTGCTCCTGCTCTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CCTCTCC 1 (Fe65) (APBB1, Accession NM_001164.2) is another GAM4895 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of APBB1, a GAM4895 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM4895 A A BACE GCTGCTCCTGCTCTC CCTCTCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) is another GAM4895 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of BACE, a GAM4895 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4895 A A CRAT GCTGCTCCTGCTCTC CCTCTCC Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is another GAM4895 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of CRAT, a GAM4895 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM4895 CRH GCTGCTCCTGCTCTC Corticotropin Releasing Hormone (CRH, Accession NM_000756.1) is A A

CCTCTCC another GAM4895 target gene. CRH BINDING SITE1 through CRH BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CRH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRH BINDING SITE1 through CRH BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of CRH, a GAM4895 target gene which regulates the release of corticotropin from pituitary gland. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRH.The function of CRH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1976.

GAM4895 ESR2 GCTGCTCCTGCTCTC Estrogen Receptor 2 (ER beta) (ESR2, Accession NM_001437.1) is A A

CCTCTCC another GAM4895 target gene. ESR2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ESR2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of ESR2, a GAM4895 target gene which transcriptional activator involved in regulation of reproduction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ESR2.The function of ESR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM4188.

GAM4895 FHL2 GCTGCTCCTGCTCTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CCTCTCC another GAM4895 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of FHL2, a GAM4895 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM4895 GFAP GCTGCTCCTGCTCTC GFAP (Accession NM_002055.2) is another GAM4895 target gene. A A

CCTCTCC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of GFAP. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4895 HD GCTGCTCCTGCTCTC HD (Accession NM_002111.3) is another GAM4895 target gene. HD A A

CCTCTCC BINDING SITE1 through HD BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 through HD BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of HD. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4895 MAPT GCTGCTCCTGCTCTC Microtubule- associated Protein Tau (MAPT, Accession A A

CCTCTCC NM_005910.2) is another GAM4895 target gene. MAPT BINDING SITE1 through MAPT BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 through MAPT BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of MAPT, a GAM4895 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM4895 MME GCTGCTCCTGCTCTC Membrane Metallo- endopeptidase (neutral endopeptidase, A A

CCTCTCC enkephalinase, (MME, Accession NM_000902.2) is another GAM4895 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of MME, a GAM4895 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4895 PSEN1 GCTGCTCCTGCTCTC PSEN1 (Accession NM_007318.1) is another GAM4895 target gene. A A

CCTCTCC PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of PSEN1. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM4895 TGFB1 GCTGCTCCTGCTCTC TGFB1 (Accession NM_000660.1) is another GAM4895 target gene. A A

CCTCTCC TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4895 is therefore inhibition of TGFB1. Accordingly, utilities of GAM4895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM4904 APBB2 TGGGGCACTGTGGAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GTGTCAT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM4904 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4904 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4904 is therefore inhibition of APBB2, a GAM4904 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4904 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4904 ARHA TGGGGCACTGTGGAG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GTGTCAT is another GAM4904 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4904 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4904 is therefore inhibition of ARHA, a GAM4904 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4904 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM4904 CTSG TGGGGCACTGTGGAG Cathepsin G (CTSG, Accession NM_001911.2) is another GAM4904 A A

GTGTCAT target gene. CTSG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSG BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM4904 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4904 is therefore inhibition of CTSG, a GAM4904 target gene which is a member of the peptidase S1 protein family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4904 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSG.The function of CTSG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2514.

GAM4904 MAPK10 TGGGGCACTGTGGAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A GTGTCAT NM_138981.1) is another GAM4904 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4904 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4904 is therefore inhibition of MAPK10, a GAM4904 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4904 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM4904 UBB TGGGGCACTGTGGAG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM4904 A A GTGTCAT target gene. UBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4904 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4904 is therefore inhibition of UBB, a GAM4904 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM4904 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM3298.

GAM4913 APPBP2 TATAACAGCCAGCTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGATTCA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM4913 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4913 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4913 is therefore inhibition of APPBP2, a GAM4913 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4913 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4932 BACE TGGAGAATTAAAAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A GGTAGTG is a GAM4932 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4932 is therefore inhibition of BACE, a GAM4932 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM4932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM4932 MPO TGGAGAATTAAAAAG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM4932 A A GGTAGTG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4932 is therefore inhibition of

MPO, a GAM4932 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM4946 APPBP2 TGAGATGAACCCGGT ACCTCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM4946 target gene. APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4946 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4946 is therefore inhibition of APPBP2, a GAM4946 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4969 ACE AGCAGAGCCACCAAA TTTAGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM4969 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4969 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM4969 is therefore inhibition of ACE, a GAM4969 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM4969 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM4969 HD AGCAGAGCCACCAAA TTTAGTG HD (Accession NM_002111.3) is another GAM4969 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site A A

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4969 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4969 is therefore inhibition of HD. Accordingly, utilities of GAM4969 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4971 FOS TTCCTTCAGTTCAGG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
GAACCCT Accession NM_005252.2) is a GAM4971 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4971 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4971 is therefore inhibition of FOS, a GAM4971 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM4971 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM4975 GFAP TTCCCTCATTCTCCA GFAP (Accession NM_002055.2) is a GAM4975 target gene. GFAP A A
CCCAGTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4975 is therefore inhibition of GFAP. Accordingly, utilities of GAM4975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM4975 PLAU TTCCCTCATTCTCCA Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A
CCCAGTC is another GAM4975 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4975 is therefore inhibition of PLAU, a GAM4975 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM4975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM4975 TNFRSF6 TTCCCTCATTCTCCA A A CCCAGTC TNFRSF6 (Accession NM_152877.1) is another GAM4975 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4975 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM4986 HD TCTGCTGTGATGGAC A A ACTTGTA HD (Accession NM_002111.3) is a GAM4986 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4986 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM4986 is therefore inhibition of HD. Accordingly, utilities of GAM4986 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM4986 HTR2C TCTGCTGTGATGGAC A A ACTTGTA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM4986 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4986 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4986 is therefore inhibition of HTR2C, a GAM4986 target gene which activates phospholipase C and

regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM4986 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM4986 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGTA NM_000618.2) is another GAM4986 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4986 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4986 is therefore inhibition of IGF1, a GAM4986 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM4986 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM4986 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM4986 target gene. A A

ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM4986 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4986 is therefore inhibition of PSEN2. Accordingly, utilities of GAM4986 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM4986 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM4986 target gene. A A

ACTTGTA TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM4986 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM4986 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM4986 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM5000 APBB2 CAGTGCTGAGTATGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AAGGCCC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM5000 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5000 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5000 is therefore inhibition of APBB2, a GAM5000 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5000 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5008 ADAM17 CCTGGAGTGACAGGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GTAGCCT factor, (ADAM17, Accession NM_003183.3) is a GAM5008 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5008 is therefore inhibition of ADAM17, a GAM5008 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5008 GLUL CCTGGAGTGACAGGT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

GTAGCCT NM_002065.3) is another GAM5008 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5008 is therefore inhibition of GLUL, a GAM5008 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM5008 IAPP CCTGGAGTGACAGGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A GTAGCCT another GAM5008 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5008 is therefore inhibition of IAPP, a GAM5008 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5008 PLAU CCTGGAGTGACAGGT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A GTAGCCT is another GAM5008 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5008 is therefore inhibition of PLAU, a GAM5008 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM282.

GAM5008 MPO GCTGCTGCCTCAACA Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM5008 B A
TTTTAGG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5008 is therefore inhibition of MPO, a GAM5008 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM5008 NCKAP1 GCTGCTGCCTCAACA NCKAP1 (Accession NM_013436.2) is another GAM5008 target gene. B A
TTTTAGG NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5008 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5008 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM5008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM5011 CAV1 CATATCTCCAGGTTC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
TGCTGGA NM_001753.3) is a GAM5011 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5011 is therefore inhibition of CAV1, a GAM5011 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5011 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM5011 CRAT CATATCTCCAGGTTC TGCTGGA A A Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is another GAM5011 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5011 is therefore inhibition of CRAT, a GAM5011 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5011 GLUL TCCTTAGGACCTAGA GGTAGTA B A Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM5011 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5011 is therefore inhibition of GLUL, a GAM5011 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM5035 APPBP2 AGGTCCTCACACACA GCTCTGC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5035 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM5035 is therefore inhibition of APPBP2, a GAM5035 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5035 MPO AGGTCCTCACACACA Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM5035 A A
GCTCTGC target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of MPO, a GAM5035 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM5035 OGDH AGGTCCTCACACACA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
GCTCTGC NM_002541.1) is another GAM5035 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of OGDH, a GAM5035 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM5035 PRND AGGTCCTCACACACA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GCTCTGC another GAM5035 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of PRND, a GAM5035 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5035 DHCR24 GCAGGCTGGTTGGTG 24- dehydrocholesterol Reductase (DHCR24, Accession B A

AGGCAAA NM_014762.1) is another GAM5035 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of DHCR24, a GAM5035 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5035 GLUL GCAGGCTGGTTGGTG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession B A

AGGCAAA NM_002065.3) is another GAM5035 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of GLUL, a GAM5035 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM5035 B A SNCG GCAGGCTGGTTGGTG AGGCAAA SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM5035 target gene. SNCG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5035 is therefore inhibition of SNCG, a GAM5035 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM5048 A A GFAP TTTACAGATGGCAAA GATCTGG GFAP (Accession NM_002055.2) is a GAM5048 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5048 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5048 is therefore inhibition of GFAP. Accordingly, utilities of GAM5048 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM5048 A A IGF1 TTTACAGATGGCAAA GATCTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5048 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5048 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5048 is therefore inhibition of IGF1, a GAM5048 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities

of GAM5048 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5058 FHL2 ACTGCACTCCAGCCT A A GGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM5058 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5058 is therefore inhibition of FHL2, a GAM5058 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5058 IGF1 ACTGCACTCCAGCCT A A GGGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5058 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5058 is therefore inhibition of IGF1, a GAM5058 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5058 PRND ACTGCACTCCAGCCT A A GGGTGAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM5058 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM5058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5058 is therefore inhibition of PRND, a GAM5058 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5082 IAPP TAGAGTTATATGATG TGCTAGT A A Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM5082 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5082 is therefore inhibition of IAPP, a GAM5082 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5085 HD TCTGCTGTGATGGAC ACTTGTA A A HD (Accession NM_002111.3) is a GAM5085 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5085 is therefore inhibition of HD. Accordingly, utilities of GAM5085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5085 HTR2C TCTGCTGTGATGGAC ACTTGTA A A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5085 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING

SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5085 is therefore inhibition of HTR2C, a GAM5085 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5085 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A ACTTGTA NM_000618.2) is another GAM5085 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5085 is therefore inhibition of IGF1, a GAM5085 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5085 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM5085 target gene. A A ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5085 is therefore inhibition of PSEN2. Accordingly, utilities of GAM5085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM5085 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM5085 target gene. A A ACTTGTA TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA

encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5085 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5085 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM5085 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM5090 A A CTSB GTGCTGG CGGCAAGATGCCGGA CTSB (Accession NM_147783.1) is a GAM5090 target gene. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5090 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5090 is therefore inhibition of CTSB. Accordingly, utilities of GAM5090 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM5090 A A NGB GTGCTGG CGGCAAGATGCCGGA Neuroglobin (NGB, Accession NM_021257.2) is another GAM5090 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5090 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5090 is therefore inhibition of NGB, a GAM5090 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5090 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5127 A A BACE AGACCCT TCCAGGGTGGGCCTC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) is a GAM5127 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5127 is therefore inhibition of BACE, a GAM5127 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5127 CNTF TCCAGGGTGGGCCTC AGACCCT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM5127 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5127 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5127 is therefore inhibition of CNTF, a GAM5127 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM5127 PSEN1 TCCAGGGTGGGCCTC AGACCCT PSEN1 (Accession NM_007318.1) is another GAM5127 target gene. PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5127 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5127 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5142 ACE CACCCAGGCTGGAGT GCAGTGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM5142 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a A A

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5142 is therefore inhibition of ACE, a GAM5142 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5142 ADAM17 CACCCAGGCTGGAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
GCAGTGG factor, (ADAM17, Accession NM_021832.1) is another GAM5142 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of ADAM17, a GAM5142 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5142 FLNB CACCCAGGCTGGAGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GCAGTGG NM_001457.1) is another GAM5142 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of FLNB, a GAM5142 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function

of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM5142 FPRL1 CACCCAGGCTGGAGT FPRL1 (Accession NM_001462.1) is another GAM5142 target gene. A A

GCAGTGG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of FPRL1. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM5142 IAPP CACCCAGGCTGGAGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

GCAGTGG another GAM5142 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of IAPP, a GAM5142 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5142 TGFB1 CACCCAGGCTGGAGT TGFB1 (Accession NM_000660.1) is another GAM5142 target gene. A A

GCAGTGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5142 ACE TCACTGCAACCTCTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 B A
CTTCTGG (ACE, Accession NM_152831.1) is another GAM5142 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of ACE, a GAM5142 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5142 CTSK TCACTGCAACCTCTG CTSK (Accession NM_000396.2) is another GAM5142 target gene. B A
CTTCTGG CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of CTSK. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM5142 HTR2A TCACTGCAACCTCTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession B A
CTTCTGG NM_000621.1) is another GAM5142 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of HTR2A, a GAM5142 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM593.

GAM5142 HTR2C TCACTGCAACCTCTG CTTCTGG B A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5142 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of HTR2C, a GAM5142 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5142 IAPP TCACTGCAACCTCTG CTTCTGG B A Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM5142 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of IAPP, a GAM5142 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5142 MTNR1A TCACTGCAACCTCTG CTTCTGG B A Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM5142 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5142 is therefore inhibition of

MTNR1A, a GAM5142 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5209 ABCD1 CCAGCCTGAGGTTCC ABCD1 (Accession NM_000033.2) is a GAM5209 target gene.
ABCD1 A A

TGGAGGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5209 is therefore inhibition of ABCD1. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM5209 APBA1 CCAGCCTGAGGTTCC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A
A

TGGAGGG 1 (X11) (APBA1, Accession NM_001163.2) is another GAM5209 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of APBA1, a GAM5209 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5209 APOC1 CCAGCCTGAGGTTCC Apolipoprotein C- I (APOC1, Accession NM_001645.2) is another
A A

TGGAGGG GAM5209 target gene. APOC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of APOC1, a GAM5209 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM5209 APPBP2 CCAGCCTGAGGTTCC TGGAGGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM5209 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5209 is therefore inhibition of APPBP2, a GAM5209 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5209 CRAT CCAGCCTGAGGTTCC TGGAGGG Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is another GAM5209 target gene. CRAT BINDING SITE1 through CRAT BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CRAT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE1 through CRAT BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5209 is therefore inhibition of CRAT, a GAM5209 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5209 CTSB CCAGCCTGAGGTTCC CTSB (Accession NM_147780.1) is another GAM5209 target gene. A A

TGGAGGG CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of CTSB. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM5209 DHCR24 CCAGCCTGAGGTTCC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGAGGG NM_014762.1) is another GAM5209 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of DHCR24, a GAM5209 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5209 DLST CCAGCCTGAGGTTCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TGGAGGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM5209 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of DLST, a GAM5209 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM5209 A A GFAP CCAGCCTGAGGTTCC TGGAGGG — GFAP (Accession NM_002055.2) is another GAM5209 target gene. GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of GFAP. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM5209 A A NGB CCAGCCTGAGGTTCC TGGAGGG — Neuroglobin (NGB, Accession NM_021257.2) is another GAM5209 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of NGB, a GAM5209 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5209 A A PRND CCAGCCTGAGGTTCC TGGAGGG — Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM5209 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of PRND, a GAM5209 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5209 A A TGGAGGG SLC17A7 CCAGCCTGAGGTTCC SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM5209 target gene. SLC17A7 BINDING SITE1 and SLC17A7 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SLC17A7, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE1 and SLC17A7 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of SLC17A7, a GAM5209 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5209 A A TGGAGGG TGFB1 CCAGCCTGAGGTTCC TGFB1 (Accession NM_000660.1) is another GAM5209 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5209 A A TGGAGGG TRPM2 CCAGCCTGAGGTTCC TRPM2 (Accession NM_003307.1) is another GAM5209 target gene. TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5209 is therefore inhibition of

TRPM2, a GAM5209 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5217 HD TGTACAAGGGGCTCA HD (Accession NM_002111.3) is a GAM5217 target gene. HD BINDING A A
GCCAGCC SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5217 is therefore inhibition of HD. Accordingly, utilities of GAM5217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5217 TRPM2 TGTACAAGGGGCTCA TRPM2 (Accession NM_003307.1) is another GAM5217 target gene. A A
GCCAGCC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5217 is therefore inhibition of TRPM2, a GAM5217 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5217 OLR1 GATGTTGATGAGCTT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 B A
GTGTGCA (OLR1, Accession NM_002543.1) is another GAM5217 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5217 is therefore inhibition of OLR1, a GAM5217 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is

associated with Alzheimer. Accordingly, utilities of GAM5217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5222 APBB2 TCCTCATCTTTGAGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CCCAGCG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM5222 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5222 is therefore inhibition of APBB2, a GAM5222 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5222 TGFB1 TCCTCATCTTTGAGT TGFB1 (Accession NM_000660.1) is another GAM5222 target gene.
A A

CCCAGCG TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5222 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5222 APBB2 GAGCTAAGGATAGAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A

GTGAGGA 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM5222 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5222 is therefore inhibition of APBB2, a GAM5222 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5222 APLP1 GAGCTAAGGATAGAG Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession B A
GTGAGGA NM_005166.2) is another GAM5222 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5222 is therefore inhibition of APLP1, a GAM5222 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM5222 MAPK10 GAGCTAAGGATAGAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession B A
GTGAGGA NM_138981.1) is another GAM5222 target gene. MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPK10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5222 is therefore inhibition of MAPK10, a GAM5222 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to GAM55.

GAM5222 MPO GAGCTAAGGATAGAG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM5222 B A
GTGAGGA target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5222 is therefore inhibition of MPO, a GAM5222 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM5254 FHL2 TGAGTGTATGTGTGA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GAGAGAA a GAM5254 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5254 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5254 is therefore inhibition of FHL2, a GAM5254 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5254 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5254 IL1B TGAGTGTATGTGTGA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A
GAGAGAA GAM5254 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5254 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5254 is therefore inhibition of

IL1B, a GAM5254 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5254 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM5254 SNCAIP TGAGTGTATGTGTGA GAGAGAA Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM5254 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5254 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5254 is therefore inhibition of SNCAIP, a GAM5254 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5254 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM5266 ACE TCACTGCAACCTCCA CCTCCCG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM5266 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5266 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5266 is therefore inhibition of ACE, a GAM5266 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5266 IAPP TCACTGCAACCTCCA CCTCCCG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM5266 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences A A

of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5266 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5266 is therefore inhibition of IAPP, a GAM5266 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5270 IGF1 TCAGTGCAAACTAAG CAGGGCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM5270 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5270 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5270 is therefore inhibition of IGF1, a GAM5270 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5270 MAPK10 TCAGTGCAAACTAAG CAGGGCA Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_002753.2) is another GAM5270 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5270 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5270 is therefore inhibition of MAPK10, a GAM5270 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions,

has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5272 APPBP2 TTAACTGAGAGGATC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGAGTAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5272 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5272 is therefore inhibition of APPBP2, a GAM5272 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5272 DLST TTAACTGAGAGGATC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
TGAGTAG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM5272 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5272 is therefore inhibition of DLST, a GAM5272 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM5272 ARHA CTCACCAGTTACTCT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) B A
CCAGTTG is another GAM5272 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5272 is therefore inhibition of ARHA, a GAM5272 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM5272 PSEN1 CTCACCAGTTACTCT PSEN1 (Accession NM_007318.1) is another GAM5272 target gene. B A

CCAGTTG PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5272 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5278 MAPT TACCCCGATAGGGAG Microtubule- associated Protein Tau (MAPT, Accession A A

GGTGGGG NM_016835.1) is a GAM5278 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5278 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5278 is therefore inhibition of MAPT, a GAM5278 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5278 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5278 DHCR24 ACCATCTTCCCTTTC 24- dehydrocholesterol Reductase (DHCR24, Accession B A

TCGAGTA NM_014762.1) is another GAM5278 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5278 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5278 is therefore inhibition of DHCR24, a GAM5278 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5278 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5278 DSCR1 ACCATCTTCCCTTTC Down Syndrome Critical Region Gene 1 (DSCR1, Accession B A
TCGAGTA NM_004414.3) is another GAM5278 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5278 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5278 is therefore inhibition of DSCR1, a GAM5278 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5278 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM5292 FLNB GCCCTGTTGACCAGA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
ATTTGTT NM_001457.1) is a GAM5292 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5292 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5292 is therefore inhibition of FLNB, a GAM5292 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5292 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM5324 MME GATATCATGGGAAGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGTACTT enkephalinase, (MME, Accession NM_007288.1) is a GAM5324 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5324 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5324 is therefore inhibition of MME, a GAM5324 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5329 BCHE AGCAAGATGGTAGCA BCHE (Accession NM_000055.1) is a GAM5329 target gene. BCHE A A

TTGGAGA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5329 is therefore inhibition of BCHE. Accordingly, utilities of GAM5329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM5329 HD AGCAAGATGGTAGCA HD (Accession NM_002111.3) is another GAM5329 target gene. HD A A

TTGGAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5329 is therefore inhibition of HD. Accordingly, utilities of GAM5329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5329 MME AGCAAGATGGTAGCA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TTGGAGA enkephalinase, (MME, Accession NM_000902.2) is another GAM5329 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5329 is therefore inhibition of MME, a GAM5329 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5329 PRNP AGCAAGATGGTAGCA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

TTGGAGA Strausler- (PRNP, Accession NM_000311.1) is another GAM5329 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5329 is therefore inhibition of PRNP, a GAM5329 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM5340 MAPK10 TGATTGGCAATGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

ATGACGG NM_138980.1) is a GAM5340 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5340 is therefore inhibition of MAPK10, a GAM5340 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5342 PSEN1 GTTCTGCTGAGATAC PSEN1 (Accession NM_000021.2) is a GAM5342 target gene. PSEN1 A A GTGCTCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5342 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5342 TNFRSF5 GTTCTGCTGAGATAC TNFRSF5 (Accession NM_001250.3) is another GAM5342 target gene. A A GTGCTCT TNFRSF5 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5342 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM5342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM5354 FOS TACAGCTCTGCTTCT V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A GGCTCAC Accession NM_005252.2) is a GAM5354 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5354 is therefore inhibition of FOS, a GAM5354 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM5354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM846.

GAM5354 SNCB TACAGCTCTGCTTCT GGCTCAC Synuclein, Beta (SNCB, Accession NM_003085.2) is another GAM5354 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5354 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5354 is therefore inhibition of SNCB, a GAM5354 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5370 CAV1 AAAGTGGCTGGAGTG GAGTCTT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM5370 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5370 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5370 is therefore inhibition of CAV1, a GAM5370 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM5370 IDE AAAGTGGCTGGAGTG GAGTCTT Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM5370 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5370 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5370 is therefore inhibition of IDE, a GAM5370 target gene which may play a role in the cellular

processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM5370 SLC6A4 AAAGTGGCTGGAGTG GAGTCTT Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM5370 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5370 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5370 is therefore inhibition of SLC6A4, a GAM5370 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM5371 ACE CTCACTGCAACCTCC GCCTCCC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM5371 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5371 is therefore inhibition of ACE, a GAM5371 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5371 ADAM10 CTCACTGCAACCTCC GCCTCCC A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is another GAM5371 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated A A

region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of ADAM10, a GAM5371 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM5371 IAPP CTCACTGCAACCTCC A A GCCTCCC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM5371 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of IAPP, a GAM5371 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5371 MPO CTCACTGCAACCTCC A A GCCTCCC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM5371 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of MPO, a GAM5371 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM1032.

GAM5371 NCKAP1 CTCACTGCAACCTCC NCKAP1 (Accession NM_013436.2) is another GAM5371 target gene. A A

GCCTCCC NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM5371 NOTCH1 CTCACTGCAACCTCC Notch (Drosophila) Homolog 1 (translocation- associated) A A

GCCTCCC (NOTCH1, Accession NM_017617.2) is another GAM5371 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of NOTCH1, a GAM5371 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM5371 ACE CCCAGGCTGGAGTGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 B A

AGTGGTG (ACE, Accession NM_152831.1) is another GAM5371 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of ACE, a GAM5371 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5371 ADAM17 CCCAGGCTGGAGTGC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis B A

AGTGGTG factor, (ADAM17, Accession NM_003183.3) is another GAM5371 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of ADAM17, a GAM5371 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5371 FLNB CCCAGGCTGGAGTGC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession B A

AGTGGTG NM_001457.1) is another GAM5371 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of FLNB, a GAM5371 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM5371 FPRL1 CCCAGGCTGGAGTGC FPRL1 (Accession NM_001462.1) is another GAM5371 target gene. B A

AGTGGTG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of FPRL1. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM5371 HTR2A CCCAGGCTGGAGTGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession B A
AGTGGTG NM_000621.1) is another GAM5371 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of HTR2A, a GAM5371 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM5371 IAPP CCCAGGCTGGAGTGC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A
AGTGGTG another GAM5371 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of IAPP, a GAM5371 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5371 NOTCH1 CCCAGGCTGGAGTGC Notch (Drosophila) Homolog 1 (translocation- associated) B A
AGTGGTG (NOTCH1, Accession NM_017617.2) is another GAM5371 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of NOTCH1, a GAM5371 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM5371 TGFB1 CCCAGGCTGGAGTGC TGFB1 (Accession NM_000660.1) is another GAM5371 target gene. B A

AGTGGTG TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5371 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5374 ADAMTS5 TACTCATTTATGCAT A Disintegrin- like and Metalloprotease (reprolysin type) with A A TGTTTTG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM5374 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5374 is therefore inhibition of ADAMTS5, a GAM5374 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM5374 CASP3 TACTCATTTATGCAT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

TGTTTTG Accession NM_004346.2) is another GAM5374 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5374 is therefore inhibition of CASP3, a GAM5374 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM5374 MME TACTCATTTATGCAT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TGTTTTG enkephalinase, (MME, Accession NM_007288.1) is another GAM5374 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5374 is therefore inhibition of MME, a GAM5374 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5385 IGF1 TCACAGTGAACCGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CTCTTTC NM_000618.2) is a GAM5385 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5385 is therefore inhibition of IGF1, a GAM5385 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of

GAM5385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5385 MTNR1A TCACAGTGAACCGGT A A CTCTTTC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM5385 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5385 is therefore inhibition of MTNR1A, a GAM5385 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5415 ACE TGATCCTCTGGCTTC A A AGCCTCC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM5415 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5415 is therefore inhibition of ACE, a GAM5415 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5415 HTR2A TGATCCTCTGGCTTC A A AGCCTCC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM5415 target gene. HTR2A BINDING SITE1 and HTR2A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE1 and HTR2A BINDING

SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5415 is therefore inhibition of HTR2A, a GAM5415 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM5415 MTNR1A TGATCCTCTGGCTTC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

AGCCTCC another GAM5415 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5415 is therefore inhibition of MTNR1A, a GAM5415 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5415 TGFB1 TGATCCTCTGGCTTC TGFB1 (Accession NM_000660.1) is another GAM5415 target gene. A A

AGCCTCC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5415 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5422 CASP3 ATGAGAGTAGGAGTT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

TGGGCTC Accession NM_004346.2) is a GAM5422 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5422 is therefore inhibition of CASP3, a GAM5422 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM5422 IGF1 ATGAGAGTAGGAGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TGGGCTC NM_000618.2) is another GAM5422 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5422 is therefore inhibition of IGF1, a GAM5422 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5422 MAPT ATGAGAGTAGGAGTT Microtubule- associated Protein Tau (MAPT, Accession A A TGGGCTC NM_016835.1) is another GAM5422 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5422 is therefore inhibition of MAPT, a GAM5422 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5444 HD TGGAGACCTGTGTGG HD (Accession NM_002111.3) is a GAM5444 target gene. HD BINDING A A

TTTGTGG SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5444 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5444 is therefore inhibition of HD. Accordingly, utilities of GAM5444 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5444 TNFRSF6 TGGAGACCTGTGTGG TNFRSF6 (Accession NM_152876.1) is another GAM5444 target gene. A A

TTTGTGG TNFRSF6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5444 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5444 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM5444 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM5454 DLST ATACCAGCACAGTGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

ATGGGGA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM5454 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5454 is therefore inhibition of DLST, a GAM5454 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM240.

GAM5454 MAPT ATACCAGCACAGTGG ATGGGGA Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM5454 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5454 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5454 is therefore inhibition of MAPT, a GAM5454 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5454 NGB ATACCAGCACAGTGG ATGGGGA Neuroglobin (NGB, Accession NM_021257.2) is another GAM5454 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5454 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5454 is therefore inhibition of NGB, a GAM5454 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5486 APPBP2 TGAGGAAGGTGTGAG AAATGAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5486 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5486 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5486 is therefore inhibition of APPBP2, a

GAM5486 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5486 IL1A TGAGGAAGGTGTGAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

AAATGAG GAM5486 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5486 is therefore inhibition of IL1A, a GAM5486 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5498 DLST TTCACAGTGGCTGAA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GCTGTTC oxo- glutarat (DLST, Accession NM_001933.2) is a GAM5498 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5498 is therefore inhibition of DLST, a GAM5498 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM5498 HD TTCACAGTGGCTGAA HD (Accession NM_002111.3) is another GAM5498 target gene. HD A A

GCTGTTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5498 is therefore inhibition of HD. Accordingly, utilities of GAM5498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5498 OGDH TTCACAGTGGCTGAA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

GCTGTTC NM_002541.1) is another GAM5498 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5498 is therefore inhibition of OGDH, a GAM5498 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM5512 ACE GGCCCAGGAGGGGGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GAAAGGC (ACE, Accession NM_152830.1) is a GAM5512 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5512 is therefore inhibition of ACE, a GAM5512 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5512 ADAMTS5 GGCCCAGGAGGGGGA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GAAAGGC Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM5512 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of ADAMTS5, a GAM5512 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM5512 APBB1 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAAAGGC 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM5512 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of APBB1, a GAM5512 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5512 APBB2 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAAAGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM5512 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of APBB2, a GAM5512 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5512 APLP2 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
GAAAGGC NM_001642.1) is another GAM5512 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of APLP2, a GAM5512 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM5512 BACE2 GGCCCAGGAGGGGGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GAAAGGC NM_138992.1) is another GAM5512 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of BACE2, a GAM5512 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5512 DHCR24 GGCCCAGGAGGGGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GAAAGGC NM_014762.1) is another GAM5512 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of DHCR24, a GAM5512 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5512 A A FOS GGCCCAGGAGGGGGA GAAAGGC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is another GAM5512 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of FOS, a GAM5512 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM5512 A A GFAP GGCCCAGGAGGGGGA GAAAGGC GFAP (Accession NM_002055.2) is another GAM5512 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of GFAP. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with GFAP.

GAM5512 IGF1 GGCCCAGGAGGGGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GAAAGGC NM_000618.2) is another GAM5512 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of IGF1, a GAM5512 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5512 IL1A GGCCCAGGAGGGGGA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
GAAAGGC GAM5512 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of IL1A, a GAM5512 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5512 OGDH GGCCCAGGAGGGGGA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
GAAAGGC NM_002541.1) is another GAM5512 target gene. OGDH BINDING SITE1 and OGDH BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 and OGDH BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM5512 is therefore inhibition of OGDH, a GAM5512 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM5512 PRND GGCCCAGGAGGGGGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GAAAGGC another GAM5512 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5512 is therefore inhibition of PRND, a GAM5512 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5514 APLP1 TGAGGAGGTGCTACC Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A AGCGTCT NM_005166.2) is a GAM5514 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5514 is therefore inhibition of APLP1, a GAM5514 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM5526 MAPK10 AATGCTGTGCCAGAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A CTGCACC NM_002753.2) is a GAM5526 target gene. MAPK10 BINDING SITE is a

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5526 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5526 is therefore inhibition of MAPK10, a GAM5526 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5526 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5526 THOP1 AATGCTGTGCCAGAG Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is
A A
CTGCACC another GAM5526 target gene. THOP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5526 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5526 is therefore inhibition of THOP1, a GAM5526 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5526 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM5560 BACE TGAAATGCTTTTAGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1)
A A
ACACTGC is a GAM5560 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5560 is therefore inhibition of BACE, a GAM5560 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5560 A A BCHE TGAAATGCTTTTAGG ACACTGC BCHE (Accession NM_000055.1) is another GAM5560 target gene. BCHE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5560 is therefore inhibition of BCHE. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM5560 A A CAV2 TGAAATGCTTTTAGG ACACTGC Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM5560 target gene. CAV2 BINDING SITE1 and CAV2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 and CAV2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5560 is therefore inhibition of CAV2, a GAM5560 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5560 A A CNTF TGAAATGCTTTTAGG ACACTGC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM5560 target gene. CNTF BINDING SITE1 and CNTF BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CNTF, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE1 and CNTF BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5560 is therefore inhibition of CNTF, a GAM5560 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM5560 FLNB TGAAATGCTTTTAGG ACACTGC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM5560 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5560 is therefore inhibition of FLNB, a GAM5560 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM5560 HTR2A TGAAATGCTTTTAGG ACACTGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM5560 target gene. HTR2A BINDING SITE1 and HTR2A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE1 and HTR2A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5560 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5560 is therefore inhibition of HTR2A, a GAM5560 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM5597 IGF1 TTGTTTTAGAAGAAG GTCAGAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM5597 target gene. IGF1 BINDING SITE is a target A A

binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5597 is therefore inhibition of IGF1, a GAM5597 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5597 PRND TTGTTTTAGAAGAAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GTCAGAA another GAM5597 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5597 is therefore inhibition of PRND, a GAM5597 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5597 PSEN1 TTGTTTTAGAAGAAG PSEN1 (Accession NM_000021.2) is another GAM5597 target gene. A A GTCAGAA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5597 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5615 ACE AAATCCAGAATCTAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A ACTGAAT (ACE, Accession NM_152831.1) is a GAM5615 target gene. ACE BINDING

SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5615 is therefore inhibition of ACE, a GAM5615 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5615 FOS ATTTGGGGAAATGTG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, B A

TTTCTGG Accession NM_005252.2) is another GAM5615 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5615 is therefore inhibition of FOS, a GAM5615 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM5615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM5615 NCKAP1 ATTTGGGGAAATGTG NCKAP1 (Accession NM_013436.2) is another GAM5615 target gene. B A

TTTCTGG NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5615 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM5615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM5617 MME ACCAGCTGTGTGAAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TTAGGAA enkephalinase, (MME, Accession NM_000902.2) is a GAM5617 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5617 is therefore inhibition of MME, a GAM5617 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5617 MAPT CTTCCTGGGTTCATA Microtubule- associated Protein Tau (MAPT, Accession B A
TCCTGGT NM_016835.1) is another GAM5617 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5617 is therefore inhibition of MAPT, a GAM5617 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5623 CAV2 GGAAGAATGTGCTTT Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM5623 target A A
TGTTGTT gene. CAV2 BINDING SITE1 and CAV2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 and CAV2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5623 is therefore inhibition of CAV2, a GAM5623 target gene which may function as an accessory protein in

conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5623 CNTF GGAAGAATGTGCTTT TGTTGTT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM5623 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5623 is therefore inhibition of CNTF, a GAM5623 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM5623 ESR2 GGAAGAATGTGCTTT TGTTGTT Estrogen Receptor 2 (ER beta) (ESR2, Accession NM_001437.1) is another GAM5623 target gene. ESR2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ESR2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5623 is therefore inhibition of ESR2, a GAM5623 target gene which transcriptional activator involved in regulation of reproduction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ESR2.The function of ESR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM4188.

GAM5623 IGF1 GGAAGAATGTGCTTT TGTTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5623 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5623 is therefore inhibition of IGF1, a GAM5623 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5623 IL1A GGAAGAATGTGCTTT TGTTGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM5623 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5623 is therefore inhibition of IL1A, a GAM5623 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5623 MME GGAAGAATGTGCTTT TGTTGTT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is another GAM5623 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5623 is therefore inhibition of MME, a GAM5623 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5623 MTNR1A GGAAGAATGTGCTTT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

TGTTGTT another GAM5623 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5623 is therefore inhibition of MTNR1A, a GAM5623 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5623 SNCAIP GGAAGAATGTGCTTT Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, A A

TGTTGTT Accession NM_005460.1) is another GAM5623 target gene. SNCAIP BINDING SITE1 and SNCAIP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SNCAIP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE1 and SNCAIP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5623 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5623 is therefore inhibition of SNCAIP, a GAM5623 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM5640 DHCR24 CTTTTCCTGGGTCTG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GGCTGTG NM_014762.1) is a GAM5640 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5640 is therefore inhibition of DHCR24, a GAM5640 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5640 LRP1 CTTTTCCTGGGTCTG GGCTGTG Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM5640 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5640 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5640 is therefore inhibition of LRP1, a GAM5640 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM5653 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5653 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5653 is therefore inhibition of APPBP2, a GAM5653 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5653 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM5653 target gene. BACE2 BINDING SITE is a A A

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of BACE2, a GAM5653 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5653 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM5653 target gene.
A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of BCHE. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM5653 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM5653 target gene.
A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of CTSB. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM5653 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM5653 target gene.
A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of CTSK. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM5653 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM5653 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of FHL2, a GAM5653 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5653 HD CACTGCACTCCAGCC A A TGGGCAA HD (Accession NM_002111.3) is another GAM5653 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of HD. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5653 IGF1 CACTGCACTCCAGCC A A TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5653 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING

SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of IGF1, a GAM5653 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5653 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A TGGGCAA GAM5653 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of IL1A, a GAM5653 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5653 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM5653 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5653 is therefore inhibition of NGB, a GAM5653 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM281.

GAM5653 PRND CACTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM5653 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5653 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5653 is therefore inhibition of PRND, a GAM5653 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5654 PIN1 TACAAATTCCTGGGT CTCCTGG Protein (peptidyl- prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1, Accession NM_006221.1) is a GAM5654 target gene. PIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5654 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5654 is therefore inhibition of PIN1, a GAM5654 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5654 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PIN1.The function of PIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM5654 S100B TACAAATTCCTGGGT CTCCTGG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is another GAM5654 target gene. S100B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5654 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5654 is therefore inhibition of S100B, a GAM5654 target gene which weakly binds calcium but binds

zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5654 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM5657 FHL2 ACTGCACTCCTGCCT A A AGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM5657 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5657 is therefore inhibition of FHL2, a GAM5657 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5657 IGF1 ACTGCACTCCTGCCT A A AGGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5657 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5657 is therefore inhibition of IGF1, a GAM5657 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5657 PRND ACTGCACTCCTGCCT A A AGGTGAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM5657 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5657 is therefore inhibition of PRND, a GAM5657 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5657 PRNP ACTGCACTCCTGCCT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

AGGTGAC Strausler- (PRNP, Accession NM_000311.1) is another GAM5657 target gene. PRNP BINDING SITE1 and PRNP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRNP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE1 and PRNP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5657 is therefore inhibition of PRNP, a GAM5657 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM5673 IGF1 GGAAAGTTAAAGATG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TATGTAT NM_000618.2) is a GAM5673 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5673 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5673 is therefore inhibition of IGF1, a GAM5673 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of

GAM5673 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5673 MAPK10 GGAAAGTTAAAGATG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

TATGTAT NM_138981.1) is another GAM5673 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5673 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5673 is therefore inhibition of MAPK10, a GAM5673 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5673 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5691 ACE GGCCCAGGAGGGGGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GAAAGGC (ACE, Accession NM_152830.1) is a GAM5691 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5691 is therefore inhibition of ACE, a GAM5691 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5691 ADAMTS5 GGCCCAGGAGGGGGA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GAAAGGC Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM5691 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of ADAMTS5, a GAM5691 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM5691 APBB1 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAAAGGC 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM5691 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of APBB1, a GAM5691 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5691 APBB2 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAAAGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM5691 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of APBB2, a GAM5691 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5691 APLP2 GGCCCAGGAGGGGGA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

GAAAGGC NM_001642.1) is another GAM5691 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of APLP2, a GAM5691 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM5691 BACE2 GGCCCAGGAGGGGGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GAAAGGC NM_138992.1) is another GAM5691 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of BACE2, a GAM5691 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5691 DHCR24 GGCCCAGGAGGGGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GAAAGGC NM_014762.1) is another GAM5691 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of DHCR24, a GAM5691 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5691 FOS GGCCCAGGAGGGGGA V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
GAAAGGC Accession NM_005252.2) is another GAM5691 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of FOS, a GAM5691 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM5691 GFAP GGCCCAGGAGGGGGA GFAP (Accession NM_002055.2) is another GAM5691 target gene. A A
GAAAGGC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of GFAP. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM5691 IGF1 GGCCCAGGAGGGGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAAAGGC NM_000618.2) is another GAM5691 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of IGF1, a GAM5691 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5691 IL1A GGCCCAGGAGGGGGA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

GAAAGGC GAM5691 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of IL1A, a GAM5691 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5691 OGDH GGCCCAGGAGGGGGA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

GAAAGGC NM_002541.1) is another GAM5691 target gene. OGDH BINDING SITE1 and OGDH BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 and OGDH BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of

OGDH, a GAM5691 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM5691 PRND GGCCCAGGAGGGGGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GAAAGGC another GAM5691 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5691 is therefore inhibition of PRND, a GAM5691 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5697 APPBP2 TATTGATCTGTCCCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GCCTGTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5697 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5697 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5697 is therefore inhibition of APPBP2, a GAM5697 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5697 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5703 ABCD1 GTCCAGTGCTCACTG ABCD1 (Accession NM_000033.2) is a GAM5703 target gene. ABCD1 A A
CCGACAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5703 is therefore inhibition of ABCD1. Accordingly, utilities of GAM5703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM5703 DHCR24 GTCCAGTGCTCACTG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

CCGACAT NM_014762.1) is another GAM5703 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5703 is therefore inhibition of DHCR24, a GAM5703 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5703 GLUL GTCCAGTGCTCACTG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

CCGACAT NM_002065.3) is another GAM5703 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5703 is therefore inhibition of GLUL, a GAM5703 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM5728 ADAMTS5 GGCATGTGTGAGCAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CTGCAGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM5728 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5728 is therefore inhibition of ADAMTS5, a GAM5728 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM5728 APLP2 GGCATGTGTGAGCAG A A CTGCAGG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is another GAM5728 target gene. APLP2 BINDING SITE1 and APLP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APLP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE1 and APLP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of APLP2, a GAM5728 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM5728 APPBP2 GGCATGTGTGAGCAG A A CTGCAGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM5728 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of APPBP2, a GAM5728 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5728 CNTF GGCATGTGTGAGCAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

CTGCAGG another GAM5728 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of CNTF, a GAM5728 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM5728 HD GGCATGTGTGAGCAG HD (Accession NM_002111.3) is another GAM5728 target gene. HD A A

CTGCAGG BINDING SITE1 through HD BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 through HD BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of HD. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5728 MAPK10 GGCATGTGTGAGCAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

CTGCAGG NM_138981.1) is another GAM5728 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of

MAPK10, a GAM5728 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5728 TRPM2 GGCATGTGTGAGCAG TRPM2 (Accession NM_003307.1) is another GAM5728 target gene. A A

CTGCAGG TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5728 is therefore inhibition of TRPM2, a GAM5728 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5744 ADAMTS5 TTCACATGTTGCTCA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GTTTTGC Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM5744 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5744 is therefore inhibition of ADAMTS5, a GAM5744 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM5744 APLP2 TTCACATGTTGCTCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

GTTTTGC NM_001642.1) is another GAM5744 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5744 is therefore inhibition of APLP2, a GAM5744 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM5744 GFAP TTCACATGTTGCTCA GFAP (Accession NM_002055.2) is another GAM5744 target gene. A A

GTTTTGC GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5744 is therefore inhibition of GFAP. Accordingly, utilities of GAM5744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM5744 GYPA TTCACATGTTGCTCA Glycophorin A (includes MN blood group) (GYPA, Accession A A

GTTTTGC NM_002099.2) is another GAM5744 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5744 is therefore inhibition of GYPA, a GAM5744 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5744 TRPM2 TTCACATGTTGCTCA TRPM2 (Accession NM_003307.1) is another GAM5744 target gene. A A

GTTTTGC TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites

found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5744 is therefore inhibition of TRPM2, a GAM5744 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5749 A A DSCR1 CTGCACTAGAAGGCA CTATGTT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM5749 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5749 is therefore inhibition of DSCR1, a GAM5749 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM5749 A A HTR2C CTGCACTAGAAGGCA CTATGTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5749 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5749 is therefore inhibition of HTR2C, a GAM5749 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5749 A A PLCD1 CTGCACTAGAAGGCA CTATGTT Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is another GAM5749 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5749 is therefore inhibition of PLCD1, a GAM5749 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM5749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM5764 A A HD BINDING SITE TCTGCTGTGATGGAC ACTTGTA HD (Accession NM_002111.3) is a GAM5764 target gene. HD is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5764 is therefore inhibition of HD. Accordingly, utilities of GAM5764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM5764 A A HTR2C TCTGCTGTGATGGAC ACTTGTA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5764 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5764 is therefore inhibition of HTR2C, a GAM5764 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM5764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5764 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGTA NM_000618.2) is another GAM5764 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5764 is therefore inhibition of IGF1, a GAM5764 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5764 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM5764 target gene. A A

ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5764 is therefore inhibition of PSEN2. Accordingly, utilities of GAM5764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM5764 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM5764 target gene. A A

ACTTGTA TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5764 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM5764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM5798 ARHA GAAAGTAGTAAGTTG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A TATAGTT is a GAM5798 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5798 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5798 is therefore inhibition of ARHA, a GAM5798 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM5800 CAV2 AGTATTACAGCAGGT Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM5800 target A A ACTGGTT gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5800 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5800 is therefore inhibition of CAV2, a GAM5800 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5800 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5806 ABCD1 GCCTGGATGTGACCA ABCD1 (Accession NM_000033.2) is a GAM5806 target gene. ABCD1 A A CCCTCAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5806 RNA

are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5806 is therefore inhibition of ABCD1. Accordingly, utilities of GAM5806 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM5806 DHCR24 GCCTGGATGTGACCA CCCTCAC A A

24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM5806 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5806 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5806 is therefore inhibition of DHCR24, a GAM5806 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5806 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5809 CAV1 GACAAGAGGCACAGA CAGCAGG A A

Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM5809 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5809 is therefore inhibition of CAV1, a GAM5809 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM5809 CRAT GACAAGAGGCACAGA CAGCAGG A A

Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is another GAM5809 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of CRAT, a GAM5809 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5809 HTR2C GACAAGAGGCACAGA A A CAGCAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5809 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of HTR2C, a GAM5809 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5809 MAPT GACAAGAGGCACAGA A A CAGCAGG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM5809 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of MAPT, a GAM5809 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM144.

GAM5809 PLCD1 GACAAGAGGCACAGA Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is
A A
CAGCAGG another GAM5809 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of PLCD1, a GAM5809 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM5809 PSEN1 GACAAGAGGCACAGA PSEN1 (Accession NM_007318.1) is another GAM5809 target gene.
A A
CAGCAGG PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5809 THOP1 GACAAGAGGCACAGA Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is
A A
CAGCAGG another GAM5809 target gene. THOP1 BINDING SITE1 and THOP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by THOP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE1 and THOP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of THOP1, a GAM5809 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore

is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM5809 TNF GACAAGAGGCACAGA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A
CAGCAGG Accession NM_000594.2) is another GAM5809 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5809 is therefore inhibition of TNF, a GAM5809 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM5809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5814 ADAM17 TGCAAGTCTGTGATT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TTGTGTT factor, (ADAM17, Accession NM_003183.3) is a GAM5814 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5814 is therefore inhibition of ADAM17, a GAM5814 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5814 FHL2 TGCAAGTCTGTGATT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TTGTGTT another GAM5814 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5814 is therefore inhibition of FHL2, a GAM5814 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5814 FPRL1 TGCAAGTCTGTGATT A A TTGTGTT FPRL1 (Accession NM_001462.1) is another GAM5814 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5814 is therefore inhibition of FPRL1. Accordingly, utilities of GAM5814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM5814 HTR2C TGCAAGTCTGTGATT A A TTGTGTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM5814 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5814 is therefore inhibition of HTR2C, a GAM5814 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM5814 IGF1 TGCAAGTCTGTGATT A A TTGTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5814 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5814 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5814 is therefore inhibition of IGF1, a GAM5814 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5823 IGF1 GGAAAGTTAAAGATG TATGTAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM5823 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5823 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5823 is therefore inhibition of IGF1, a GAM5823 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5823 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5823 MAPK10 GGAAAGTTAAAGATG TATGTAT Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is another GAM5823 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5823 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5823 is therefore inhibition of MAPK10, a GAM5823 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM5823 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5826 ABCD1 TGAGGTCATGTTCTG ABCD1 (Accession NM_000033.2) is a GAM5826 target gene. ABCD1 A A
TCAGGTT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5826 is therefore inhibition of ABCD1. Accordingly, utilities of GAM5826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM5826 IGF1 TGAGGTCATGTTCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCAGGTT NM_000618.2) is another GAM5826 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5826 is therefore inhibition of IGF1, a GAM5826 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5826 IL1B TGAGGTCATGTTCTG Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A
TCAGGTT GAM5826 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5826 is therefore inhibition of IL1B, a GAM5826 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5826 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM5826 MME TGAGGTCATGTTCTG TCAGGTT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM5826 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5826 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5826 is therefore inhibition of MME, a GAM5826 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5826 TRPM2 TGAGGTCATGTTCTG TCAGGTT TRPM2 (Accession NM_003307.1) is another GAM5826 target gene. TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5826 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5826 is therefore inhibition of TRPM2, a GAM5826 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5836 ACE CACCCAGGCTGGAGT GCAGTGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM5836 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence A A

of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5836 is therefore inhibition of ACE, a GAM5836 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5836 ADAM17 CACCCAGGCTGGAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
GCAGTGG factor, (ADAM17, Accession NM_021832.1) is another GAM5836 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of ADAM17, a GAM5836 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM5836 FLNB CACCCAGGCTGGAGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GCAGTGG NM_001457.1) is another GAM5836 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of FLNB, a GAM5836 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM5836 FPRL1 CACCCAGGCTGGAGT FPRL1 (Accession NM_001462.1) is another GAM5836 target gene. A A

GCAGTGG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of FPRL1. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM5836 IAPP CACCCAGGCTGGAGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

GCAGTGG another GAM5836 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of IAPP, a GAM5836 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5836 TGFB1 CACCCAGGCTGGAGT TGFB1 (Accession NM_000660.1) is another GAM5836 target gene. A A

GCAGTGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of TGFB1. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM5836 ACE TCACTGCAACCTCCG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 B A

CCTGCCG (ACE, Accession NM_152831.1) is another GAM5836 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of ACE, a GAM5836 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5836 AGER TCACTGCAACCTCCG Advanced Glycosylation End Product- specific Receptor (AGER, B A CCTGCCG Accession NM_172197.1) is another GAM5836 target gene. AGER BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AGER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of AGER, a GAM5836 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AGER.The function of AGER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2350.

GAM5836 IAPP TCACTGCAACCTCCG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A CCTGCCG another GAM5836 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5836 is therefore inhibition of IAPP, a GAM5836 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM5836 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM5859 ACHE TCCCTGAGCCCTGAA Acetylcholinesterase (YT blood group) (ACHE, Accession A A

GGGTGTT NM_015831.1) is a GAM5859 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5859 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5859 is therefore inhibition of ACHE, a GAM5859 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5859 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM5859 MTNR1A TCCCTGAGCCCTGAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

GGGTGTT another GAM5859 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5859 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5859 is therefore inhibition of MTNR1A, a GAM5859 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5859 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5868 ARHA TCAAAGCTGCAGATT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GCCTGTG is a GAM5868 target gene. ARHA BINDING SITE1 and ARHA BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARHA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE1 and ARHA BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM5868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5868 is therefore inhibition of ARHA, a GAM5868 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM5868 DLST TCAAAGCTGCAGATT GCCTGTG Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM5868 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5868 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5868 is therefore inhibition of DLST, a GAM5868 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM5868 TNF TCAAAGCTGCAGATT GCCTGTG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM5868 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5868 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5868 is therefore inhibition of TNF, a GAM5868 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM5868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5868 VLDLR TCAAAGCTGCAGATT Very Low Density Lipoprotein Receptor (VLDLR, Accession A A
GCCTGTG NM_003383.1) is another GAM5868 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5868 is therefore inhibition of VLDLR, a GAM5868 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM5868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM5872 ACE GTTGTGTGGAAGATG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
CTTTGCC (ACE, Accession NM_152831.1) is a GAM5872 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5872 is therefore inhibition of ACE, a GAM5872 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM5872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5872 APBA1 GTTGTGTGGAAGATG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
CTTTGCC 1 (X11) (APBA1, Accession NM_001163.2) is another GAM5872 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5872 is therefore inhibition of

APBA1, a GAM5872 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5874 BACE TCCAAAATTAAAGGT A A TGTAGAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is a GAM5874 target gene. BACE BINDING SITE1 through BACE BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 through BACE BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM5874 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5874 is therefore inhibition of BACE, a GAM5874 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5874 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5874 IGF1 TCCAAAATTAAAGGT A A TGTAGAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5874 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5874 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5874 is therefore inhibition of IGF1, a GAM5874 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5874 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5874 MME TCCAAAATTAAAGGT A A TGTAGAA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM5874 target gene. MME BINDING SITE is a target binding site found in the

3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5874 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5874 is therefore inhibition of MME, a GAM5874 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5874 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5884 DLST TAGCTCATTTTTGAA ATCAGTT — Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is a GAM5884 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5884 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5884 is therefore inhibition of DLST, a GAM5884 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5884 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM5884 IGF1 TAGCTCATTTTTGAA ATCAGTT — Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM5884 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5884 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5884 is therefore inhibition of IGF1, a GAM5884 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5884 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5884 NOTCH1 TAGCTCATTTTTGAA ATCAGTT Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM5884 target gene. NOTCH1 BINDING SITE1 and NOTCH1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NOTCH1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE1 and NOTCH1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5884 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5884 is therefore inhibition of NOTCH1, a GAM5884 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5884 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM5886 BACE2 TATCTCTTGCCTTGA CCTCCTA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is a GAM5886 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5886 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5886 is therefore inhibition of BACE2, a GAM5886 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM5886 PSEN1 TATCTCTTGCCTTGA CCTCCTA PSEN1 (Accession NM_000021.2) is another GAM5886 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5886 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5886 is therefore inhibition of PSEN1. Accordingly, utilities of GAM5886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM5910 ACT AGCAAGTGTTGAAAC Activator of CAMP- responsive Element Modulator (CR (ACT, A A AGCTGGT Accession NM_020482.3) is a GAM5910 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5910 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5910 is therefore inhibition of ACT, a GAM5910 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5910 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM5910 DSCR1 AGCAAGTGTTGAAAC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A AGCTGGT NM_004414.3) is another GAM5910 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5910 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5910 is therefore inhibition of DSCR1, a GAM5910 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5910 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM5916 BACE AAGCAGCCTTGGACC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A AGGAGGG is a GAM5916 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5916 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM5916 is therefore inhibition of BACE, a GAM5916 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM5916 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM5916 IL1A AAGCAGCCTTGGACC AGGAGGG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM5916 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5916 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5916 is therefore inhibition of IL1A, a GAM5916 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5916 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5958 CASP3 AAGCTGGCCTGTACC TGCTGAG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM5958 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5958 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM5958 is therefore inhibition of CASP3, a GAM5958 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5958 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM5958 CTSG AAGCTGGCCTGTACC Cathepsin G (CTSG, Accession NM_001911.2) is another GAM5958 A A

TGCTGAG target gene. CTSG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5958 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5958 is therefore inhibition of CTSG, a GAM5958 target gene which is a member of the peptidase S1 protein family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5958 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSG.The function of CTSG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2514.

GAM5963 ARHA GAGGACCCTTAGGTC Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

AGACAGA is a GAM5963 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5963 is therefore inhibition of ARHA, a GAM5963 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM5963 NGB GAGGACCCTTAGGTC Neuroglobin (NGB, Accession NM_021257.2) is another GAM5963 A A

AGACAGA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5963 is therefore inhibition of NGB, a GAM5963 target gene which has function in oxygen transport

and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM5971 APPBP2 TTTTTGTGGAATATT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TTTTTAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM5971 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5971 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5971 is therefore inhibition of APPBP2, a GAM5971 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5971 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5971 MTNR1A TTTTTGTGGAATATT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A TTTTTAA another GAM5971 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5971 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5971 is therefore inhibition of MTNR1A, a GAM5971 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5971 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM5973 IGF1 TGGCAGATTTGGTTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A CTGTTGG NM_000618.2) is a GAM5973 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5973 is therefore inhibition of IGF1, a GAM5973 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM5973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5973 MAPK10 TGGCAGATTTGGTTG CTGTTGG Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_002753.2) is another GAM5973 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5973 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5973 is therefore inhibition of MAPK10, a GAM5973 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM5973 MAPT TGGCAGATTTGGTTG CTGTTGG Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM5973 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5973 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM5973 is therefore inhibition of MAPT, a GAM5973 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5973 A PRNP TGGCAGATTTGGTTG CTGTTGG A Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM5973 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5973 is therefore inhibition of PRNP, a GAM5973 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM5973 A TRPM2 TGGCAGATTTGGTTG CTGTTGG A TRPM2 (Accession NM_003307.1) is another GAM5973 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5973 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5973 is therefore inhibition of TRPM2, a GAM5973 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5973 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM5990 A DSCR1 TCCTTTGGACATGGG CAAGGGT A Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM5990 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM5990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5990 is therefore inhibition of DSCR1, a GAM5990 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM5990	MAPT	TGCTCTTGCTCTTTC TTCTGGA	Microtubule- associated Protein Tau (MAPT, Accession NM_016834.1) is another GAM5990 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM5990 is therefore inhibition of MAPT, a GAM5990 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM5990	MME	TGCTCTTGCTCTTTC TTCTGGA	Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM5990 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM5990 is therefore inhibition of MME, a GAM5990 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM5990	PRND	TGCTCTTGCTCTTTC	Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is	B	A

TTCTGGA another GAM5990 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5990 is therefore inhibition of PRND, a GAM5990 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5998 CRAT CTTGGCCCTGTGAGG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is a A A

CTTCACC GAM5998 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5998 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM5998 is therefore inhibition of CRAT, a GAM5998 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5998 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5998 DHCR24 CTTGGCCCTGTGAGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

CTTCACC NM_014762.1) is another GAM5998 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM5998 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5998 is therefore inhibition of DHCR24, a GAM5998 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5998 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM5998 MPO CTTGGCCCTGTGAGG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM5998 A A
CTTCACC target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5998 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5998 is therefore inhibition of MPO, a GAM5998 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5998 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM5998 SNCB CTTGGCCCTGTGAGG Synuclein, Beta (SNCB, Accession NM_003085.2) is another A A
CTTCACC GAM5998 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5998 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM5998 is therefore inhibition of SNCB, a GAM5998 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM5998 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM5998 TRPM2 CTTGGCCCTGTGAGG TRPM2 (Accession NM_003307.1) is another GAM5998 target gene. A A
CTTCACC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM5998 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM5998 is therefore inhibition of TRPM2, a GAM5998 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM5998 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6014 IL1A TACAAGTGCTCCAGT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a GAM6014 A A

ACGGCC target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6014 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6014 is therefore inhibition of IL1A, a GAM6014 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6014 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM6024 BACE TGGAGAATTAAAAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

GGTAGTG is a GAM6024 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6024 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6024 is therefore inhibition of BACE, a GAM6024 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6024 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6024 MPO TGGAGAATTAAAAAG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM6024 A A

GGTAGTG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6024 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6024 is therefore inhibition of MPO, a GAM6024 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6024 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM6051 ADAM10 CTCCCTCCACTTCTG A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

AGGACGT Accession NM_001110.1) is a GAM6051 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6051 is therefore inhibition of ADAM10, a GAM6051 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM6055 DHCR24 TTCACCCATCTTTCC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

ACCCAC NM_014762.1) is a GAM6055 target gene. DHCR24 BINDING SITE1 through DHCR24 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 through DHCR24 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM6055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6055 is therefore inhibition of DHCR24, a GAM6055 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM6055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6055 PRND TTCACCCATCTTTCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

ACCCAC another GAM6055 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6055 is therefore inhibition of PRND, a GAM6055 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6055 PSEN1 TTCACCCATCTTTCC PSEN1 (Accession NM_007318.1) is another GAM6055 target gene. A A

ACCCAC PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6055 is therefore inhibition of PSEN1. Accordingly, utilities of GAM6055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM6055 UBB TTCACCCATCTTTCC Ubiquitin B (UBB, Accession NM_018955.2) is another GAM6055 A A

ACCCAC target gene. UBB BINDING SITE1 and UBB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by UBB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE1 and UBB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6055 is therefore inhibition of UBB, a GAM6055 target gene which marks cellular proteins for

degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM6055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM6083 ABCD1 GGCCTGAGGTCAGCA ABCD1 (Accession NM_000033.2) is a GAM6083 target gene.
ABCD1 A A
GTAGAGG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6083 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6083 APBB1 GGCCTGAGGTCAGCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A
A
GTAGAGG 1 (Fe65) (APBB1, Accession NM_145689.1) is another GAM6083 target gene. APBB1 BINDING SITE1 and APBB1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APBB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE1 and APBB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of APBB1, a GAM6083 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM6083 APLP2 GGCCTGAGGTCAGCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A
A
GTAGAGG NM_001642.1) is another GAM6083 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of APLP2, a GAM6083 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM6083 BAX GGCCTGAGGTCAGCA AA GTAGAGG BCL2- associated X Protein (BAX, Accession NM_004324.2) is another GAM6083 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of BAX, a GAM6083 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM6083 PRND GGCCTGAGGTCAGCA AA GTAGAGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM6083 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of PRND, a GAM6083 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6083 SLC17A7 GGCCTGAGGTCAGCA AA GTAGAGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM6083 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of SLC17A7, a GAM6083 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM6083 TRPM2 GGCCTGAGGTCAGCA TRPM2 (Accession NM_003307.1) is another GAM6083 target gene. A A

GTAGAGG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6083 is therefore inhibition of TRPM2, a GAM6083 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM6083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6102 ABCD1 CTGAGGTCAGGAGTT ABCD1 (Accession NM_000033.2) is a GAM6102 target gene. ABCD1 A A

CGAGACC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6102 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6102 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6102 IGF1 CTGAGGTCAGGAGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CGAGACC NM_000618.2) is another GAM6102 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6102 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6102 is therefore inhibition of IGF1, a GAM6102 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6102 PRND CTGAGGTCAGGAGTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
CGAGACC another GAM6102 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6102 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6102 is therefore inhibition of PRND, a GAM6102 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6102 TRPM2 CTGAGGTCAGGAGTT TRPM2 (Accession NM_003307.1) is another GAM6102 target gene. A A
CGAGACC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6102 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6102 is therefore inhibition of TRPM2, a GAM6102 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM6102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6121 APLP2 GAGGTAGAGGTTGCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
GTGAGTC NM_001642.1) is a GAM6121 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6121 is therefore inhibition of APLP2, a GAM6121 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM6121 APPBP2 GAGGTAGAGGTTGCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GTGAGTC Protein 2 (APPBP2, Accession NM_006380.2) is another GAM6121 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of APPBP2, a GAM6121 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6121 BACE GAGGTAGAGGTTGCA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A
GTGAGTC is another GAM6121 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of BACE, a GAM6121 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6121 CNTF GAGGTAGAGGTTGCA GTGAGTC AA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM6121 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of CNTF, a GAM6121 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM6121 DLST GAGGTAGAGGTTGCA GTGAGTC AA Dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo- glutarat (DLST, Accession NM_001933.2) is another GAM6121 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of DLST, a GAM6121 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM6121 FHL2 GAGGTAGAGGTTGCA AA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is

GTGAGTC another GAM6121 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of FHL2, a GAM6121 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6121 GYPA GAGGTAGAGGTTGCA Glycophorin A (includes MN blood group) (GYPA, Accession A A

GTGAGTC NM_002099.2) is another GAM6121 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of GYPA, a GAM6121 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6121 HTR2C GAGGTAGAGGTTGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

GTGAGTC NM_000868.1) is another GAM6121 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of HTR2C, a GAM6121 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM6121 IGF1 GAGGTAGAGGTTGCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GTGAGTC NM_000618.2) is another GAM6121 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of IGF1, a GAM6121 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6121 MAPK10 GAGGTAGAGGTTGCA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
GTGAGTC NM_002753.2) is another GAM6121 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of MAPK10, a GAM6121 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM6121 MAPT GAGGTAGAGGTTGCA Microtubule- associated Protein Tau (MAPT, Accession A A
GTGAGTC NM_173727.1) is another GAM6121 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE

III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of MAPT, a GAM6121 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM6121 PRND GAGGTAGAGGTTGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GTGAGTC another GAM6121 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of PRND, a GAM6121 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6121 TNF GAGGTAGAGGTTGCA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

GTGAGTC Accession NM_000594.2) is another GAM6121 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of TNF, a GAM6121 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM99.

GAM6121 TNFRSF6 GAGGTAGAGGTTGCA TNFRSF6 (Accession NM_000043.3) is another GAM6121 target gene. A A

GTGAGTC TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6121 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM6121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM6161 ADAM17 TTTGCACACTTTCCA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AGTTGCC factor, (ADAM17, Accession NM_003183.3) is a GAM6161 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6161 is therefore inhibition of ADAM17, a GAM6161 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6161 B2M TTTGCACACTTTCCA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A

AGTTGCC GAM6161 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6161 is therefore inhibition of B2M, a GAM6161 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6161 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM6161 CTNND2 TTTGCACACTTTCCA AGTTGCC Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM6161 target gene. CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTNND2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6161 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6161 is therefore inhibition of CTNND2, a GAM6161 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6161 IGF1 TTTGCACACTTTCCA AGTTGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM6161 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6161 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6161 is therefore inhibition of IGF1, a GAM6161 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6161 PRNP TTTGCACACTTTCCA AGTTGCC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM6161 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide A A

sequence of GAM6161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6161 is therefore inhibition of PRNP, a GAM6161 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6172 ACE AGTGGTTTCAGGGAC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TTCTGTA (ACE, Accession NM_152831.1) is a GAM6172 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6172 is therefore inhibition of ACE, a GAM6172 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM6172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6172 CRH AGTGGTTTCAGGGAC Corticotropin Releasing Hormone (CRH, Accession NM_000756.1) is A A TTCTGTA another GAM6172 target gene. CRH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6172 is therefore inhibition of CRH, a GAM6172 target gene which regulates the release of corticotropin from pituitary gland. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRH.The function of CRH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM1976.

GAM6172 IGF1 AGTGGTTTCAGGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTCTGTA NM_000618.2) is another GAM6172 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6172 is therefore inhibition of IGF1, a GAM6172 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6172 SNCA AGTGGTTTCAGGGAC SNCA (Accession NM_000345.2) is another GAM6172 target gene. A A

TTCTGTA SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6172 is therefore inhibition of SNCA. Accordingly, utilities of GAM6172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM6234 APLP2 AACCTGCTGGTAAAG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

CACTGGC NM_001642.1) is a GAM6234 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6234 is therefore inhibition of APLP2, a GAM6234 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM6234 BACE AACCTGCTGGTAAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A
CACTGGC is another GAM6234 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6234 is therefore inhibition of BACE, a GAM6234 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6234 SLC6A4 AACCTGCTGGTAAAG Solute Carrier Family 6 (neurotransmitter transporter, A A
CACTGGC serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM6234 target gene. SLC6A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6234 is therefore inhibition of SLC6A4, a GAM6234 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM6250 CTSB TGTAAACTTGTCTTG CTSB (Accession NM_147783.1) is a GAM6250 target gene. CTSB A A
AATGGAA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6250 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

A function of GAM6250 is therefore inhibition of CTSB. Accordingly, utilities of GAM6250 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM6265 ADAMTS5 TGGGTTAGTGGTTGA ATAGTTT A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM6265 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6265 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6265 is therefore inhibition of ADAMTS5, a GAM6265 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6265 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM6265 TNF TGGGTTAGTGGTTGA ATAGTTT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM6265 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6265 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6265 is therefore inhibition of TNF, a GAM6265 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM6265 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6271 BCHE AGCAAGATGGTAGCA TTGGAGA BCHE (Accession NM_000055.1) is a GAM6271 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of A A

Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6271 is therefore inhibition of BCHE. Accordingly, utilities of GAM6271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM6271 HD AGCAAGATGGTAGCA HD (Accession NM_002111.3) is another GAM6271 target gene. HD A A

TTGGAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6271 is therefore inhibition of HD. Accordingly, utilities of GAM6271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6271 MME AGCAAGATGGTAGCA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TTGGAGA enkephalinase, (MME, Accession NM_000902.2) is another GAM6271 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6271 is therefore inhibition of MME, a GAM6271 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6271 PRNP AGCAAGATGGTAGCA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

TTGGAGA Strausler- (PRNP, Accession NM_000311.1) is another GAM6271 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6271 is therefore inhibition of PRNP, a GAM6271 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6296 APOC1 TCCCTTCAGAGCCCA Apolipoprotein C- I (APOC1, Accession NM_001645.2) is a GAM6296 A A
TGGGTTT target gene. APOC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6296 is therefore inhibition of APOC1, a GAM6296 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM6296 PLAU TCCCTTCAGAGCCCA Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A
TGGGTTT is another GAM6296 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of PLAU, a GAM6296 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM6296 PRND TCCCTTCAGAGCCCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGTTT another GAM6296 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of PRND, a GAM6296 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6296 ABCD1 AAATCCTGGGGATCT ABCD1 (Accession NM_000033.2) is another GAM6296 target gene. B A

GGAGGGA ABCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6296 FHL2 AAATCCTGGGGATCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is B A

GGAGGGA another GAM6296 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of FHL2, a GAM6296 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM6296 HD AAATCCTGGGGATCT HD (Accession NM_002111.3) is another GAM6296 target gene. HD B A

GGAGGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of HD. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6296 MME AAATCCTGGGGATCT Membrane Metallo- endopeptidase (neutral endopeptidase, B A

GGAGGGA enkephalinase, (MME, Accession NM_000902.2) is another GAM6296 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6296 is therefore inhibition of MME, a GAM6296 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6306 ADAMTS5 GCTGTGTTAACTGTT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CAAACTC Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM6306 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6306 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6306 is therefore inhibition of ADAMTS5, a GAM6306 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM6306 APPBP2 GCTGTGTTAACTGTT CAAACTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM6306 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6306 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6306 is therefore inhibition of APPBP2, a GAM6306 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6306 DHCR24 GCTGTGTTAACTGTT CAAACTC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM6306 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6306 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6306 is therefore inhibition of DHCR24, a GAM6306 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6306 PRNP GCTGTGTTAACTGTT CAAACTC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM6306 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6306 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6306 is therefore inhibition of PRNP, a GAM6306 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6329 HD AAAGACAGTTCAGTG HD (Accession NM_002111.3) is a GAM6329 target gene. HD BINDING A A

ACAAGTT SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6329 is therefore inhibition of HD. Accordingly, utilities of GAM6329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6361 BACE GCAGCAGGCAGGGCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

AGGCAGG is a GAM6361 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6361 is therefore inhibition of BACE, a GAM6361 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6361 BACE2 GCAGCAGGCAGGGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

AGGCAGG NM_138992.1) is another GAM6361 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and

secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of BACE2, a GAM6361 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6361 GFAP GCAGCAGGCAGGGCC GFAP (Accession NM_002055.2) is another GAM6361 target gene. A A

AGGCAGG GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of GFAP. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM6361 HTR2C GCAGCAGGCAGGGCC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

AGGCAGG NM_000868.1) is another GAM6361 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of HTR2C, a GAM6361 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM6361 LRP1 GCAGCAGGCAGGGCC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

AGGCAGG macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM6361 target gene. LRP1 BINDING SITE1 and LRP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LRP1,

corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 and LRP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of LRP1, a GAM6361 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM6361 MAPT GCAGCAGGCAGGGCC AGGCAGG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM6361 target gene. MAPT BINDING SITE1 and MAPT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 and MAPT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6361 is therefore inhibition of MAPT, a GAM6361 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM6361 NGB GCAGCAGGCAGGGCC AGGCAGG Neuroglobin (NGB, Accession NM_021257.2) is another GAM6361 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6361 is therefore inhibition of NGB, a GAM6361 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM6361 SERPINA GCAGCAGGCAGGGCC Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 A A

3 AGGCAGG antiprotei (SERPINA3, Accession NM_001085.2) is another GAM6361 target gene. SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINA3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE1 and SERPINA3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of SERPINA3, a GAM6361 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM6361 SNCG GCAGCAGGCAGGGCC SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another A A

AGGCAGG GAM6361 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of SNCG, a GAM6361 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM6361 TGFB1 GCAGCAGGCAGGGCC TGFB1 (Accession NM_000660.1) is another GAM6361 target gene. A A

AGGCAGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of TGFB1. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM6361 TRPM2 GCAGCAGGCAGGGCC TRPM2 (Accession NM_003307.1) is another GAM6361 target gene. A A
AGGCAGG TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6361 is therefore inhibition of TRPM2, a GAM6361 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM6361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6366 CAV1 TGAGGTTAGTAGTTT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
GAGACCA NM_001753.3) is a GAM6366 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6366 is therefore inhibition of CAV1, a GAM6366 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM6366 DSCR1 TGAGGTTAGTAGTTT Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A
GAGACCA NM_004414.3) is another GAM6366 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6366 is therefore inhibition of DSCR1, a GAM6366 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM6366 IGF1 TGAGGTTAGTAGTTT GAGACCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM6366 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6366 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6366 is therefore inhibition of IGF1, a GAM6366 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6388 ABCD1 AGGCAGTGTTGTTCC TGATTGC ABCD1 (Accession NM_000033.2) is a GAM6388 target gene. ABCD1 BINDING SITE1 and ABCD1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ABCD1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE1 and ABCD1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6388 RNA are set forth in Tables 6 and 7, hereby incorporated herein. ABCD1 A A A A

A function of GAM6388 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6388 ACE AGGCAGTGTTGTTCC TGATTGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is another GAM6388 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated A A

region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6388 is therefore inhibition of ACE, a GAM6388 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM6388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6388 MPO AGGCAGTGTTGTTCC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM6388 A A TGATTGC target gene. MPO BINDING SITE1 and MPO BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE1 and MPO BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6388 is therefore inhibition of MPO, a GAM6388 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM6414 HTR2C TCTAACACTGACTTC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A TATTCCA NM_000868.1) is a GAM6414 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6414 is therefore inhibition of HTR2C, a GAM6414 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM6417 BACE TGGAGAATTAAAAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

GGTAGTG is a GAM6417 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6417 is therefore inhibition of BACE, a GAM6417 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6417 MPO TGGAGAATTAAAAAG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM6417 A A

GGTAGTG target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6417 is therefore inhibition of MPO, a GAM6417 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM6431 DLST TGAAAAGCCTTTGGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TAGTGAT oxo- glutarat (DLST, Accession NM_001933.2) is a GAM6431 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary

structure complementarity to the nucleotide sequence of GAM6431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6431 is therefore inhibition of DLST, a GAM6431 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM6440 ADAMTS5 TGTGAGAGAAATGGC A Disintegrin- like and Metalloprotease (reprolysin type) with A A AAGTTGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM6440 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6440 is therefore inhibition of ADAMTS5, a GAM6440 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM6440 CASP3 TGTGAGAGAAATGGC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A AAGTTGG Accession NM_032991.1) is another GAM6440 target gene. CASP3 BINDING SITE1 and CASP3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE1 and CASP3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6440 is therefore inhibition of CASP3, a GAM6440 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM6440 MAPT TGTGAGAGAAATGGC AAGTTGG Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM6440 target gene. MAPT BINDING SITE1 through MAPT BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 through MAPT BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM6440 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6440 is therefore inhibition of MAPT, a GAM6440 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM6440 MME TGTGAGAGAAATGGC AAGTTGG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is another GAM6440 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6440 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6440 is therefore inhibition of MME, a GAM6440 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6459 DSCR1 TCCTTTGGACATGGG CAAGGGT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM6459 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6459 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6459 is therefore inhibition of DSCR1, a GAM6459 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM6459 MAPT TGCTCTTGCTCTTTC TTCTGGA Microtubule- associated Protein Tau (MAPT, Accession NM_016834.1) is another GAM6459 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6459 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM6459 is therefore inhibition of MAPT, a GAM6459 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM6459 MME TGCTCTTGCTCTTTC TTCTGGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM6459 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6459 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM6459 is therefore inhibition of MME, a GAM6459 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6459 PRND TGCTCTTGCTCTTTC TTCTGGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM6459 target gene. PRND BINDING SITE is a target binding B A

site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6459 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6459 is therefore inhibition of PRND, a GAM6459 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6466 APLP2 TGGAATGGCTGAAGA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A CTGTGAA NM_001642.1) is a GAM6466 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6466 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6466 is therefore inhibition of APLP2, a GAM6466 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6466 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM6466 FLNB TGGAATGGCTGAAGA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A CTGTGAA NM_001457.1) is another GAM6466 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6466 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6466 is therefore inhibition of FLNB, a GAM6466 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6466 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM1193.

GAM6466 SLC17A7 TGGAATGGCTGAAGA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A CTGTGAA NM_020309.1) is another GAM6466 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6466 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6466 is therefore inhibition of SLC17A7, a GAM6466 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM6466 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM6467 BACE GGTAGCTAGAGGGGA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A GATAGCA is a GAM6467 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6467 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6467 is therefore inhibition of BACE, a GAM6467 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6467 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6467 BACE2 GGTAGCTAGAGGGGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A GATAGCA NM_138992.1) is another GAM6467 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6467 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6467 is therefore inhibition of BACE2, a GAM6467 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6467 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6506 ABCD1 GCCCAGGAGTCTGAG ABCD1 (Accession NM_000033.2) is a GAM6506 target gene. ABCD1 A A

GCTGGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6506 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6506 ADAM17 GCCCAGGAGTCTGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GCTGGAG factor, (ADAM17, Accession NM_021832.1) is another GAM6506 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6506 is therefore inhibition of ADAM17, a GAM6506 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6506 DHCR24 GCCCAGGAGTCTGAG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GCTGGAG NM_014762.1) is another GAM6506 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6506 is therefore inhibition of DHCR24, a GAM6506 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6506 GFAP GCCCAGGAGTCTGAG GFAP (Accession NM_002055.2) is another GAM6506 target gene. A A

GCTGGAG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6506 is therefore inhibition of GFAP. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM6506 IGF1 GCCCAGGAGTCTGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCTGGAG NM_000618.2) is another GAM6506 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6506 is therefore inhibition of IGF1, a GAM6506 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6506 LRP1 GCCCAGGAGTCTGAG Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

GCTGGAG macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM6506 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6506 is therefore inhibition of LRP1, a GAM6506 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM6506	UBB	CAGCTATTCAGGAGC TTGAGGT	Ubiquitin B (UBB, Accession NM_018955.2) is another GAM6506 target gene. UBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	B	A

Another function of GAM6506 is therefore inhibition of UBB, a GAM6506 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM6506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM6509	ACHE	TCTTCCCCACCTTCG GCTTGCA	Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM6509 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

A function of GAM6509 is therefore inhibition of ACHE, a GAM6509 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM6509 APP TCTTCCCCACCTTCG APP (Accession NM_000484.1) is another GAM6509 target gene. APP A A
GCTTGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of APP. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM6509 B2M TCTTCCCCACCTTCG Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A
GCTTGCA GAM6509 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of B2M, a GAM6509 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM6509 BACE2 TCTTCCCCACCTTCG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GCTTGCA NM_138991.1) is another GAM6509 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of BACE2, a GAM6509 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM189.

GAM6509 NGB TCTTCCCCACCTTCG Neuroglobin (NGB, Accession NM_021257.2) is another GAM6509
A A
GCTTGCA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of NGB, a GAM6509 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM6509 TGFB1 TCTTCCCCACCTTCG TGFB1 (Accession NM_000660.1) is another GAM6509 target gene.
A A
GCTTGCA TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of TGFB1. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM6509 APBA1 GGCCTCAGAAGCTGA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member B
A
GGGGAGA 1 (X11) (APBA1, Accession NM_001163.2) is another GAM6509 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of APBA1, a GAM6509 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM6509 GFAP GGCCTCAGAAGCTGA GFAP (Accession NM_002055.2) is another GAM6509 target gene. B A

GGGGAGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of GFAP. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM6509 SNCB GGCCTCAGAAGCTGA Synuclein, Beta (SNCB, Accession NM_003085.2) is another B A

GGGGAGA GAM6509 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6509 is therefore inhibition of SNCB, a GAM6509 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM6531 HD GGCAATATTCCAGGA HD (Accession NM_002111.3) is a GAM6531 target gene. HD BINDING A A

TAGGCTG SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6531 is therefore inhibition of HD. Accordingly, utilities of GAM6531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6531 HTR2C GGCAATATTCCAGGA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
TAGGCTG NM_000868.1) is another GAM6531 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6531 is therefore inhibition of HTR2C, a GAM6531 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM6541 CTNND2 TAAGTAAAGAGAGAA Catenin (cadherin- associated protein), Delta 2 (neural A A
GCCAGAA plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM6541 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6541 is therefore inhibition of CTNND2, a GAM6541 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6541 HD TAAGTAAAGAGAGAA HD (Accession NM_002111.3) is another GAM6541 target gene. HD A A
GCCAGAA BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6541 is therefore inhibition of HD.

Accordingly, utilities of GAM6541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6541 OLR1 TAAGTAAAGAGAGAA GCCAGAA Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM6541 target gene. OLR1 BINDING SITE1 and OLR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OLR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE1 and OLR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6541 is therefore inhibition of OLR1, a GAM6541 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6564 APLP2 TGGAATGGCTGAAGA CTGTGAA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM6564 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6564 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6564 is therefore inhibition of APLP2, a GAM6564 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM6564 FLNB TGGAATGGCTGAAGA CTGTGAA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM6564 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6564 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6564 is therefore inhibition of

FLNB, a GAM6564 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM6564 SLC17A7 TGGAATGGCTGAAGA A A CTGTGAA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM6564 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6564 is therefore inhibition of SLC17A7, a GAM6564 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM6564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM6567 ARHA TGGAGAGATAGTGAT A A TTAGCTC Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) is a GAM6567 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6567 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6567 is therefore inhibition of ARHA, a GAM6567 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM6567 PSEN2 TGGAGAGATAGTGAT A A TTAGCTC PSEN2 (Accession NM_012486.1) is another GAM6567 target gene. PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by

PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6567 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6567 is therefore inhibition of PSEN2. Accordingly, utilities of GAM6567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM6567 A A TGFB1 TTAGCTC TGGAGAGATAGTGAT TGFB1 (Accession NM_000660.1) is another GAM6567 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6567 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6567 is therefore inhibition of TGFB1. Accordingly, utilities of GAM6567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM6618 A A BACE2 CTTTGCC TTCAGGCACCAGGCA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is a GAM6618 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6618 is therefore inhibition of BACE2, a GAM6618 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6618 A A THOP1 CTTTGCC TTCAGGCACCAGGCA Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is another GAM6618 target gene. THOP1 BINDING SITE1 and THOP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by THOP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of THOP1 BINDING SITE1 and THOP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6618 is therefore inhibition of THOP1, a GAM6618 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM6618 TRPM2 TTCAGGCACCAGGCA TRPM2 (Accession NM_003307.1) is another GAM6618 target gene. A A

CTTTGCC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6618 is therefore inhibition of TRPM2, a GAM6618 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM6618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6638 DLST CAGAGCTGCCTTTCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

CTTCCTG oxo- glutarat (DLST, Accession NM_001933.2) is a GAM6638 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6638 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6638 is therefore inhibition of DLST, a GAM6638 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6638 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM240.

GAM6638 LRP1 CAGAGCTGCCTTTCC CTTCCTG Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM6638 target gene. LRP1 BINDING SITE1 and LRP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LRP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 and LRP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6638 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6638 is therefore inhibition of LRP1, a GAM6638 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6638 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM6638 OGDH CAGAGCTGCCTTTCC CTTCCTG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM6638 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6638 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6638 is therefore inhibition of OGDH, a GAM6638 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6638 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM6638 PSEN1 CAGAGCTGCCTTTCC CTTCCTG PSEN1 (Accession NM_000021.2) is another GAM6638 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6638 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6638 is therefore inhibition of PSEN1. Accordingly, utilities of GAM6638 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM6674 TGFB1 GAACCTTCAACTGCT TGFB1 (Accession NM_000660.1) is a GAM6674 target gene. TGFB1 A A

TAGCCTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6674 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6674 is therefore inhibition of TGFB1. Accordingly, utilities of GAM6674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM6700 IGF1 TCAGAGTAGGCTTGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGTAATC NM_000618.2) is a GAM6700 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6700 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6700 is therefore inhibition of IGF1, a GAM6700 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6700 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6700 HD GTGATTAAATTAAGG HD (Accession NM_002111.3) is another GAM6700 target gene. HD B A

CTCTTGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6700 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6700 is therefore inhibition of HD. Accordingly, utilities of GAM6700 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6773 BACE CTAGCCTGTTTGTCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TCACCCC is a GAM6773 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6773 is therefore inhibition of BACE, a GAM6773 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6773 CNTF CTAGCCTGTTTGTCC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A
TCACCCC another GAM6773 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6773 is therefore inhibition of CNTF, a GAM6773 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM6773 LRP1 CTAGCCTGTTTGTCC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
TCACCCC macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM6773 target gene. LRP1 BINDING SITE1 and LRP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LRP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 and LRP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6773 is therefore inhibition of LRP1, a GAM6773 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6773 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM6773 MTNR1A CTAGCCTGTTTGTCC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A
TCACCCC another GAM6773 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6773 is therefore inhibition of MTNR1A, a GAM6773 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM6773 S100B CTAGCCTGTTTGTCC S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A
TCACCCC NM_006272.1) is another GAM6773 target gene. S100B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6773 is therefore inhibition of S100B, a GAM6773 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM6773 TNFRSF5 CTAGCCTGTTTGTCC TNFRSF5 (Accession NM_152854.1) is another GAM6773 target gene. A A
TCACCCC TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6773 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM6773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM6774 APPBP2 AAATTGCCGAGATGA TGTTTGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM6774 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6774 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6774 is therefore inhibition of APPBP2, a GAM6774 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6774 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6774 IL1A CCAGAGGTGAGTCTT GATTTTG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM6774 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6774 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM6774 is therefore inhibition of IL1A, a GAM6774 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6774 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM6774 OLR1 CCAGAGGTGAGTCTT GATTTTG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM6774 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding B A

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6774 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6774 is therefore inhibition of OLR1, a GAM6774 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6774 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6799 ARHA TCAAAGCTGCAGATT GCCTGTG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A is a GAM6799 target gene. ARHA BINDING SITE1 and ARHA BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARHA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE1 and ARHA BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6799 is therefore inhibition of ARHA, a GAM6799 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM6799 DLST TCAAAGCTGCAGATT GCCTGTG Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM6799 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6799 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6799 is therefore inhibition of DLST, a GAM6799 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM6799 TNF TCAAAGCTGCAGATT GCCTGTG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM6799 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6799 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6799 is therefore inhibition of TNF, a GAM6799 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM6799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM6799 VLDLR TCAAAGCTGCAGATT GCCTGTG Very Low Density Lipoprotein Receptor (VLDLR, Accession NM_003383.1) is another GAM6799 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6799 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6799 is therefore inhibition of VLDLR, a GAM6799 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM6799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM6807 GYPA TGAGGTAAGTATGTT ATTGGAA Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is a GAM6807 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6807 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6807 is therefore inhibition of GYPA, a GAM6807 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6807 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6811 MPO TCAGGTTCCTGATTG GAGTTCT Myeloperoxidase (MPO, Accession NM_000250.1) is a GAM6811 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6811 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6811 is therefore inhibition of MPO, a GAM6811 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6811 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM6811 OLR1 TCAGGTTCCTGATTG GAGTTCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM6811 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6811 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6811 is therefore inhibition of OLR1, a GAM6811 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6811 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6818 CTNND2 TTCTTTTTCCGCTTT CTGAGCC Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM6818 target gene. CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTNND2, corresponding to target binding sites such as BINDING SITE A A

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6818 is therefore inhibition of CTNND2, a GAM6818 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM6818 GYPA TTCTTTTTCCGCTTT CTGAGCC Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM6818 target gene. GYPA BINDING SITE1 and GYPA BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GYPA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE1 and GYPA BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6818 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6818 is therefore inhibition of GYPA, a GAM6818 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6818 OLR1 TTCTTTTTCCGCTTT CTGAGCC Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM6818 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6818 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6818 is therefore inhibition of OLR1, a GAM6818 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6818 TNFRSF6 TTCTTTTTCCGCTTT TNFRSF6 (Accession NM_152875.1) is another GAM6818 target gene. A A

CTGAGCC TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6818 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM6818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM6836 FHL2 ACTGCACTCTAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGGTGAT a GAM6836 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6836 is therefore inhibition of FHL2, a GAM6836 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6836 IGF1 ACTGCACTCTAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGGTGAT NM_000618.2) is another GAM6836 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6836 is therefore inhibition of IGF1, a GAM6836 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6836 PRND ACTGCACTCTAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

AGGTGAT another GAM6836 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6836 is therefore inhibition of PRND, a GAM6836 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6836 TFCP2 ACTGCACTCTAGCCT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

AGGTGAT another GAM6836 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6836 is therefore inhibition of TFCP2, a GAM6836 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM6840 DHCR24 GCTGAATTTTGACTC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

CATCTCC NM_014762.1) is a GAM6840 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6840 is therefore inhibition of DHCR24, a GAM6840 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6840 HD GCTGAATTTTGACTC HD (Accession NM_002111.3) is another GAM6840 target gene. HD A A

CATCTCC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6840 is therefore inhibition of HD. Accordingly, utilities of GAM6840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM6840 ARHA GTTCTTCTGGGAGAA Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) B A

AAATGGC is another GAM6840 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6840 is therefore inhibition of ARHA, a GAM6840 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM6840 MME GTTCTTCTGGGAGAA Membrane Metallo- endopeptidase (neutral endopeptidase, B A

AAATGGC enkephalinase, (MME, Accession NM_000902.2) is another GAM6840 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6840 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

Another function of GAM6840 is therefore inhibition of MME, a GAM6840 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6842 IGF1 TCATATCATTTTGAA AGCTGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM6842 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM6842 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM6842 is therefore inhibition of IGF1, a GAM6842 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6842 IL1A TCATATCATTTTGAA AGCTGAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM6842 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6842 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6842 is therefore inhibition of IL1A, a GAM6842 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM6858 PSEN2 GGTGCAGATCATGGA PSEN2 (Accession NM_000447.1) is a GAM6858 target gene. PSEN2 A A

TAGAGCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6858 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6858 is therefore inhibition of PSEN2. Accordingly, utilities of GAM6858 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM6978 BACE2 TTCAGGCACCAGGCA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

CTTTGCC NM_138991.1) is a GAM6978 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6978 is therefore inhibition of BACE2, a GAM6978 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM6978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM6978 THOP1 TTCAGGCACCAGGCA Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is A A

CTTTGCC another GAM6978 target gene. THOP1 BINDING SITE1 and THOP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by THOP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE1 and THOP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM6978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6978 is therefore inhibition of THOP1, a GAM6978 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM6978 TRPM2 TTCAGGCACCAGGCA TRPM2 (Accession NM_003307.1) is another GAM6978 target gene. A A

CTTTGCC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6978 is therefore inhibition of TRPM2, a GAM6978 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM6978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM6982 GYPA GAAGGCAGTAGGTTG Glycophorin A (includes MN blood group) (GYPA, Accession A A

TATAGTT NM_002099.2) is a GAM6982 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6982 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6982 is therefore inhibition of GYPA, a GAM6982 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6982 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6982 IGF1 GAAGGCAGTAGGTTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TATAGTT NM_000618.2) is another GAM6982 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6982 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6982 is therefore inhibition of IGF1, a GAM6982 target gene which are structurally and functionally

related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6982 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6994 ACE TTGCCTAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TGCAGTG (ACE, Accession NM_152831.1) is a GAM6994 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6994 is therefore inhibition of ACE, a GAM6994 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM6994 ADAM17 TTGCCTAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TGCAGTG factor, (ADAM17, Accession NM_021832.1) is another GAM6994 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6994 is therefore inhibition of ADAM17, a GAM6994 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM6994 IAPP TTGCCTAGGCTGGAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
TGCAGTG another GAM6994 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6994 is therefore inhibition of IAPP, a GAM6994 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM6994 IGF1 TTGCCTAGGCTGGAG TGCAGTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM6994 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6994 is therefore inhibition of IGF1, a GAM6994 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM6994 MAPT TTGCCTAGGCTGGAG TGCAGTG Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM6994 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM6994 is therefore inhibition of MAPT, a GAM6994 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM6994 NOTCH1 TTGCCTAGGCTGGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGCAGTG (NOTCH1, Accession NM_017617.2) is another GAM6994 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6994 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6994 is therefore inhibition of NOTCH1, a GAM6994 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM6994 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM6996 ABCD1 TTCCTGGTGGAGGCA ABCD1 (Accession NM_000033.2) is a GAM6996 target gene. ABCD1 A A

TTCGGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6996 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM6996 is therefore inhibition of ABCD1. Accordingly, utilities of GAM6996 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM6996 BLMH TTCCTGGTGGAGGCA Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another A A

TTCGGAG GAM6996 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM6996 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM6996 is therefore inhibition of BLMH, a GAM6996 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM6996 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM7017 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM7017 target gene. HD BINDING A A

ACTTGTA SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7017 is therefore inhibition of HD. Accordingly, utilities of GAM7017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7017 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACTTGTA NM_000868.1) is another GAM7017 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7017 is therefore inhibition of HTR2C, a GAM7017 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7017 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGTA NM_000618.2) is another GAM7017 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7017 is therefore inhibition of IGF1, a GAM7017 target gene which are structurally and functionally

related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7017 PSEN2 TCTGCTGTGATGGAC A A ACTTGTA PSEN2 (Accession NM_000447.1) is another GAM7017 target gene. PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7017 is therefore inhibition of PSEN2. Accordingly, utilities of GAM7017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM7017 TNFRSF6 TCTGCTGTGATGGAC A A ACTTGTA TNFRSF6 (Accession NM_152872.1) is another GAM7017 target gene. TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7017 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM7017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM7022 APPBP2 TTGGTTGCTGATGAG A A CTTTGAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM7022 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7022 is therefore inhibition of APPBP2, a GAM7022 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7022 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7022 BACE TTGGTTGCTGATGAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

CTTTGAG is another GAM7022 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7022 is therefore inhibition of BACE, a GAM7022 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7022 IGF1 TTGGTTGCTGATGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTTTGAG NM_000618.2) is another GAM7022 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7022 is therefore inhibition of IGF1, a GAM7022 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7022 MTNR1A TTGGTTGCTGATGAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CTTTGAG another GAM7022 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7022 is therefore inhibition of MTNR1A, a GAM7022 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM7067 ADAM10 TTGAGCAAAATATCT A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A
GGTTTCA Accession NM_001110.1) is a GAM7067 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7067 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7067 is therefore inhibition of ADAM10, a GAM7067 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7067 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM7067 APPBP2 TTGAGCAAAATATCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGTTTCA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM7067 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7067 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7067 is therefore inhibition of APPBP2, a GAM7067 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7067 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM7067 GYPA TTGAGCAAAATATCT Glycophorin A (includes MN blood group) (GYPA, Accession A A
GGTTTCA NM_002099.2) is another GAM7067 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7067 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7067 is therefore inhibition of GYPA, a GAM7067 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7067 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7067 HD TTGAGCAAAATATCT HD (Accession NM_002111.3) is another GAM7067 target gene. HD A A
GGTTTCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7067 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7067 is therefore inhibition of HD. Accordingly, utilities of GAM7067 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7067 OLR1 TTGAGCAAAATATCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A
GGTTTCA (OLR1, Accession NM_002543.1) is another GAM7067 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7067 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7067 is therefore inhibition of OLR1, a GAM7067 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7067 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7078 HD TAGGGGGTCACCTAT HD (Accession NM_002111.3) is a GAM7078 target gene. HD BINDING A A
GTGGGAG SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7078 is therefore inhibition of HD. Accordingly, utilities of GAM7078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7078 HD CTCCTACAACTGACT HD (Accession NM_002111.3) is another GAM7078 target gene. HD B A
CTCTGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7078 is therefore inhibition of HD. Accordingly, utilities of GAM7078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7078 IGF1 CTCCTACAACTGACT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession B A
CTCTGGA NM_000618.2) is another GAM7078 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7078 is therefore inhibition of IGF1, a GAM7078 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7080 APLP2 TTTCCACAGCGGCCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A
ATTCTTC NM_001642.1) is a GAM7080 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7080 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7080 is therefore inhibition of APLP2, a GAM7080 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7080 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM7080 HTR2C TTTCCACAGCGGCCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
ATTCTTC NM_000868.1) is another GAM7080 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7080 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7080 is therefore inhibition of HTR2C, a GAM7080 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7080 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7080 TNF TTTCCACAGCGGCCA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A
ATTCTTC Accession NM_000594.2) is another GAM7080 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7080 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7080 is therefore inhibition of TNF, a GAM7080 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM7080 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7095 ADAMTS5 TGTGAGAGAAATGGC A Disintegrin- like and Metalloprotease (reprolysin type) with A A
AAGTTGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM7095 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7095 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7095 is therefore inhibition of ADAMTS5, a GAM7095 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7095 CASP3 TGTGAGAGAAATGGC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A
AAGTTGG Accession NM_032991.1) is another GAM7095 target gene. CASP3 BINDING SITE1 and CASP3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE1 and CASP3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7095 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7095 is therefore inhibition of CASP3, a GAM7095 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM7095 MAPT TGTGAGAGAAATGGC Microtubule- associated Protein Tau (MAPT, Accession A A
AAGTTGG NM_173727.1) is another GAM7095 target gene. MAPT BINDING SITE1 through MAPT BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 through MAPT BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM7095 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7095 is therefore inhibition of MAPT, a GAM7095 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM7095 MME TGTGAGAGAAATGGC AAGTTGG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is another GAM7095 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7095 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7095 is therefore inhibition of MME, a GAM7095 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7102 ACE TCACTGCAACCTCCA CCTCCCG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM7102 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7102 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7102 is therefore inhibition of ACE, a GAM7102 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7102 IAPP TCACTGCAACCTCCA CCTCCCG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM7102 target gene. IAPP BINDING SITE is a target binding A A

site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7102 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7102 is therefore inhibition of IAPP, a GAM7102 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7102 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7124 ACHE TAGCACCTTCTGAAA TAACGTG Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM7124 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7124 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7124 is therefore inhibition of ACHE, a GAM7124 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM7124 SNCA TAGCACCTTCTGAAA TAACGTG SNCA (Accession NM_000345.2) is another GAM7124 target gene. SNCA BINDING SITE1 and SNCA BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SNCA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE1 and SNCA BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7124 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7124 is therefore inhibition of SNCA. Accordingly, utilities of GAM7124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM7135 APPBP2 TTGGTTGCTGATGAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CTTTGAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM7135 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7135 is therefore inhibition of APPBP2, a GAM7135 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7135 BACE TTGGTTGCTGATGAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A
CTTTGAG is another GAM7135 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7135 is therefore inhibition of BACE, a GAM7135 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7135 IGF1 TTGGTTGCTGATGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CTTTGAG NM_000618.2) is another GAM7135 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7135 is therefore inhibition of

IGF1, a GAM7135 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7135 MTNR1A TTGGTTGCTGATGAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CTTTGAG another GAM7135 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7135 is therefore inhibition of MTNR1A, a GAM7135 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM7140 ADAMTS5 TACAGGCAGGCACAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

AGGCAGT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM7140 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7140 is therefore inhibition of ADAMTS5, a GAM7140 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7140 APBA2 TACAGGCAGGCACAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AGGCAGT 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM7140 target

gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of APBA2, a GAM7140 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7140 DLST TACAGGCAGGCACAG AA AGGCAGT Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is another GAM7140 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of DLST, a GAM7140 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM7140 NGB TACAGGCAGGCACAG AA AGGCAGT Neuroglobin (NGB, Accession NM_021257.2) is another GAM7140 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of NGB, a GAM7140 target gene which has function in oxygen transport

and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7140 A A SNCG AGGCAGT TACAGGCAGGCACAG SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM7140 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of SNCG, a GAM7140 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7140 A A TFCP2 AGGCAGT TACAGGCAGGCACAG Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM7140 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of TFCP2, a GAM7140 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM7140 A A TGFB1 AGGCAGT TACAGGCAGGCACAG TGFB1 (Accession NM_000660.1) is another GAM7140 target gene. TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7140 is therefore inhibition of TGFB1. Accordingly, utilities of GAM7140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM7146 APLP2 TGCTGTAGTATGTAT ATAGTAT Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM7146 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7146 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7146 is therefore inhibition of APLP2, a GAM7146 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM7146 MME TGCTGTAGTATGTAT ATAGTAT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM7146 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7146 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7146 is therefore inhibition of MME, a GAM7146 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7162 HD CTGGGTGGCCTTCAG TCCATGA HD (Accession NM_002111.3) is a GAM7162 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7162 is therefore inhibition of HD. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7162 PLAU CTGGGTGGCCTTCAG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

TCCATGA is another GAM7162 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7162 is therefore inhibition of PLAU, a GAM7162 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM7162 TNFRSF5 CTGGGTGGCCTTCAG TNFRSF5 (Accession NM_001250.3) is another GAM7162 target gene. A A

TCCATGA TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7162 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM7162 APBB2 TCAGGCTGAGGTCAT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A

CTGCATC 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM7162 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7162 is therefore inhibition of APBB2, a GAM7162 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7162 BACE2 TCAGGCTGAGGTCAT CTGCATC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM7162 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM7162 is therefore inhibition of BACE2, a GAM7162 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7162 TRPM2 TCAGGCTGAGGTCAT CTGCATC TRPM2 (Accession NM_003307.1) is another GAM7162 target gene. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7162 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM7162 is therefore inhibition of TRPM2, a GAM7162 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM7162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7166 CAV1 AGGGAGTTTACATGT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
TTTCTAA NM_001753.3) is a GAM7166 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7166 is therefore inhibition of CAV1, a GAM7166 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7166 MME AGGGAGTTTACATGT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TTTCTAA enkephalinase, (MME, Accession NM_007287.1) is another GAM7166 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7166 is therefore inhibition of MME, a GAM7166 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7169 ACE TAGACTGAGGCTTCC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TGCAGGG (ACE, Accession NM_152831.1) is a GAM7169 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7169 is therefore inhibition of ACE, a GAM7169 target gene which Angiotensin I- converting enzyme

(dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7169 DHCR24 TAGACTGAGGCTTCC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGCAGGG NM_014762.1) is another GAM7169 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7169 is therefore inhibition of DHCR24, a GAM7169 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7169 DLST TAGACTGAGGCTTCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TGCAGGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM7169 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7169 is therefore inhibition of DLST, a GAM7169 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM7169 DSCR1 TAGACTGAGGCTTCC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

TGCAGGG NM_004414.3) is another GAM7169 target gene. DSCR1 BINDING SITE1 and

DSCR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DSCR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7169 is therefore inhibition of DSCR1, a GAM7169 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM7169 A A TGFB1 TAGACTGAGGCTTCC TGCAGGG TGFB1 (Accession NM_000660.1) is another GAM7169 target gene. TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7169 is therefore inhibition of TGFB1. Accordingly, utilities of GAM7169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM7199 A A CAV2 TGGCAAAGAAGGCAG TACAGTT Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM7199 target gene. CAV2 BINDING SITE1 and CAV2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE1 and CAV2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7199 is therefore inhibition of CAV2, a GAM7199 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM55.

GAM7201 ACE TGTCCTTTGTTTTGA GATGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM7201 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7201 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7201 is therefore inhibition of ACE, a GAM7201 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7201 ADAM17 TGTCCTTTGTTTTGA GATGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is another GAM7201 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7201 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7201 is therefore inhibition of ADAM17, a GAM7201 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7201 TNF TGTCCTTTGTTTTGA GATGGAG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM7201 target gene. TNF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7201 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7201 is therefore inhibition of

TNF, a GAM7201 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM7201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7212 A2M GGCCAGGACTCTTGC AGAACTG Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a GAM7212 target gene. A2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7212 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7212 is therefore inhibition of A2M, a GAM7212 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM7212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM7212 IL1B GGCCAGGACTCTTGC AGAACTG Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another GAM7212 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7212 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7212 is therefore inhibition of IL1B, a GAM7212 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM7212 SERPINA3 GGCCAGGACTCTTGC AGAACTG Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 antiprotei (SERPINA3, Accession NM_001085.2) is another GAM7212 target gene. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences A A

of SERPINA3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7212 is therefore inhibition of SERPINA3, a GAM7212 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM7212 SLC6A4 GGCCAGGACTCTTGC AGAACTG Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM7212 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7212 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7212 is therefore inhibition of SLC6A4, a GAM7212 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM7212 TFCP2 GGCCAGGACTCTTGC AGAACTG Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM7212 target gene. TFCP2 BINDING SITE1 through TFCP2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TFCP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE1 through TFCP2 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM7212 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7212 is therefore inhibition of TFCP2, a GAM7212 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM7241 A MPO A CTCAGTGTGAAGAAC TACGGGT Myeloperoxidase (MPO, Accession NM_000250.1) is a GAM7241 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7241 is therefore inhibition of MPO, a GAM7241 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM7250 A ADAM17 A GAAGAGCTGTGTGCT GTGATGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is a GAM7250 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7250 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7250 is therefore inhibition of ADAM17, a GAM7250 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7250 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7255 A DSCR1 A TGGTCTCTTGAAAGA GGCTCTT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM7255 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7255 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7255 is therefore inhibition of DSCR1, a GAM7255 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM7255 IL1B TGGTCTCTTGAAAGA GGCTCTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another GAM7255 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7255 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7255 is therefore inhibition of IL1B, a GAM7255 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM7257 IAPP TGGGGTTTCTCCATG TTGGTCA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM7257 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7257 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7257 is therefore inhibition of IAPP, a GAM7257 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7257 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7260 MME ATGTCAGTGAAGAGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TCTGGCA enkephalinase, (MME, Accession NM_007289.1) is a GAM7260 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7260 is therefore inhibition of MME, a GAM7260 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7260 A A PSEN1 ATGTCAGTGAAGAGG TCTGGCA PSEN1 (Accession NM_000021.2) is another GAM7260 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7260 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7264 A A MAPK10 ACTGGCACAGACATC TGTCAAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is a GAM7264 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7264 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7264 is therefore inhibition of MAPK10, a GAM7264 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7264 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM55.

GAM7264 A A MTNR1A ACTGGCACAGACATC TGTCAAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM7264 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7264 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7264 is therefore inhibition of MTNR1A, a GAM7264 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7264 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM7272 A A APP CTGGGCAGTAATGTA GTTGAGA APP (Accession NM_000484.1) is a GAM7272 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7272 is therefore inhibition of APP. Accordingly, utilities of GAM7272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM7302 A A HTR2C GAAACTAGTGTTGGG ACAAAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is a GAM7302 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7302 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7302 is therefore inhibition of HTR2C, a GAM7302 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7302 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7302 MME GAAACTAGTGTTGGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
ACAAAGG enkephalinase, (MME, Accession NM_007288.1) is another GAM7302 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7302 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7302 is therefore inhibition of MME, a GAM7302 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7302 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7320 GYPA GGTTCTCAAATGAGG Glycophorin A (includes MN blood group) (GYPA, Accession A A
GACATTT NM_002099.2) is a GAM7320 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7320 is therefore inhibition of GYPA, a GAM7320 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7320 NGB GGTTCTCAAATGAGG Neuroglobin (NGB, Accession NM_021257.2) is another GAM7320 A A
GACATTT target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7320 is therefore inhibition of NGB, a GAM7320 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7320 PLAU GGTTCTCAAATGAGG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GACATTT is another GAM7320 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7320 is therefore inhibition of PLAU, a GAM7320 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM7320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM7320 PSEN1 GGTTCTCAAATGAGG PSEN1 (Accession NM_000021.2) is another GAM7320 target gene. A A

GACATTT PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7320 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7320 CHAT ACATTTCCAATGTTT Choline Acetyltransferase (CHAT, Accession NM_020986.1) is B A

GGGGACA another GAM7320 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7320 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7320 is therefore inhibition of CHAT, a GAM7320 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7331 FHL2 ACTGCACTCCAGCCT ATGGGAT A A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM7331 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7331 is therefore inhibition of FHL2, a GAM7331 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7331 IGF1 ACTGCACTCCAGCCT ATGGGAT A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM7331 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7331 is therefore inhibition of IGF1, a GAM7331 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7331 PRND ACTGCACTCCAGCCT A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is

ATGGGAT another GAM7331 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7331 is therefore inhibition of PRND, a GAM7331 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7345 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM7345 target gene. HD BINDING A A

ACTTGTA SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7345 is therefore inhibition of HD. Accordingly, utilities of GAM7345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7345 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACTTGTA NM_000868.1) is another GAM7345 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7345 is therefore inhibition of HTR2C, a GAM7345 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7345 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGTA NM_000618.2) is another GAM7345 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7345 is therefore inhibition of IGF1, a GAM7345 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7345 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM7345 target gene. A A

ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7345 is therefore inhibition of PSEN2. Accordingly, utilities of GAM7345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM7345 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM7345 target gene. A A

ACTTGTA TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7345 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM7345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM7349 ADAM17 TGGAGTGTCTGGAGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TGTCTCT factor, (ADAM17, Accession NM_021832.1) is a GAM7349 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7349 is therefore inhibition of ADAM17, a GAM7349 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7349 DHCR24 TGGAGTGTCTGGAGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGTCTCT NM_014762.1) is another GAM7349 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of DHCR24, a GAM7349 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7349 HD TGGAGTGTCTGGAGG HD (Accession NM_002111.3) is another GAM7349 target gene. HD A A

TGTCTCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of HD. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with HD.

GAM7349 OLR1 TGGAGTGTCTGGAGG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A TGTCTCT (OLR1, Accession NM_002543.1) is another GAM7349 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of OLR1, a GAM7349 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7349 PLAU TGGAGTGTCTGGAGG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A TGTCTCT is another GAM7349 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of PLAU, a GAM7349 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM7349 TGFB1 TGGAGTGTCTGGAGG TGFB1 (Accession NM_000660.1) is another GAM7349 target gene. A A TGTCTCT TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of TGFB1. Accordingly, utilities of GAM7349 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM7349 TNFSF5 TGGAGTGTCTGGAGG TNFSF5 (Accession NM_000074.1) is another GAM7349 target gene. A A

TGTCTCT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7349 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM7349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM7350 ADAM17 CTAATTGTTCCTGCA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GGTAGTA factor, (ADAM17, Accession NM_021832.1) is a GAM7350 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7350 is therefore inhibition of ADAM17, a GAM7350 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7363 HD GTCAGCAAGGAGGGG HD (Accession NM_002111.3) is a GAM7363 target gene. HD BINDING A A

TGGACAA SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7363 is therefore inhibition of HD. Accordingly, utilities of GAM7363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7366 APPBP2 TATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM7366 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7366 is therefore inhibition of APPBP2, a GAM7366 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7366 FHL2 TATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM7366 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7366 is therefore inhibition of FHL2, a GAM7366 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7366 HD TATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM7366 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7366 is therefore inhibition of HD. Accordingly, utilities of GAM7366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with HD.

GAM7366 IGF1 TATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM7366 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7366 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7366 is therefore inhibition of IGF1, a GAM7366 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7366 PRND TATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM7366 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM7366 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7366 is therefore inhibition of PRND, a GAM7366 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7369 APBB2 TCTTGGTGCTTTTGC TGGATGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM7369 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7369 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7369 is therefore inhibition of APBB2, a GAM7369 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7369 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7369 APOC1 TCTTGGTGCTTTTGC TGGATGA Apolipoprotein C- I (APOC1, Accession NM_001645.2) is another GAM7369 target gene. APOC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7369 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7369 is therefore inhibition of APOC1, a GAM7369 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7369 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM7369 CHAT TCTTGGTGCTTTTGC TGGATGA Choline Acetyltransferase (CHAT, Accession NM_020986.1) is another GAM7369 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7369 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7369 is therefore inhibition of CHAT, a GAM7369 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7369 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7369 CLU TCTTGGTGCTTTTGC TGGATGA Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is another GAM7369 target A A

gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7369 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7369 is therefore inhibition of CLU, a GAM7369 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7369 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM7371 A2M AGAAGGTTGGGGCTG Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a A A GAGGTCT GAM7371 target gene. A2M BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7371 is therefore inhibition of A2M, a GAM7371 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM7371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM7371 BACE AGAAGGTTGGGGCTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A GAGGTCT is another GAM7371 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7371 is therefore inhibition of BACE, a GAM7371 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7371 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7371 SLC17A7 AGAAGGTTGGGGCTG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A
GAGGTCT NM_020309.1) is another GAM7371 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7371 is therefore inhibition of SLC17A7, a GAM7371 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM7371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM7371 SLC6A4 AGAAGGTTGGGGCTG Solute Carrier Family 6 (neurotransmitter transporter, A A
GAGGTCT serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM7371 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7371 is therefore inhibition of SLC6A4, a GAM7371 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM7374 IL1B GCAGCTGTTTATTTA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is a GAM7374 A A
GAACCTG target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM7374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7374 is therefore inhibition of IL1B, a GAM7374 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM7374 MME GCAGCTGTTTATTTA GAACCTG Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is another GAM7374 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7374 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7374 is therefore inhibition of MME, a GAM7374 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7374 TNFSF5 GCAGCTGTTTATTTA GAACCTG TNFSF5 (Accession NM_000074.1) is another GAM7374 target gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7374 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7374 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM7374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM7374 ACT CAGATCTGGGATACA GCTGTGG Activator of CAMP- responsive Element Modulator (CR (ACT, Accession NM_020482.3) is another GAM7374 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. B A

Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7374 is therefore inhibition of ACT, a GAM7374 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM7374 APBB2 CAGATCTGGGATACA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member B A

GCTGTGG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM7374 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7374 is therefore inhibition of APBB2, a GAM7374 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7400 TNFRSF6 TTAATGCTTTTTGTC TNFRSF6 (Accession NM_152873.1) is a GAM7400 target gene. A A

ATACTCA TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7400 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM7400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM7415 ADAMTS5 TACAGGCAGGCACAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

AGGCAGT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM7415 target gene.

ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7415 is therefore inhibition of ADAMTS5, a GAM7415 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7415 APBA2 TACAGGCAGGCACAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AGGCAGT 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM7415 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of APBA2, a GAM7415 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7415 DLST TACAGGCAGGCACAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

AGGCAGT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM7415 target gene. DLST BINDING SITE1 and DLST BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DLST, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE1 and DLST BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of

DLST, a GAM7415 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM7415 A A NGB TACAGGCAGGCACAG AGGCAGT Neuroglobin (NGB, Accession NM_021257.2) is another GAM7415 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of NGB, a GAM7415 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7415 A A SNCG TACAGGCAGGCACAG AGGCAGT SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM7415 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of SNCG, a GAM7415 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7415 A A TFCP2 TACAGGCAGGCACAG AGGCAGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM7415 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of TFCP2, a GAM7415 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM7415 TGFB1 TACAGGCAGGCACAG TGFB1 (Accession NM_000660.1) is another GAM7415 target gene. A A

AGGCAGT TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7415 is therefore inhibition of TGFB1. Accordingly, utilities of GAM7415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM7440 IAPP TGTGACTGAGGTGCG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a A A

CATAAAG GAM7440 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7440 is therefore inhibition of IAPP, a GAM7440 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7446 ACE TCACTGCAACCTCTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

CTGCCTG (ACE, Accession NM_152831.1) is a GAM7446 target gene. ACE BINDING

SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7446 is therefore inhibition of ACE, a GAM7446 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7446 APBA1 TCACTGCAACCTCTG CTGCCTG A A Amyloid Beta (A4) Precursor Protein- binding, Family A, Member 1 (X11) (APBA1, Accession NM_001163.2) is another GAM7446 target gene. APBA1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of APBA1, a GAM7446 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM7446 APLP1 TCACTGCAACCTCTG CTGCCTG A A Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession NM_005166.2) is another GAM7446 target gene. APLP1 BINDING SITE1 and APLP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APLP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE1 and APLP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of APLP1, a GAM7446 target gene which is a membrane- associated

glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM7446 APPBP2 TCACTGCAACCTCTG CTGCCTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM7446 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7446 is therefore inhibition of APPBP2, a GAM7446 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7446 AVP TCACTGCAACCTCTG CTGCCTG AVP (Accession NM_000490.2) is another GAM7446 target gene. AVP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7446 is therefore inhibition of AVP. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM7446 CHAT TCACTGCAACCTCTG CTGCCTG Choline Acetyltransferase (CHAT, Accession NM_020985.1) is another GAM7446 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7446 is therefore inhibition of

CHAT, a GAM7446 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7446 CTNND2 TCACTGCAACCTCTG CTGCCTG Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM7446 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7446 is therefore inhibition of CTNND2, a GAM7446 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM7446 FLNB TCACTGCAACCTCTG CTGCCTG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM7446 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7446 is therefore inhibition of FLNB, a GAM7446 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM7446 HD TCACTGCAACCTCTG CTGCCTG HD (Accession NM_002111.3) is another GAM7446 target gene. HD BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING A A

SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of HD. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7446 HTR2A TCACTGCAACCTCTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
CTGCCTG NM_000621.1) is another GAM7446 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of HTR2A, a GAM7446 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM7446 HTR2C TCACTGCAACCTCTG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
CTGCCTG NM_000868.1) is another GAM7446 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of HTR2C, a GAM7446 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7446 IAPP TCACTGCAACCTCTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
CTGCCTG another GAM7446 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of IAPP, a GAM7446 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7446 MAPT TCACTGCAACCTCTG CTGCCTG A A Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM7446 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of MAPT, a GAM7446 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM7446 MPO TCACTGCAACCTCTG CTGCCTG A A Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM7446 target gene. MPO BINDING SITE1 and MPO BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE1 and MPO BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of MPO, a GAM7446 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM7446 A A MTNR1A CTGCCTG TCACTGCAACCTCTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM7446 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of MTNR1A, a GAM7446 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM7446 A A NGB CTGCCTG TCACTGCAACCTCTG Neuroglobin (NGB, Accession NM_021257.2) is another GAM7446 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of NGB, a GAM7446 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7446 A A OGDH CTGCCTG TCACTGCAACCTCTG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM7446 target gene. OGDH BINDING SITE1 and OGDH BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by OGDH, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE1 and OGDH BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM7446 is therefore inhibition of OGDH, a GAM7446 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM7446 A A PSEN1 TCACTGCAACCTCTG CTGCCTG PSEN1 (Accession NM_000021.2) is another GAM7446 target gene. PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7446 A A TRPM2 TCACTGCAACCTCTG CTGCCTG TRPM2 (Accession NM_003307.1) is another GAM7446 target gene. TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TRPM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE1 and TRPM2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7446 is therefore inhibition of TRPM2, a GAM7446 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM7446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7449 A A IGF1 GGTAGCTTATTAAAG AAACTCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM7449 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7449 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

A function of GAM7449 is therefore inhibition of IGF1, a GAM7449 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7449 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7449 NOTCH1 GGGGTTTCTGTAGGC Notch (Drosophila) Homolog 1 (translocation- associated) B A

ACTTTAT (NOTCH1, Accession NM_017617.2) is another GAM7449 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7449 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7449 is therefore inhibition of NOTCH1, a GAM7449 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7449 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7464 BAX ATTTATTTTCCCTCA BCL2- associated X Protein (BAX, Accession NM_138765.1) is a A A

AGTACCT GAM7464 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7464 is therefore inhibition of BAX, a GAM7464 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM7464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM7464 BAX AGGTAGGGAGGGTAG BCL2- associated X Protein (BAX, Accession NM_004324.2) is B A

ATGCTCT another GAM7464 target gene. BAX BINDING SITE1 and BAX BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BAX, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE1 and BAX BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7464 is therefore inhibition of BAX, a GAM7464 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM7464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM7464 DLST AGGTAGGGAGGGTAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- B A

ATGCTCT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM7464 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7464 is therefore inhibition of DLST, a GAM7464 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM7464 MPO AGGTAGGGAGGGTAG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM7464 B A

ATGCTCT target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7464 is therefore inhibition of MPO, a GAM7464 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM7464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM7464 TRPM2 AGGTAGGGAGGGTAG TRPM2 (Accession NM_003307.1) is another GAM7464 target gene. B A

ATGCTCT TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7464 is therefore inhibition of TRPM2, a GAM7464 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM7464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7473 ACE TCGGCAGGGAACAGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

AAGTAGG (ACE, Accession NM_152831.1) is a GAM7473 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7473 is therefore inhibition of ACE, a GAM7473 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7473 BACE TCGGCAGGGAACAGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

AAGTAGG is another GAM7473 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING

SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7473 is therefore inhibition of BACE, a GAM7473 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7473 HTR2C TCGGCAGGGAACAGG AAGTAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM7473 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7473 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7473 is therefore inhibition of HTR2C, a GAM7473 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7473 LRP1 TCGGCAGGGAACAGG AAGTAGG Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM7473 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7473 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7473 is therefore inhibition of LRP1, a GAM7473 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM1975.

GAM7473 MT3 TCGGCAGGGAACAGG Metallothionein 3 (MT3, Accession NM_005954.1) is another A A
AAGTAGG GAM7473 target gene. MT3 BINDING SITE1 and MT3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MT3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MT3 BINDING SITE1 and MT3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7473 is therefore inhibition of MT3, a GAM7473 target gene which inhibits survival and neurite formation of cortical neurons in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MT3.The function of MT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3890.

GAM7477 AVP TGAGGACAGGAGGTT AVP (Accession NM_000490.2) is a GAM7477 target gene. AVP A A
GTGAGTT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7477 is therefore inhibition of AVP. Accordingly, utilities of GAM7477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM7477 IL1B TGAGGACAGGAGGTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A
GTGAGTT GAM7477 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7477 is therefore inhibition of IL1B, a GAM7477 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM604.

GAM7477 MAPK10 TGAGGACAGGAGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
GTGAGTT NM_138980.1) is another GAM7477 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7477 is therefore inhibition of MAPK10, a GAM7477 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM7477 MME TGAGGACAGGAGGTT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GTGAGTT enkephalinase, (MME, Accession NM_000902.2) is another GAM7477 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7477 is therefore inhibition of MME, a GAM7477 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7520 NGB TGCCTAGGCAGGACG Neuroglobin (NGB, Accession NM_021257.2) is a GAM7520 target A A
GAATGCA gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7520 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

A function of GAM7520 is therefore inhibition of NGB, a GAM7520 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7520 A A RAGE GAATGCA TGCCTAGGCAGGACG Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another GAM7520 target gene. RAGE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7520 is therefore inhibition of RAGE, a GAM7520 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM7520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM7520 A A SLC17A7 GAATGCA TGCCTAGGCAGGACG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession NM_020309.1) is another GAM7520 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7520 is therefore inhibition of SLC17A7, a GAM7520 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM7520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM7520 A A SNCG TGCCTAGGCAGGACG SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another

GAATGCA GAM7520 target gene. SNCG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7520 is therefore inhibition of SNCG, a GAM7520 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7530 ACE TAGCAGCACATAATG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GTTTGAA (ACE, Accession NM_152831.1) is a GAM7530 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7530 is therefore inhibition of ACE, a GAM7530 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7530 ADAM10 TAGCAGCACATAATG A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A
GTTTGAA Accession NM_001110.1) is another GAM7530 target gene. ADAM10 BINDING SITE1 and ADAM10 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ADAM10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE1 and ADAM10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7530 is therefore inhibition of ADAM10, a GAM7530 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM7530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM7530 HTR2A TAGCAGCACATAATG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
GTTTGAA NM_000621.1) is another GAM7530 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7530 is therefore inhibition of HTR2A, a GAM7530 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM7530 MME TAGCAGCACATAATG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GTTTGAA enkephalinase, (MME, Accession NM_000902.2) is another GAM7530 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7530 is therefore inhibition of MME, a GAM7530 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7530 SLC6A4 TAGCAGCACATAATG Solute Carrier Family 6 (neurotransmitter transporter, A A
GTTTGAA serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM7530 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM7530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7530 is therefore inhibition of SLC6A4, a GAM7530 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM7542 CAV1 AGTTATGTGATGCTT TGAAGCA Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM7542 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7542 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7542 is therefore inhibition of CAV1, a GAM7542 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7546 PSEN1 TGATGCTTGAGCACA PSEN1 (Accession NM_007318.1) is a GAM7546 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7546 RNA are set forth in Tables 6 and 7, hereby incorporated herein. PSEN1 A A GTACCTC

A function of GAM7546 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7546 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7553 ACT TAGGTAGTTTCCTGT TGTTGGG Activator of CAMP- responsive Element Modulator (CR (ACT, Accession NM_020482.3) is a GAM7553 target gene. ACT BINDING SITE1 A A

and ACT BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ACT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE1 and ACT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7553 is therefore inhibition of ACT, a GAM7553 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM7553 ADAMTS5 TAGGTAGTTTCCTGT A Disintegrin- like and Metalloprotease (reprolysin type) with A A TGTTGGG Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM7553 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7553 is therefore inhibition of ADAMTS5, a GAM7553 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7553 BACE TAGGTAGTTTCCTGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A TGTTGGG is another GAM7553 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7553 is therefore inhibition of BACE, a GAM7553 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7553 CAV1 TAGGTAGTTTCCTGT TGTTGGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM7553 target gene. CAV1 BINDING SITE1 and CAV1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE1 and CAV1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7553 is therefore inhibition of CAV1, a GAM7553 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7553 IL1A TAGGTAGTTTCCTGT TGTTGGG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM7553 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7553 is therefore inhibition of IL1A, a GAM7553 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7553 PRND TAGGTAGTTTCCTGT TGTTGGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM7553 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7553 is therefore inhibition of PRND, a GAM7553 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7553 TNFRSF6 TAGGTAGTTTCCTGT TNFRSF6 (Accession NM_152875.1) is another GAM7553 target gene. A A

TGTTGGG TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7553 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM7553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM7559 APBB1 TCTGCCTCCCTGTCT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CACTCTC 1 (Fe65) (APBB1, Accession NM_001164.2) is a GAM7559 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7559 is therefore inhibition of APBB1, a GAM7559 target gene which may modulate the internalization of beta-amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7559 APP TCTGCCTCCCTGTCT APP (Accession NM_000484.1) is another GAM7559 target gene. APP A A

CACTCTC BINDING SITE1 and APP BINDING SITE2 are target binding sites found

in untranslated regions of mRNA encoded by APP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE1 and APP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of APP. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM7559 CAV1 TCTGCCTCCCTGTCT CACTCTC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM7559 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7559 is therefore inhibition of CAV1, a GAM7559 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7559 HD TCTGCCTCCCTGTCT CACTCTC HD (Accession NM_002111.3) is another GAM7559 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7559 is therefore inhibition of HD. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7559 HTR2C TCTGCCTCCCTGTCT CACTCTC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM7559 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING A A

SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of HTR2C, a GAM7559 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7559	LRP1	TCTGCCTCCCTGTCT CACTCTC	Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM7559 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM7559 is therefore inhibition of LRP1, a GAM7559 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM7559	MAPT	TCTGCCTCCCTGTCT CACTCTC	Microtubule- associated Protein Tau (MAPT, Accession NM_016834.1) is another GAM7559 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.	A	A

Another function of GAM7559 is therefore inhibition of MAPT, a GAM7559 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM144.

GAM7559 NOTCH1 TCTGCCTCCCTGTCT Notch (Drosophila) Homolog 1 (translocation- associated) A A

CACTCTC (NOTCH1, Accession NM_017617.2) is another GAM7559 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of NOTCH1, a GAM7559 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7559 PSEN2 TCTGCCTCCCTGTCT PSEN2 (Accession NM_000447.1) is another GAM7559 target gene. A A

CACTCTC PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of PSEN2. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM7559 RAGE TCTGCCTCCCTGTCT Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

CACTCTC GAM7559 target gene. RAGE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of RAGE, a GAM7559 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM7559 S100B TCTGCCTCCCTGTCT CACTCTC A A S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is another GAM7559 target gene. S100B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of S100B, a GAM7559 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM7559 TFCP2 TCTGCCTCCCTGTCT CACTCTC A A Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM7559 target gene. TFCP2 BINDING SITE1 and TFCP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TFCP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE1 and TFCP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of TFCP2, a GAM7559 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM7559 TNFRSF5 TCTGCCTCCCTGTCT CACTCTC A A TNFRSF5 (Accession NM_001250.3) is another GAM7559 target gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7559 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM7559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM7591 ADAMTS5 TTGGAGTAATTCAGT A Disintegrin- like and Metalloprotease (reprolysin type) with A A
ATAGGTT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM7591 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7591 is therefore inhibition of ADAMTS5, a GAM7591 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7591 CAV1 TTGGAGTAATTCAGT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
ATAGGTT NM_001753.3) is another GAM7591 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7591 is therefore inhibition of CAV1, a GAM7591 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7591 CTSK TTGGAGTAATTCAGT CTSK (Accession NM_000396.2) is another GAM7591 target gene. A A
ATAGGTT CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7591 is therefore inhibition of CTSK. Accordingly, utilities of GAM7591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM7591 IGF1 TTGGAGTAATTCAGT ATAGGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM7591 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7591 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7591 is therefore inhibition of IGF1, a GAM7591 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7591 PRND TTGGAGTAATTCAGT ATAGGTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM7591 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7591 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7591 is therefore inhibition of PRND, a GAM7591 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7592 CHAT TAGGTTGTGCGCTCC TTATGAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a GAM7592 target gene. CHAT BINDING SITE1 and CHAT BINDING SITE2 are A A

target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CHAT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE1 and CHAT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7592 is therefore inhibition of CHAT, a GAM7592 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM7592 OLR1 TAGGTTGTGCGCTCC TTATGAG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A (OLR1, Accession NM_002543.1) is another GAM7592 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7592 is therefore inhibition of OLR1, a GAM7592 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7601 NOTCH1 TTAAAGTCACCATTT GTGGGTT Notch (Drosophila) Homolog 1 (translocation- associated) A A (NOTCH1, Accession NM_017617.2) is a GAM7601 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7601 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7601 is therefore inhibition of NOTCH1, a GAM7601 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7601 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7636 APPBP2 TATTACATTCATTTT GATGGTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM7636 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7636 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7636 is therefore inhibition of APPBP2, a GAM7636 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7636 IL1A TATTACATTCATTTT GATGGTT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM7636 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7636 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7636 is therefore inhibition of IL1A, a GAM7636 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7654 MAPK10 GTTTGGCACTGAATC ATATACA Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is a GAM7654 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7654 RNA are set forth in Tables 6 and 7, hereby incorporated A A

herein.

A function of GAM7654 is therefore inhibition of MAPK10, a GAM7654 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7654 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM7654 RAGE GTTTGGCACTGAATC Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

ATATACA GAM7654 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7654 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7654 is therefore inhibition of RAGE, a GAM7654 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM7654 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM7663 ABCD1 TGTGCTGGTTGCCCC ABCD1 (Accession NM_000033.2) is a GAM7663 target gene. ABCD1 A A

CGAGGGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7663 is therefore inhibition of ABCD1. Accordingly, utilities of GAM7663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM7663 BACE TGTGCTGGTTGCCCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

CGAGGGG is another GAM7663 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE

III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7663 is therefore inhibition of BACE, a GAM7663 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7663 CLU TGTGCTGGTTGCCCC CGAGGGG A A Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is another GAM7663 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7663 is therefore inhibition of CLU, a GAM7663 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM7663 NPY TGTGCTGGTTGCCCC CGAGGGG A A Neuropeptide Y (NPY, Accession NM_000905.2) is another GAM7663 target gene. NPY BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7663 is therefore inhibition of NPY, a GAM7663 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM7700 IAPP TAGAGTTATATGATG TGCTAGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM7700 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7700 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7700 is therefore inhibition of IAPP, a GAM7700 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7700 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7707 MME TGGGCACATACTGCA TCATTTA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is a GAM7707 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7707 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7707 is therefore inhibition of MME, a GAM7707 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7707 IL1B TAGAGCACCTGTTGT GTGTGCA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another GAM7707 target gene. IL1B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7707 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM7707 is therefore inhibition of IL1B, a GAM7707 target gene which stimulates thymocyte

proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM7729 IL1A GTGCTTCCATTTCCC CATCTGT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein. GAM7729 A A

A function of GAM7729 is therefore inhibition of IL1A, a GAM7729 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM7729 MAPT GTGCTTCCATTTCCC CATCTGT Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM7729 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7729 is therefore inhibition of MAPT, a GAM7729 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM7729 PSEN1 GTGCTTCCATTTCCC CATCTGT PSEN1 (Accession NM_000021.2) is another GAM7729 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A A

PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7729 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7729 TNFSF5 GTGCTTCCATTTCCC TNFSF5 (Accession NM_000074.1) is another GAM7729 target gene. A A

CATCTGT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7729 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM7729 BACE ACAGGAGCATGGAGA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) B A

GGCTA is another GAM7729 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7729 is therefore inhibition of BACE, a GAM7729 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7729 CLU ACAGGAGCATGGAGA Clusterin (complement lysis inhibitor, SP- 40,40, sulfated B A

GGCTA glycoprotein (CLU, Accession NM_001831.1) is another GAM7729 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE,

and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7729 is therefore inhibition of CLU, a GAM7729 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM7729 NCSTN ACAGGAGCATGGAGA NCSTN (Accession NM_015331.1) is another GAM7729 target gene. B A
GGCTA NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7729 is therefore inhibition of NCSTN, a GAM7729 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7776 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM7776 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7776 is therefore inhibition of APPBP2, a GAM7776 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions,

has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7776 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM7776 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7776 is therefore inhibition of BACE2, a GAM7776 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7776 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM7776 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7776 is therefore inhibition of FHL2, a GAM7776 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7776 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM7776 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7776 is therefore inhibition of HD. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7776 IGF1 CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM7776 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7776 is therefore inhibition of IGF1, a GAM7776 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7776 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM7776 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM7776 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7776 is therefore inhibition of PRND, a GAM7776 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7777 FLNB GCCCTGTTGACCAGA ATTTGTT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM7777 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the A A

nucleotide sequence of GAM7777 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7777 is therefore inhibition of FLNB, a GAM7777 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7777 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM7784 BACE2 CTGTGAGCTATTTGT TTTGGTT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is a GAM7784 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7784 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7784 is therefore inhibition of BACE2, a GAM7784 target gene which cleaves intracellularly the b- secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7784 CNTF CTGTGAGCTATTTGT TTTGGTT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM7784 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7784 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7784 is therefore inhibition of CNTF, a GAM7784 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM7784 HTR2C CTGTGAGCTATTTGT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
TTTGGTT NM_000868.1) is another GAM7784 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7784 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7784 is therefore inhibition of HTR2C, a GAM7784 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM7784 PRNP CTGTGAGCTATTTGT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A
TTTGGTT Strausler- (PRNP, Accession NM_000311.1) is another GAM7784 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7784 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7784 is therefore inhibition of PRNP, a GAM7784 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM7784 TFCP2 AATTTAACAGACAGC Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is B A
CACAGCC another GAM7784 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7784 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7784 is therefore inhibition of TFCP2, a GAM7784 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM7817 ACE TCACCCAGGCTGGAG TGCAGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM7817 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7817 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7817 is therefore inhibition of ACE, a GAM7817 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7817 ADAM17 TCACCCAGGCTGGAG TGCAGTG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is another GAM7817 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7817 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7817 is therefore inhibition of ADAM17, a GAM7817 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM7817 FLNB TCACCCAGGCTGGAG TGCAGTG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM7817 target gene. FLNB BINDING SITE is a A A

target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7817 is therefore inhibition of FLNB, a GAM7817 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM7817 IAPP TCACCCAGGCTGGAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A TGCAGTG another GAM7817 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7817 is therefore inhibition of IAPP, a GAM7817 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM7817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM7817 NOTCH1 TCACCCAGGCTGGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A TGCAGTG (NOTCH1, Accession NM_017617.2) is another GAM7817 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7817 is therefore inhibition of NOTCH1, a GAM7817 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7817 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7837 B2M AGAAGTGTAAATAAG TATGTAT Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a GAM7837 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7837 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7837 is therefore inhibition of B2M, a GAM7837 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7837 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM7837 FLNB AGAAGTGTAAATAAG TATGTAT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM7837 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7837 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7837 is therefore inhibition of FLNB, a GAM7837 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7837 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM7845 ADAM10 TGAGGGCAGGTGTGA AAATGCT A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is a GAM7845 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7845 is therefore inhibition of ADAM10, a GAM7845 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM7845 APBB2 TGAGGGCAGGTGTGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AAATGCT 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM7845 target gene. APBB2 BINDING SITE1 and APBB2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APBB2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE1 and APBB2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7845 is therefore inhibition of APBB2, a GAM7845 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7845 FPRL1 TGAGGGCAGGTGTGA FPRL1 (Accession NM_001462.1) is another GAM7845 target gene. A A

AAATGCT FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7845 is therefore inhibition of FPRL1. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM7845 IGF1 TGAGGGCAGGTGTGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AAATGCT NM_000618.2) is another GAM7845 target gene. IGF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7845 is therefore inhibition of IGF1, a GAM7845 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7845 MAPK10 TGAGGGCAGGTGTGA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
AAATGCT NM_138981.1) is another GAM7845 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7845 is therefore inhibition of MAPK10, a GAM7845 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM7845 SNCA TGAGGGCAGGTGTGA SNCA (Accession NM_007308.1) is another GAM7845 target gene. A A
AAATGCT SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7845 is therefore inhibition of SNCA. Accordingly, utilities of GAM7845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM7854 APLP2 ATACAGCTCTCTCTG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

GGGACTT NM_001642.1) is a GAM7854 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7854 is therefore inhibition of APLP2, a GAM7854 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM7854 IGF1 ATACAGCTCTCTCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGACTT NM_000618.2) is another GAM7854 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of IGF1, a GAM7854 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7854 ACE CTGTGCCCAGCCAGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 B A
GCTGTGT (ACE, Accession NM_152831.1) is another GAM7854 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of ACE, a GAM7854 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7854 BACE2 CTGTGCCCAGCCAGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession B A
GCTGTGT NM_138992.1) is another GAM7854 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of BACE2, a GAM7854 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM7854 HD CTGTGCCCAGCCAGG HD (Accession NM_002111.3) is another GAM7854 target gene. HD B A
GCTGTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of HD. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM7854 MPO CTGTGCCCAGCCAGG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM7854 B A
GCTGTGT target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of MPO, a GAM7854 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM7854 MTNR1A CTGTGCCCAGCCAGG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is B A

GCTGTGT another GAM7854 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of MTNR1A, a GAM7854 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM7854 NOTCH1 CTGTGCCCAGCCAGG Notch (Drosophila) Homolog 1 (translocation- associated) B A

GCTGTGT (NOTCH1, Accession NM_017617.2) is another GAM7854 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of NOTCH1, a GAM7854 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM7854 PRND CTGTGCCCAGCCAGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

GCTGTGT another GAM7854 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of PRND, a GAM7854 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7854 TNFRSF6 CTGTGCCCAGCCAGG TNFRSF6 (Accession NM_152877.1) is another GAM7854 target gene. B A

GCTGTGT TNFRSF6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7854 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM7854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM7865 BACE TGGAGAGATAAGCCA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

AGTATCC is a GAM7865 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7865 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7865 is therefore inhibition of BACE, a GAM7865 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7865 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7865 CTSK TGGAGAGATAAGCCA CTSK (Accession NM_000396.2) is another GAM7865 target gene. A A

AGTATCC CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7865 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7865 is therefore inhibition of CTSK. Accordingly, utilities of GAM7865 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM7865 TNF TGGAGAGATAAGCCA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

AGTATCC Accession NM_000594.2) is another GAM7865 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7865 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7865 is therefore inhibition of TNF, a GAM7865 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM7865 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7884 CTSB TTTGCACTGTAATAC CTSB (Accession NM_147783.1) is a GAM7884 target gene. CTSB A A

CTCGGTC BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7884 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7884 is therefore inhibition of CTSB. Accordingly, utilities of GAM7884 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM7889 OGDH TCTTAGATTGAGAAG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

ATGTGGC NM_002541.1) is a GAM7889 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7889 RNA are set forth in Tables 6 and 7,

hereby incorporated herein.

A function of GAM7889 is therefore inhibition of OGDH, a GAM7889 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7889 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM7898 ACHE TTTGTAATAGCAAAA TACTGGA Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM7898 target gene. ACHE BINDING SITE1 and ACHE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACHE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE1 and ACHE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7898 is therefore inhibition of ACHE, a GAM7898 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM7898 ADAMTS5 TTTGTAATAGCAAAA TACTGGA A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM7898 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7898 is therefore inhibition of ADAMTS5, a GAM7898 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7898 BACE TTTGTAATAGCAAAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

TACTGGA is another GAM7898 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of BACE, a GAM7898 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM7898 CAV1 TTTGTAATAGCAAAA Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
TACTGGA NM_001753.3) is another GAM7898 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of CAV1, a GAM7898 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7898 GLUL TTTGTAATAGCAAAA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
TACTGGA NM_002065.3) is another GAM7898 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of GLUL, a GAM7898 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM7898 MME TTTGTAATAGCAAAA TACTGGA A A Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is another GAM7898 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of MME, a GAM7898 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7898 NCSTN TTTGTAATAGCAAAA TACTGGA A A NCSTN (Accession NM_015331.1) is another GAM7898 target gene. NCSTN BINDING SITE1 and NCSTN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCSTN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE1 and NCSTN BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of NCSTN, a GAM7898 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7898 OLR1 TTTGTAATAGCAAAA TACTGGA A A Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM7898 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM7898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7898 is therefore inhibition of OLR1, a GAM7898 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7902 ABCD1 TCCCTGAGACTCTTT ABCD1 (Accession NM_000033.2) is a GAM7902 target gene. ABCD1 A A

AACTTCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7902 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7902 is therefore inhibition of ABCD1. Accordingly, utilities of GAM7902 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM7911 PSEN2 TTCCTTCAGCCCTAG PSEN2 (Accession NM_012486.1) is a GAM7911 target gene. PSEN2 A A

CTGCTTT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7911 is therefore inhibition of PSEN2. Accordingly, utilities of GAM7911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM7915 APLP2 AGACTGTTCCGTCAG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

ACTCAGT NM_001642.1) is a GAM7915 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7915 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7915 is therefore inhibition of APLP2, a

GAM7915 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7915 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM7915 ADAMTS5 AATGTGTGGGAGAAC AGTCTTT A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM7915 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7915 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM7915 is therefore inhibition of ADAMTS5, a GAM7915 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7915 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM7933 ACE TAGCAGCACATAATG GTTTGAA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM7933 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7933 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7933 is therefore inhibition of ACE, a GAM7933 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM7933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7933 ADAM10 TAGCAGCACATAATG GTTTGAA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is another GAM7933 target gene. ADAM10 BINDING SITE1 and ADAM10 BINDING SITE2 are target binding sites A A

found in untranslated regions of mRNA encoded by ADAM10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE1 and ADAM10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7933 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7933 is therefore inhibition of ADAM10, a GAM7933 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM7933 HTR2A TAGCAGCACATAATG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
GTTTGAA NM_000621.1) is another GAM7933 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7933 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7933 is therefore inhibition of HTR2A, a GAM7933 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM7933 MME TAGCAGCACATAATG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GTTTGAA enkephalinase, (MME, Accession NM_000902.2) is another GAM7933 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7933 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7933 is therefore inhibition of MME, a GAM7933 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7933 include diagnosis, prevention and treatment of Alzheimer,

and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM7933 SLC6A4 TAGCAGCACATAATG GTTTGAA Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM7933 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7933 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7933 is therefore inhibition of SLC6A4, a GAM7933 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM7954 DHCR24 TTCACCCATCTTTCC ACCCACG 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM7954 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7954 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7954 is therefore inhibition of DHCR24, a GAM7954 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM7954 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM7954 PSEN1 TTCACCCATCTTTCC ACCCACG PSEN1 (Accession NM_007318.1) is another GAM7954 target gene. PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, A A

and secondary structure complementarity to the nucleotide sequence of GAM7954 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7954 is therefore inhibition of PSEN1. Accordingly, utilities of GAM7954 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM7954 UBB TTCACCCATCTTTCC ACCCACG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM7954 target gene. UBB BINDING SITE1 and UBB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by UBB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE1 and UBB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM7954 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM7954 is therefore inhibition of UBB, a GAM7954 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM7954 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM7966 CAV1 TGTTAACATTTTGGC TAGATAG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM7966 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7966 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM7966 is therefore inhibition of CAV1, a GAM7966 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM7966 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM7966 UBB TGTTAACATTTTGGC TAGATAG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM7966 target gene. UBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or A A

BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7966 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM7966 is therefore inhibition of UBB, a GAM7966 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM7966 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM7980 TRPM2 CCTGGCTTAGGAAGC TRPM2 (Accession NM_003307.1) is a GAM7980 target gene. TRPM2 A A TCACAAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM7980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM7980 is therefore inhibition of TRPM2, a GAM7980 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM7980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM8013 ACE TTGCCCAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TGCAGTG (ACE, Accession NM_152831.1) is a GAM8013 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8013 is therefore inhibition of ACE, a GAM8013 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8013 ADAM17 TTGCCCAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TGCAGTG factor, (ADAM17, Accession NM_003183.3) is another GAM8013 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of ADAM17, a GAM8013 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8013 CHAT TTGCCCAGGCTGGAG A A
TGCAGTG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is another GAM8013 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of CHAT, a GAM8013 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM8013 FLNB TTGCCCAGGCTGGAG A A
TGCAGTG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM8013 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of FLNB, a GAM8013 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM8013 A HTR2A TGCAGTG A TTGCCCAGGCTGGAG A 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM8013 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of HTR2A, a GAM8013 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8013 A IAPP TGCAGTG A TTGCCCAGGCTGGAG A Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM8013 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of IAPP, a GAM8013 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM8013 A NOTCH1 TGCAGTG A TTGCCCAGGCTGGAG A Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM8013 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of NOTCH1, a GAM8013 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM8013 TGFB1 TTGCCCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM8013 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of TGFB1. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM8013 IAPP CACTGCAACCTCTGC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A

CACCTGG another GAM8013 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of IAPP, a GAM8013 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM8013 MTNR1A CACTGCAACCTCTGC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is B A

CACCTGG another GAM8013 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8013 is therefore inhibition of MTNR1A, a GAM8013 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM8013 A | OGDH | CACTGCAACCTCTGC CACCTGG | Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM8013 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8013 RNA are set forth in Tables 6 and 7, hereby incorporated herein. | B

Another function of GAM8013 is therefore inhibition of OGDH, a GAM8013 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM8026 A A | APP | CAGCAGAGCCCATGT GTTCATG | APP (Accession NM_000484.1) is a GAM8026 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8026 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8026 is therefore inhibition of APP. Accordingly, utilities of GAM8026 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM8026 A | MAPK10 | AACGATGGGCTGGAT TGTTTTG | Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM8026 target gene. MAPK10 BINDING SITE is | B

a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8026 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8026 is therefore inhibition of MAPK10, a GAM8026 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8026 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM8031 MME ATATTGTGTATTCAG GATAGCA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007289.1) is a GAM8031 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8031 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8031 is therefore inhibition of MME, a GAM8031 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8031 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8047 ADAM17 ATCACAGAGGCTTAA GTGCTGA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM8047 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8047 is therefore inhibition of ADAM17, a GAM8047 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8047 GFAP ATCACAGAGGCTTAA GFAP (Accession NM_002055.2) is another GAM8047 target gene. A A

GTGCTGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of GFAP. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM8047 MME ATCACAGAGGCTTAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GTGCTGA enkephalinase, (MME, Accession NM_007288.1) is another GAM8047 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of MME, a GAM8047 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8047 MTNR1A ATCACAGAGGCTTAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

GTGCTGA another GAM8047 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of MTNR1A, a GAM8047 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM8047 NCKAP1 ATCACAGAGGCTTAA NCKAP1 (Accession NM_013436.2) is another GAM8047 target gene. A A

GTGCTGA NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM8047 PSEN1 ATCACAGAGGCTTAA PSEN1 (Accession NM_007318.1) is another GAM8047 target gene. A A

GTGCTGA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of PSEN1. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM8047 RAGE ATCACAGAGGCTTAA Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

GTGCTGA GAM8047 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8047 is therefore inhibition of RAGE, a GAM8047 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is

associated with Alzheimer. Accordingly, utilities of GAM8047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM8100 CAV2 CTGCAGATTTTGGGG A A TCCACAG Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM8100 target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8100 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8100 is therefore inhibition of CAV2, a GAM8100 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8100 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM8109 ADAMTS5 TCCAGTACAGGTCTC A A TCATTTC A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM8109 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8109 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8109 is therefore inhibition of ADAMTS5, a GAM8109 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8109 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM8109 TFCP2 TCCAGTACAGGTCTC A A TCATTTC Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM8109 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8109 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8109 is therefore inhibition of TFCP2, a GAM8109 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8109 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM8109 TNFRSF5 TCCAGTACAGGTCTC TNFRSF5 (Accession NM_152854.1) is another GAM8109 target gene. A A
TCATTTC TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8109 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8109 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM8109 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM8145 BLMH ACATGATCTCCTCAC Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a GAM8145 A A
TCTAGGA target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8145 is therefore inhibition of BLMH, a GAM8145 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM8145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM8145 GSK3B ACATGATCTCCTCAC Glycogen Synthase Kinase 3 Beta (GSK3B, Accession NM_002093.2) A A
TCTAGGA is another GAM8145 target gene. GSK3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

GSK3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSK3B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8145 is therefore inhibition of GSK3B, a GAM8145 target gene which b subunit of glycogen synthase kinase 3 which phosphorylates regulatory proteins. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSK3B.The function of GSK3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2027.

GAM8145 MAPT ACATGATCTCCTCAC TCTAGGA A A Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM8145 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8145 is therefore inhibition of MAPT, a GAM8145 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM8145 PSEN2 ACATGATCTCCTCAC TCTAGGA A A PSEN2 (Accession NM_012486.1) is another GAM8145 target gene. PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8145 is therefore inhibition of PSEN2. Accordingly, utilities of GAM8145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM8164 ABCD1 GCTTCTCCTGTCCCC ABCD1 A A ABCD1 (Accession NM_000033.2) is a GAM8164 target gene.

TCCCTAC BINDING SITE1 and ABCD1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ABCD1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE1 and ABCD1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8164 is therefore inhibition of ABCD1. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM8164 APBB1 GCTTCTCCTGTCCCC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TCCCTAC 1 (Fe65) (APBB1, Accession NM_001164.2) is another GAM8164 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of APBB1, a GAM8164 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM8164 AVP GCTTCTCCTGTCCCC AVP (Accession NM_000490.2) is another GAM8164 target gene. AVP A A

TCCCTAC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of AVP. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM8164 BLMH GCTTCTCCTGTCCCC Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another A A

TCCCTAC GAM8164 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of BLMH, a GAM8164 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM8164 DHCR24 GCTTCTCCTGTCCCC 24- dehydrocholesterol Reductase (DHCR24, Accession A A
TCCCTAC NM_014762.1) is another GAM8164 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of DHCR24, a GAM8164 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8164 GLUL GCTTCTCCTGTCCCC Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
TCCCTAC NM_002065.3) is another GAM8164 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of GLUL, a GAM8164 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM8164 LRP1 GCTTCTCCTGTCCCC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
TCCCTAC macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM8164 target gene. LRP1 BINDING SITE1 and LRP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LRP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 and LRP1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of LRP1, a GAM8164 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM8164 NCKAP1 GCTTCTCCTGTCCCC NCKAP1 (Accession NM_013436.2) is another GAM8164 target gene. A A
TCCCTAC NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM8164 NGB GCTTCTCCTGTCCCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM8164 A A
TCCCTAC target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8164 is therefore inhibition of NGB, a GAM8164 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM8164 OGDH GCTTCTCCTGTCCCC TCCCTAC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM8164 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8164 is therefore inhibition of OGDH, a GAM8164 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM8164 PIN1 GCTTCTCCTGTCCCC TCCCTAC Protein (peptidyl- prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1, Accession NM_006221.1) is another GAM8164 target gene. PIN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8164 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8164 is therefore inhibition of PIN1, a GAM8164 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PIN1.The function of PIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM8206 APPBP2 TTGCACTCCAGCCTG GGTAACA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM8206 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8206 RNA are set forth in Tables 6 and 7, hereby A A

incorporated herein.

A function of GAM8206 is therefore inhibition of APPBP2, a GAM8206 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8206 FHL2 TTGCACTCCAGCCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGTAACA another GAM8206 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8206 is therefore inhibition of FHL2, a GAM8206 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8206 IGF1 TTGCACTCCAGCCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGTAACA NM_000618.2) is another GAM8206 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8206 is therefore inhibition of IGF1, a GAM8206 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8206 PRND TTGCACTCCAGCCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGTAACA another GAM8206 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM8206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8206 is therefore inhibition of PRND, a GAM8206 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8276 FHL2 ACTGTACTCCACCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCGAC a GAM8276 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8276 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8276 is therefore inhibition of FHL2, a GAM8276 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8276 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8276 HD ACTGTACTCCACCCT HD (Accession NM_002111.3) is another GAM8276 target gene. HD A A

GGGCGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8276 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8276 is therefore inhibition of HD. Accordingly, utilities of GAM8276 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM8285 IGF1 AGTAGACAGTGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CATAGTC NM_000618.2) is a GAM8285 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8285 is therefore inhibition of IGF1, a GAM8285 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8285 MME AGTAGACAGTGGCAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

CATAGTC enkephalinase, (MME, Accession NM_000902.2) is another GAM8285 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8285 is therefore inhibition of MME, a GAM8285 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8288 HTR2A GTGCTCATCTTCTGT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

AACTGTT NM_000621.1) is a GAM8288 target gene. HTR2A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8288 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8288 is therefore inhibition of HTR2A, a GAM8288 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8288 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8311 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TGGGTGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM8311 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8311 is therefore inhibition of APPBP2, a GAM8311 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8311 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147783.1) is another GAM8311 target gene. A A TGGGTGA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8311 is therefore inhibition of CTSB. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM8311 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM8311 target gene. A A TGGGTGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8311 is therefore inhibition of

CTSK. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM8311 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGTGA another GAM8311 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8311 is therefore inhibition of FHL2, a GAM8311 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8311 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGTGA NM_000618.2) is another GAM8311 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8311 is therefore inhibition of IGF1, a GAM8311 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8311 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGTGA another GAM8311 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM8311 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM8311 is therefore inhibition of PRND, a GAM8311 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8339 ACE TGGAGCCTTGTTGTT TGTTCAC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM8339 target gene. ACE BINDING SITE1 and ACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE1 and ACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8339 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8339 is therefore inhibition of ACE, a GAM8339 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM8339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8339 ADAMTS5 TGGAGCCTTGTTGTT TGTTCAC A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is another GAM8339 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8339 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8339 is therefore inhibition of ADAMTS5, a GAM8339 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM8339 CTNND2 TGGAGCCTTGTTGTT TGTTCAC Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM8339 A A

target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8339 is therefore inhibition of CTNND2, a GAM8339 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM8339 PRND TGGAGCCTTGTTGTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM8339 target gene. PRND BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8339 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

TGTTCAC

Another function of GAM8339 is therefore inhibition of PRND, a GAM8339 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8339 TNFRSF6 TGGAGCCTTGTTGTT TNFRSF6 (Accession NM_152871.1) is another GAM8339 target gene. A A

TGTTCAC TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8339 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM8339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM8349 ADAM17 ATCACAGAGGCTTAA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GTGCTGA factor, (ADAM17, Accession NM_021832.1) is a GAM8349 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8349 is therefore inhibition of ADAM17, a GAM8349 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8349 GFAP ATCACAGAGGCTTAA GFAP (Accession NM_002055.2) is another GAM8349 target gene. A A

GTGCTGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8349 is therefore inhibition of GFAP. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM8349 MME ATCACAGAGGCTTAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GTGCTGA enkephalinase, (MME, Accession NM_007288.1) is another GAM8349 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8349 is therefore inhibition of MME, a GAM8349 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM25.

GAM8349 MTNR1A ATCACAGAGGCTTAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM8349 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A

GTGCTGA

Another function of GAM8349 is therefore inhibition of MTNR1A, a GAM8349 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM8349 NCKAP1 ATCACAGAGGCTTAA NCKAP1 (Accession NM_013436.2) is another GAM8349 target gene. A A

GTGCTGA NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8349 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM8349 PSEN1 ATCACAGAGGCTTAA PSEN1 (Accession NM_007318.1) is another GAM8349 target gene. A A

GTGCTGA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8349 is therefore inhibition of PSEN1. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM8349 RAGE ATCACAGAGGCTTAA Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

GTGCTGA GAM8349 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8349 is therefore inhibition of RAGE, a GAM8349 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM8349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM8362 HTR2A ACAGCAAGTCTTTGT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

CAAAGCT NM_000621.1) is a GAM8362 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8362 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8362 is therefore inhibition of HTR2A, a GAM8362 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8362 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8362 VLDLR ACAGCAAGTCTTTGT Very Low Density Lipoprotein Receptor (VLDLR, Accession A A

CAAAGCT NM_003383.1) is another GAM8362 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8362 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8362 is therefore inhibition of VLDLR, a GAM8362 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM8362 include diagnosis, prevention and

treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8380 APBB2 GGAGGTGACTGTTAC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AGATCGG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM8380 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8380 is therefore inhibition of APBB2, a GAM8380 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8380 HTR2A CTGATTGAACCATTC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession B A

ACTTTAT NM_000621.1) is another GAM8380 target gene. HTR2A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8380 is therefore inhibition of HTR2A, a GAM8380 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8386 ABCD1 CTTTTTGGGGTTTGG ABCD1 (Accession NM_000033.2) is a GAM8386 target gene.
ABCD1 A A

GGCTTGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM8386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8386 is therefore inhibition of ABCD1. Accordingly, utilities of GAM8386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM8386 LRP1 CTTTTTGGGGTTTGG GGCTTGG Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM8386 target gene. LRP1 BINDING SITE1 through LRP1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LRP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE1 through LRP1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM8386 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8386 is therefore inhibition of LRP1, a GAM8386 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM8396 AVP TTCAGAGTGGTTAAG ATCATGG AVP (Accession NM_000490.2) is a GAM8396 target gene. AVP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8396 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8396 is therefore inhibition of AVP. Accordingly, utilities of GAM8396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM8396 CNTF TTCAGAGTGGTTAAG ATCATGG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM8396 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8396 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8396 is therefore inhibition of CNTF, a GAM8396 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM8396 GYPA TTCAGAGTGGTTAAG Glycophorin A (includes MN blood group) (GYPA, Accession A A ATCATGG NM_002099.2) is another GAM8396 target gene. GYPA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8396 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8396 is therefore inhibition of GYPA, a GAM8396 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8396 TGFB1 TTCAGAGTGGTTAAG TGFB1 (Accession NM_000660.1) is another GAM8396 target gene. A A ATCATGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8396 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8396 is therefore inhibition of TGFB1. Accordingly, utilities of GAM8396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM8439 DHCR24 GGGCCATGACAGGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A GATAGGC NM_014762.1) is a GAM8439 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8439 is therefore inhibition of DHCR24, a GAM8439 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8439 MPO GGGCCATGACAGGGA Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM8439 A A
GATAGGC target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8439 is therefore inhibition of MPO, a GAM8439 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM8439 PSEN2 GGGCCATGACAGGGA PSEN2 (Accession NM_000447.1) is another GAM8439 target gene. A A
GATAGGC PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8439 is therefore inhibition of PSEN2. Accordingly, utilities of GAM8439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM8439 SNCB GGGCCATGACAGGGA Synuclein, Beta (SNCB, Accession NM_003085.2) is another A A
GATAGGC GAM8439 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM8439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8439 is therefore inhibition of SNCB, a GAM8439 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM8439 TGFB1 GGGCCATGACAGGGA A A GATAGGC TGFB1 (Accession NM_000660.1) is another GAM8439 target gene. TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8439 is therefore inhibition of TGFB1. Accordingly, utilities of GAM8439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM8447 ACE CCCAGGAGGTGGAGG A A TTACAGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM8447 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8447 is therefore inhibition of ACE, a GAM8447 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8447 IGF1 CCCAGGAGGTGGAGG A A TTACAGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM8447 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of IGF1, a GAM8447 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8447 OGDH CCCAGGAGGTGGAGG A A TTACAGT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM8447 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of OGDH, a GAM8447 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM8447 PRND CCCAGGAGGTGGAGG A A TTACAGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM8447 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of PRND, a GAM8447 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8447 APPBP2 CGTGTAATCCCAGCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding B A
ACTTGGG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM8447 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of APPBP2, a GAM8447 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8447 FHL2 CGTGTAATCCCAGCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is B A
ACTTGGG another GAM8447 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of FHL2, a GAM8447 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8447 GFAP CGTGTAATCCCAGCT GFAP (Accession NM_002055.2) is another GAM8447 target gene. B A
ACTTGGG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8447 is therefore inhibition of GFAP. Accordingly, utilities of GAM8447 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM8447 IGF1 CGTGTAATCCCAGCT ACTTGGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM8447 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM8447 is therefore inhibition of IGF1, a GAM8447 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8447 PRND CGTGTAATCCCAGCT ACTTGGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM8447 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM8447 is therefore inhibition of PRND, a GAM8447 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8447 TRPM2 CGTGTAATCCCAGCT ACTTGGG TRPM2 (Accession NM_003307.1) is another GAM8447 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8447 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM8447 is therefore inhibition of TRPM2, a GAM8447 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM8447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM8452 FLNB CCTCCTTTCATCAAA TTCGAGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM8452 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8452 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8452 is therefore inhibition of FLNB, a GAM8452 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM8452 PRND CCTCCTTTCATCAAA TTCGAGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM8452 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8452 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8452 is therefore inhibition of PRND, a GAM8452 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8473 APBB2 GACCAGCCATCCTGG TTTACAT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM8473 target gene. APBB2 BINDING SITE1 and APBB2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APBB2, A A

corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE1 and APBB2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8473 is therefore inhibition of APBB2, a GAM8473 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8473 DSCR1 GACCAGCCATCCTGG A A TTTACAT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is another GAM8473 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8473 is therefore inhibition of DSCR1, a GAM8473 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM8473 MAPT GACCAGCCATCCTGG A A TTTACAT Microtubule- associated Protein Tau (MAPT, Accession NM_016841.1) is another GAM8473 target gene. MAPT BINDING SITE1 and MAPT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 and MAPT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8473 is therefore inhibition of MAPT, a GAM8473 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM8473 MME GACCAGCCATCCTGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TTTACAT enkephalinase, (MME, Accession NM_007289.1) is another GAM8473 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8473 is therefore inhibition of MME, a GAM8473 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8473 PRND GACCAGCCATCCTGG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TTTACAT another GAM8473 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8473 is therefore inhibition of PRND, a GAM8473 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8473 TNFRSF6 GACCAGCCATCCTGG TNFRSF6 (Accession NM_152872.1) is another GAM8473 target gene. A A
TTTACAT TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8473 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM8473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM8489 HD GTATGGAGATCTCTG HD (Accession NM_002111.3) is a GAM8489 target gene. HD BINDING A A
CCCTTGT SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8489 is therefore inhibition of HD. Accordingly, utilities of GAM8489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM8489 MAPT GTATGGAGATCTCTG Microtubule- associated Protein Tau (MAPT, Accession A A
CCCTTGT NM_173727.1) is another GAM8489 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8489 is therefore inhibition of MAPT, a GAM8489 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM8489 PLAU GTATGGAGATCTCTG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A
CCCTTGT is another GAM8489 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8489 is therefore inhibition of PLAU, a GAM8489 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM8489 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM8489 GYPA ACAAGGCAGGGCAGG Glycophorin A (includes MN blood group) (GYPA, Accession B A
TGTCTGT NM_002099.2) is another GAM8489 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8489 is therefore inhibition of GYPA, a GAM8489 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8506 IGF1 TGTCATATAGAATGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCTATGA NM_000618.2) is a GAM8506 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8506 is therefore inhibition of IGF1, a GAM8506 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8531 ADAM10 GGCAAGGAAGAAAGC A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A
AGAAGTT Accession NM_001110.1) is a GAM8531 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8531 is therefore inhibition of ADAM10, a GAM8531 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM8531 APCS GGCAAGGAAGAAAGC Amyloid P Component, Serum (APCS, Accession NM_001639.2) is A A

AGAAGTT another GAM8531 target gene. APCS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8531 is therefore inhibition of APCS, a GAM8531 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM772.

GAM8531 CNTF GGCAAGGAAGAAAGC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

AGAAGTT another GAM8531 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8531 is therefore inhibition of CNTF, a GAM8531 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM8531 FHL2 GGCAAGGAAGAAAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGAAGTT another GAM8531 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8531 is therefore inhibition of FHL2, a GAM8531 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8531 HTR2A GGCAAGGAAGAAAGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
AGAAGTT NM_000621.1) is another GAM8531 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8531 is therefore inhibition of HTR2A, a GAM8531 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM8531 MAPT GGCAAGGAAGAAAGC Microtubule- associated Protein Tau (MAPT, Accession A A
AGAAGTT NM_173727.1) is another GAM8531 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8531 is therefore inhibition of MAPT, a GAM8531 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8531 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM8539 ARHA TGGAGAGATAGTGAT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

TTAGCTC is a GAM8539 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8539 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8539 is therefore inhibition of ARHA, a GAM8539 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8539 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM8539 PSEN2 TGGAGAGATAGTGAT PSEN2 (Accession NM_012486.1) is another GAM8539 target gene. A A

TTAGCTC PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8539 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8539 is therefore inhibition of PSEN2. Accordingly, utilities of GAM8539 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM8539 TGFB1 TGGAGAGATAGTGAT TGFB1 (Accession NM_000660.1) is another GAM8539 target gene. A A

TTAGCTC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8539 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8539 is therefore inhibition of TGFB1. Accordingly, utilities of GAM8539 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM8542 APBA2 CTTTGGCAAGGGAGA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
AGTCAC 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM8542 target gene. APBA2 BINDING SITE1 and APBA2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APBA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE1 and APBA2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8542 is therefore inhibition of APBA2, a GAM8542 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM8542 CTSK CTTTGGCAAGGGAGA CTSK (Accession NM_000396.2) is another GAM8542 target gene. A A
AGTCAC CTSK BINDING SITE1 and CTSK BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTSK, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE1 and CTSK BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8542 is therefore inhibition of CTSK. Accordingly, utilities of GAM8542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM8542 FLNB CTTTGGCAAGGGAGA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
AGTCAC NM_001457.1) is another GAM8542 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8542 is therefore inhibition of FLNB, a GAM8542 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8542 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM8542 OGDH CTTTGGCAAGGGAGA AGTCAC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM8542 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8542 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM8542 is therefore inhibition of OGDH, a GAM8542 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM8563 ACE TTTGAAGTGGGTCCT CGAAATG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM8563 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8563 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8563 is therefore inhibition of ACE, a GAM8563 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM8563 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8563 GFAP TTTGAAGTGGGTCCT CGAAATG GFAP (Accession NM_002055.2) is another GAM8563 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide A A

sequence of GAM8563 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8563 is therefore inhibition of GFAP. Accordingly, utilities of GAM8563 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM8598 BACE TCCAAAATTAAAGGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
TGTAGAA is a GAM8598 target gene. BACE BINDING SITE1 through BACE BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 through BACE BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM8598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8598 is therefore inhibition of BACE, a GAM8598 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM8598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM8598 IGF1 TCCAAAATTAAAGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGTAGAA NM_000618.2) is another GAM8598 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8598 is therefore inhibition of IGF1, a GAM8598 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8598 MME TCCAAAATTAAAGGT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
TGTAGAA enkephalinase, (MME, Accession NM_000902.2) is another GAM8598 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8598 is therefore inhibition of MME, a GAM8598 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8601 DHCR24 TGGAATGACAGAAGA TGAGAGC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM8601 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8601 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8601 is therefore inhibition of DHCR24, a GAM8601 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8601 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8631 MME AGAAGATCCCTGCTC TGAGTCA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is a GAM8631 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8631 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM8631 is therefore inhibition of MME, a GAM8631 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8636 DSCR1 TGAGGTAGGTGCTGA Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A
AACTGCT NM_004414.3) is a GAM8636 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8636 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8636 is therefore inhibition of DSCR1, a GAM8636 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM8636 FLNB TGAGGTAGGTGCTGA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
AACTGCT NM_001457.1) is another GAM8636 target gene. FLNB BINDING SITE1 and FLNB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLNB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE1 and FLNB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8636 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8636 is therefore inhibition of FLNB, a GAM8636 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM8636 IAPP TGAGGTAGGTGCTGA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
AACTGCT another GAM8636 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8636 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8636 is therefore inhibition of IAPP, a GAM8636 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM8636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM8636 IGF1 TGAGGTAGGTGCTGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AACTGCT NM_000618.2) is another GAM8636 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8636 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8636 is therefore inhibition of IGF1, a GAM8636 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8636 NOTCH1 TGAGGTAGGTGCTGA Notch (Drosophila) Homolog 1 (translocation- associated) A A

AACTGCT (NOTCH1, Accession NM_017617.2) is another GAM8636 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8636 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8636 is therefore inhibition of NOTCH1, a GAM8636 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8636 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM8647 ADAMTS5 TGTGTCTGTGGAACA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GAAGCAG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM8647 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8647 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8647 is therefore inhibition of ADAMTS5, a GAM8647 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8647 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM8647 MME TGTGTCTGTGGAACA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GAAGCAG enkephalinase, (MME, Accession NM_007289.1) is another GAM8647 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8647 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8647 is therefore inhibition of MME, a GAM8647 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8647 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8665 APLP2 AGGCAAGAGGTTGCA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A

GTGAGCT NM_001642.1) is a GAM8665 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8665 is therefore inhibition of APLP2, a GAM8665 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM8665 APP AGGCAAGAGGTTGCA APP (Accession NM_000484.1) is another GAM8665 target gene. APP A A

GTGAGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of APP. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM8665 APPBP2 AGGCAAGAGGTTGCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GTGAGCT Protein 2 (APPBP2, Accession NM_006380.2) is another GAM8665 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of APPBP2, a GAM8665 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8665 CTSB AGGCAAGAGGTTGCA CTSB (Accession NM_147783.1) is another GAM8665 target gene. A A

GTGAGCT CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of CTSB. Accordingly, utilities of GAM8665 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM8665 DHCR24 AGGCAAGAGGTTGCA 24- dehydrocholesterol Reductase (DHCR24, Accession A A
GTGAGCT NM_014762.1) is another GAM8665 target gene. DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DHCR24, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE1 and DHCR24 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of DHCR24, a GAM8665 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8665 FHL2 AGGCAAGAGGTTGCA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GTGAGCT another GAM8665 target gene. FHL2 BINDING SITE1 through FHL2 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 through FHL2 BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of FHL2, a GAM8665 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM8665 HTR2C AGGCAAGAGGTTGCA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
GTGAGCT NM_000868.1) is another GAM8665 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of HTR2C, a GAM8665 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM8665 IGF1 AGGCAAGAGGTTGCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GTGAGCT NM_000618.2) is another GAM8665 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of IGF1, a GAM8665 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM8665 PRND AGGCAAGAGGTTGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GTGAGCT another GAM8665 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8665 is therefore inhibition of PRND, a GAM8665 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8678 CHAT GTGTTCCAGGAAGTC Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a A A

GTCTTGA GAM8678 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8678 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8678 is therefore inhibition of CHAT, a GAM8678 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8678 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM8678 DHCR24 GTGTTCCAGGAAGTC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GTCTTGA NM_014762.1) is another GAM8678 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8678 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8678 is therefore inhibition of DHCR24, a GAM8678 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8678 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM8678 DSCR1 GTGTTCCAGGAAGTC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

GTCTTGA NM_004414.3) is another GAM8678 target gene. DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DSCR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8678 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8678 is therefore inhibition of DSCR1, a GAM8678 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM8678 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM8678 MAPK10 GTGTTCCAGGAAGTC GTCTTGA A A Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM8678 target gene. MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPK10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8678 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8678 is therefore inhibition of MAPK10, a GAM8678 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8678 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM8678 TNFRSF5 GTGTTCCAGGAAGTC GTCTTGA A A TNFRSF5 (Accession NM_152854.1) is another GAM8678 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM8678 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8678 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM8678 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM8693 CAV1 CAGTGGGAAAAGTTT GTCTCAT A A Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM8693 target gene. CAV1 BINDING SITE1 and CAV1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CAV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE1 and CAV1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM8693 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM8693 is therefore inhibition of CAV1, a GAM8693 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM8693 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM8693 GYPA CAGTGGGAAAAGTTT Glycophorin A (includes MN blood group) (GYPA, Accession A A
GTCTCAT NM_002099.2) is another GAM8693 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8693 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8693 is therefore inhibition of GYPA, a GAM8693 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8693 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM8693 HD CAGTGGGAAAAGTTT HD (Accession NM_002111.3) is another GAM8693 target gene. HD A A
GTCTCAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8693 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8693 is therefore inhibition of HD. Accordingly, utilities of GAM8693 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM8693 MME CAGTGGGAAAAGTTT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GTCTCAT enkephalinase, (MME, Accession NM_007287.1) is another GAM8693 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM8693 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM8693 is therefore inhibition of MME, a GAM8693 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM8693 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336121 CHAT GTGTTCCAGGAAGTC A A GTCTTGA Choline Acetyltransferase (CHAT, Accession NM_020984.1) is a GAM336121 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336121 is therefore inhibition of CHAT, a GAM336121 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336121 DHCR24 GTGTTCCAGGAAGTC A A GTCTTGA 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM336121 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336121 is therefore inhibition of DHCR24, a GAM336121 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM44.

GAM336121 DSCR1 GTGTTCCAGGAAGTC A A GTCTTGA Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is another GAM336121 target gene. DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DSCR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE1 and DSCR1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336121 is therefore inhibition of DSCR1, a GAM336121 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336121 MAPK10 GTGTTCCAGGAAGTC A A GTCTTGA Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM336121 target gene. MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPK10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE1 and MAPK10 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336121 is therefore inhibition of MAPK10, a GAM336121 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336121 TNFRSF5 GTGTTCCAGGAAGTC A A GTCTTGA TNFRSF5 (Accession NM_152854.1) is another GAM336121 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5

BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336121 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336121 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336121 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336122 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336122 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336122 is therefore inhibition of APPBP2, a GAM336122 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336122 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336122 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of BACE2, a GAM336122 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336122 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336122 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of BCHE. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336122 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336122 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of CTSB. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336122 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336122 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of CTSK. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336122 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336122 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336122 is therefore inhibition of FHL2, a GAM336122 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336122 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336122 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of HD. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336122 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336122 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of IGF1, a GAM336122 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336122 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336122 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of IL1A, a GAM336122 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336122 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336122 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of NGB, a GAM336122 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336122 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336122 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336122 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336122 is therefore inhibition of PRND, a GAM336122 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336122 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336123 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336123 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336123 is therefore inhibition of APPBP2, a GAM336123 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336123 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336123 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of BACE2, a GAM336123 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336123 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336123 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of BCHE. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336123 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336123 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of CTSB. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336123 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336123 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of CTSK. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336123 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336123 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of FHL2, a GAM336123 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336123 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336123 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of HD. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336123 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336123 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of IGF1, a GAM336123 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336123 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336123 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of IL1A, a GAM336123 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336123 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336123 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of NGB, a GAM336123 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336123 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336123 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336123 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336123 is therefore inhibition of PRND, a GAM336123 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336123 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336124 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336124 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336124 is therefore inhibition of APPBP2, a GAM336124 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336124 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336124 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of BACE2, a GAM336124 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336124 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336124 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of BCHE. Accordingly, utilities of GAM336124 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336124 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336124 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of CTSB. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336124 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336124 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of CTSK. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336124 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336124 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of FHL2, a GAM336124 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336124 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336124 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of HD. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336124 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM336124 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of IGF1, a GAM336124 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336124 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
A

TGGGCAA GAM336124 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of IL1A, a GAM336124 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336124 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336124 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of NGB, a GAM336124 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336124 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336124 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336124 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336124 is therefore inhibition of PRND, a GAM336124 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336124 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336125 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336125 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336125 is therefore inhibition of APPBP2, a GAM336125 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336125 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336125 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336125 is therefore inhibition of BACE2, a GAM336125 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336125 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336125 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336125 is therefore inhibition of FHL2, a GAM336125 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336125 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336125 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336125 is therefore inhibition of IGF1, a GAM336125 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336125 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336125 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336125 is therefore inhibition of MME, a GAM336125 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336125 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336125 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING A A

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336125 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336125 is therefore inhibition of PRND, a GAM336125 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336125 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336126 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336126 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336126 is therefore inhibition of APPBP2, a GAM336126 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336126 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336126 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336126 is therefore inhibition of BACE2, a GAM336126 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336126 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336126 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336126 is therefore inhibition of FHL2, a GAM336126 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336126 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336126 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336126 is therefore inhibition of HD. Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336126 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336126 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336126 is therefore inhibition of IGF1, a GAM336126 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336126 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336126 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336126 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336126 is therefore inhibition of PRND, a GAM336126 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336127 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336127 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336127 is therefore inhibition of APPBP2, a GAM336127 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336127 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336127 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a A A

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of BACE2, a GAM336127 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336127 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336127 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of BCHE. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336127 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336127 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of CTSB. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336127 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336127 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of CTSK. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336127 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336127 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of FHL2, a GAM336127 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336127 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336127 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of HD. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336127 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336127 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of IGF1, a GAM336127 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336127 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336127 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of IL1A, a GAM336127 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336127 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336127 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of NGB, a GAM336127 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM281.

GAM336127 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336127 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336127 is therefore inhibition of PRND, a GAM336127 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336128 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336128 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336128 is therefore inhibition of APPBP2, a GAM336128 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336128 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336128 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of BACE2, a GAM336128 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336128 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336128 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of BCHE. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336128 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336128 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of CTSB. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336128 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336128 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of

CTSK. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336128 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336128 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of FHL2, a GAM336128 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336128 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336128 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of HD. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336128 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336128 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of IGF1, a GAM336128 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336128 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336128 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of IL1A, a GAM336128 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336128 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336128 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of NGB, a GAM336128 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336128 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336128 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336128 is therefore inhibition of PRND, a GAM336128 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336129 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336129 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336129 is therefore inhibition of APPBP2, a GAM336129 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336129 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336129 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336129 is therefore inhibition of BACE2, a GAM336129 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336129 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336129 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of BCHE. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336129 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336129 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of CTSB. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336129 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336129 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of CTSK. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336129 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336129 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of FHL2, a GAM336129 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336129 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336129 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of HD. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336129 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
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TGGGCAA NM_000618.2) is another GAM336129 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of IGF1, a GAM336129 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

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GAM336129 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336129 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of IL1A, a GAM336129 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336129 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336129 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336129 is therefore inhibition of NGB, a GAM336129 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336129 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336129 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336129 RNA are set forth in Tables 6 and 7, hereby

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Another function of GAM336129 is therefore inhibition of PRND, a GAM336129 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336130 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336130 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336130 is therefore inhibition of APPBP2, a GAM336130 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336130 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

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Another function of GAM336130 is therefore inhibition of BACE2, a GAM336130 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336130 is therefore inhibition of BCHE. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336130 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336130 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of CTSB. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336130 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336130 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of CTSK. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336130 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
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and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336130 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336130 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of HD. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336130 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336130 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of IGF1, a GAM336130 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336130 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336130 target gene. IL1A BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of IL1A, a GAM336130 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336130 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336130 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of NGB, a GAM336130 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336130 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336130 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336130 is therefore inhibition of PRND, a GAM336130 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336131 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336131 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336131 is therefore inhibition of APPBP2, a GAM336131 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336131 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336131 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of BACE2, a GAM336131 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336131 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336131 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of BCHE. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336131 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336131 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of CTSB. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336131 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336131 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of CTSK. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336131 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336131 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of

FHL2, a GAM336131 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336131 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336131 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of HD. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336131 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336131 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of IGF1, a GAM336131 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336131 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336131 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and

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Another function of GAM336131 is therefore inhibition of IL1A, a GAM336131 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336131 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336131 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of NGB, a GAM336131 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336131 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336131 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336131 is therefore inhibition of PRND, a GAM336131 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336132 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336132 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336132 is therefore inhibition of APPBP2, a GAM336132 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336132 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336132 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of BACE2, a GAM336132 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336132 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336132 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of BCHE. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336132 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336132 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of CTSB. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336132 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336132 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of CTSK. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336132 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336132 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of FHL2, a GAM336132 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336132 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336132 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of HD. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336132 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336132 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of IGF1, a GAM336132 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336132 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336132 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of IL1A, a GAM336132 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation &

proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336132 NGB CACTGCACTCCAGCC TGGGCAA A A Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of NGB, a GAM336132 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336132 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336132 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336132 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336132 is therefore inhibition of PRND, a GAM336132 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336132 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336133 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336133 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336133 is therefore inhibition of APPBP2, a GAM336133 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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Another function of GAM336133 is therefore inhibition of BACE2, a GAM336133 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336133 is therefore inhibition of BCHE. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336133 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336133 target gene. A A

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Another function of GAM336133 is therefore inhibition of CTSB. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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Another function of GAM336133 is therefore inhibition of CTSK. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336133 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336133 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336133 is therefore inhibition of FHL2, a GAM336133 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336133 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336133 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336133 is therefore inhibition of HD. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336133 IGF1 CACTGCACTCCAGCC TGGGCAA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336133 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336133 is therefore inhibition of IGF1, a GAM336133 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336133 IL1A CACTGCACTCCAGCC TGGGCAA A A Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336133 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336133 is therefore inhibition of IL1A, a GAM336133 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM281.

GAM336133 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336133 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336133 is therefore inhibition of NGB, a GAM336133 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336133 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336133 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336133 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

TGGGCAA

Another function of GAM336133 is therefore inhibition of PRND, a GAM336133 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336134 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336134 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

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A function of GAM336134 is therefore inhibition of APPBP2, a GAM336134 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336134 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336134 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of BACE2, a GAM336134 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336134 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336134 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of BCHE. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336134 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336134 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of CTSB. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336134 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336134 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of CTSK. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336134 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336134 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of FHL2, a GAM336134 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336134 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336134 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of HD. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336134 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336134 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of IGF1, a GAM336134 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336134 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336134 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of IL1A, a GAM336134 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336134 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336134 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of NGB, a GAM336134 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336134 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336134 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336134 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336134 is therefore inhibition of PRND, a GAM336134 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336134 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336135 AVP TCTTGTGAAATCTGT AVP (Accession NM_000490.2) is a GAM336135 target gene. AVP A A

GGACCCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336135 is therefore inhibition of AVP. Accordingly, utilities of GAM336135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336136 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336136 target

gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336136 is therefore inhibition of APPBP2, a GAM336136 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336136 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336136 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of BACE2, a GAM336136 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336136 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336136 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of BCHE. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with BCHE.

GAM336136 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336136 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of CTSB. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336136 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336136 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of CTSK. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336136 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336136 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of FHL2, a GAM336136 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336136 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336136 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of HD. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336136 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM336136 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of IGF1, a GAM336136 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336136 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
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TGGGCAA GAM336136 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of IL1A, a GAM336136 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336136 NGB CACTGCACTCCAGCC TGGGCAA A A

Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of NGB, a GAM336136 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336136 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336136 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336136 is therefore inhibition of PRND, a GAM336136 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336137 APPBP2 CACTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336137 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336137 is therefore inhibition of APPBP2, a GAM336137 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336137 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336137 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of BACE2, a GAM336137 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336137 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336137 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of BCHE. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336137 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336137 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA

encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of CTSB. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336137 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336137 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of CTSK. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336137 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336137 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of FHL2, a GAM336137 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336137 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336137 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of HD. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336137 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336137 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of IGF1, a GAM336137 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336137 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336137 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of IL1A, a GAM336137 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336137 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336137 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of NGB, a GAM336137 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336137 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336137 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336137 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336137 is therefore inhibition of PRND, a GAM336137 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336137 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336138 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336138 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336138 is therefore inhibition of APPBP2, a GAM336138 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336138 BACE2 CACTGCACTCCAGCC TGGGCAA A A

Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336138 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of BACE2, a GAM336138 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336138 BCHE CACTGCACTCCAGCC TGGGCAA A A

BCHE (Accession NM_000055.1) is another GAM336138 target gene.

BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of BCHE. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336138 CTSB CACTGCACTCCAGCC TGGGCAA A A

CTSB (Accession NM_147782.1) is another GAM336138 target gene.

CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of CTSB. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336138 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336138 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of CTSK. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336138 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336138 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of FHL2, a GAM336138 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336138 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336138 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of HD. Accordingly, utilities of GAM336138 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336138 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336138 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of IGF1, a GAM336138 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336138 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336138 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of IL1A, a GAM336138 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336138 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336138 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence

of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of NGB, a GAM336138 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336138 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336138 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336138 is therefore inhibition of PRND, a GAM336138 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336139 APPBP2 CACTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336139 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336139 is therefore inhibition of APPBP2, a GAM336139 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM336139 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336139 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of BACE2, a GAM336139 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336139 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336139 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of BCHE. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336139 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336139 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of CTSB. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336139 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336139 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of CTSK. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336139 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336139 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of FHL2, a GAM336139 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336139 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336139 target gene. HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of HD. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336139 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336139 target gene. IGF1 BINDING SITE1

and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of IGF1, a GAM336139 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336139 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336139 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of IL1A, a GAM336139 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336139 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336139 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of NGB, a GAM336139 target gene which has function in oxygen transport

and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336139 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336139 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336139 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336139 is therefore inhibition of PRND, a GAM336139 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336139 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336140 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336140 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336140 is therefore inhibition of APPBP2, a GAM336140 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336140 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336140 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of BACE2, a GAM336140 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336140 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336140 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of BCHE. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336140 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336140 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of CTSB. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336140 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336140 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of CTSK. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336140 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336140 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of FHL2, a GAM336140 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336140 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336140 target gene. HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of HD. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336140 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336140 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure

complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of IGF1, a GAM336140 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336140 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336140 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of IL1A, a GAM336140 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336140 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336140 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of NGB, a GAM336140 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM281.

GAM336140 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336140 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336140 is therefore inhibition of PRND, a GAM336140 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336141 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336141 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336141 is therefore inhibition of APPBP2, a GAM336141 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336141 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336141 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336141 is therefore inhibition of BACE2, a GAM336141 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336141 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336141 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of BCHE. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336141 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336141 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of CTSB. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336141 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336141 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of CTSK. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336141 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336141 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of FHL2, a GAM336141 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336141 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336141 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of HD. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336141 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336141 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of IGF1, a GAM336141 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336141 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336141 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of IL1A, a GAM336141 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336141 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336141 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of NGB, a GAM336141 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336141 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336141 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336141 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336141 is therefore inhibition of PRND, a GAM336141 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336141 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336142 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336142 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336142 is therefore inhibition of APPBP2, a GAM336142 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336142 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336142 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336142 is therefore inhibition of BACE2, a GAM336142 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336142 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336142 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of BCHE. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336142 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336142 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of CTSB. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336142 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336142 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of CTSK. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336142 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336142 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of FHL2, a GAM336142 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336142 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336142 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of HD. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336142 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
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TGGGCAA NM_000618.2) is another GAM336142 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of IGF1, a GAM336142 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

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GAM336142 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336142 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of IL1A, a GAM336142 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336142 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336142 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336142 is therefore inhibition of NGB, a GAM336142 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336142 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336142 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336142 RNA are set forth in Tables 6 and 7, hereby

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Another function of GAM336142 is therefore inhibition of PRND, a GAM336142 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336142 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336143 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336143 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336143 is therefore inhibition of APPBP2, a GAM336143 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336143 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336143 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336143 is therefore inhibition of BACE2, a GAM336143 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336143 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336143 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of BCHE. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336143 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336143 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of CTSB. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336143 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336143 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of CTSK. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336143 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336143 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of FHL2, a GAM336143 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336143 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336143 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of HD. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336143 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336143 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of IGF1, a GAM336143 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336143 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336143 target gene. IL1A BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of IL1A, a GAM336143 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336143 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336143 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of NGB, a GAM336143 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336143 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336143 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336143 is therefore inhibition of PRND, a GAM336143 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336144 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336144 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336144 is therefore inhibition of APPBP2, a GAM336144 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336144 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336144 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of BACE2, a GAM336144 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336144 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336144 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of BCHE. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336144 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147782.1) is another GAM336144 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of CTSB. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336144 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336144 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of CTSK. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336144 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336144 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of

FHL2, a GAM336144 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336144 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336144 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of HD. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336144 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336144 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of IGF1, a GAM336144 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336144 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336144 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of IL1A, a GAM336144 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336144 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336144 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of NGB, a GAM336144 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336144 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336144 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336144 is therefore inhibition of PRND, a GAM336144 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336145 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336145 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336145 is therefore inhibition of APPBP2, a GAM336145 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336145 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336145 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of BACE2, a GAM336145 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336145 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336145 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of BCHE. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336145 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336145 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of CTSB. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336145 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336145 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of CTSK. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336145 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336145 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of FHL2, a GAM336145 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336145 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336145 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of HD. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336145 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336145 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of IGF1, a GAM336145 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336145 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336145 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of IL1A, a GAM336145 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation &

proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336145 NGB CACTGCACTCCAGCC TGGGCAA A A Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of NGB, a GAM336145 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336145 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336145 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336145 is therefore inhibition of PRND, a GAM336145 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336146 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336146 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336146 is therefore inhibition of APPBP2, a GAM336146 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336146 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336146 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336146 is therefore inhibition of BACE2, a GAM336146 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336146 BCHE CACTGCACTCCAGCC TGGGCAA BCHE (Accession NM_000055.1) is another GAM336146 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336146 is therefore inhibition of BCHE. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336146 CTSB CACTGCACTCCAGCC TGGGCAA CTSB (Accession NM_147782.1) is another GAM336146 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of CTSB. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336146 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336146 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of CTSK. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336146 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336146 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of FHL2, a GAM336146 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336146 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336146 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of HD. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336146 IGF1 CACTGCACTCCAGCC TGGGCAA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336146 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of IGF1, a GAM336146 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336146 IL1A CACTGCACTCCAGCC TGGGCAA A A Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336146 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of IL1A, a GAM336146 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM281.

GAM336146 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336146 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of NGB, a GAM336146 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336146 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336146 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336146 is therefore inhibition of PRND, a GAM336146 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336147 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336147 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336147 is therefore inhibition of APPBP2, a GAM336147 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336147 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336147 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of BACE2, a GAM336147 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336147 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336147 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of BCHE. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336147 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336147 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of CTSB. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336147 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336147 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of CTSK. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336147 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336147 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of FHL2, a GAM336147 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336147 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336147 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of HD. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336147 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336147 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of IGF1, a GAM336147 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336147 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336147 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of IL1A, a GAM336147 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336147 NGB A A CACTGCACTCCAGCC TGGGCAA Neuroglobin (NGB, Accession NM_021257.2) is another GAM336147 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of NGB, a GAM336147 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336147 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336147 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336147 is therefore inhibition of PRND, a GAM336147 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336148 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336148 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336148 is therefore inhibition of APPBP2, a GAM336148 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336148 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336148 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336148 is therefore inhibition of BACE2, a GAM336148 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336148 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336148 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336148 is therefore inhibition of FHL2, a GAM336148 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336148 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336148 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336148 is therefore inhibition of IGF1, a GAM336148 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336148 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336148 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336148 is therefore inhibition of MME, a GAM336148 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336148 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336148 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336148 is therefore inhibition of PRND, a GAM336148 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336149 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336149 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336149 is therefore inhibition of APPBP2, a GAM336149 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336149 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336149 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of BACE2, a GAM336149 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336149 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336149 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of BCHE. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336149 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336149 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of CTSB. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336149 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336149 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of CTSK. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336149 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336149 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of FHL2, a GAM336149 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336149 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336149 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of HD. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336149 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336149 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of IGF1, a GAM336149 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336149 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336149 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of IL1A, a GAM336149 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336149 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336149 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of NGB, a GAM336149 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336149 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336149 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336149 is therefore inhibition of PRND, a GAM336149 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336150 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336150 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336150 is therefore inhibition of APPBP2, a GAM336150 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336150 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336150 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of BACE2, a GAM336150 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336150 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336150 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of BCHE. Accordingly, utilities of GAM336150 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336150 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336150 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of CTSB. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336150 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336150 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of CTSK. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336150 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336150 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of FHL2, a GAM336150 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336150 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336150 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of HD. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336150 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336150 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of IGF1, a GAM336150 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336150 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336150 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of IL1A, a GAM336150 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336150 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336150 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of NGB, a GAM336150 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336150 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336150 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336150 is therefore inhibition of PRND, a GAM336150 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336151 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336151 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336151 is therefore inhibition of APPBP2, a GAM336151 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336151 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336151 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of BACE2, a GAM336151 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336151 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336151 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of BCHE. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336151 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336151 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of CTSB. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336151 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336151 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of CTSK. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336151 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336151 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of FHL2, a GAM336151 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336151 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336151 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of HD. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336151 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
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TGGGCAA NM_000618.2) is another GAM336151 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of IGF1, a GAM336151 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336151 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
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TGGGCAA GAM336151 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of IL1A, a GAM336151 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336151 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336151 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of NGB, a GAM336151 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336151 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336151 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336151 is therefore inhibition of PRND, a GAM336151 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336152 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336152 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336152 is therefore inhibition of APPBP2,

a GAM336152 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336152 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336152 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of BACE2, a GAM336152 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336152 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336152 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of BCHE. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336152 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336152 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of CTSB. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336152 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336152 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of CTSK. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336152 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336152 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of FHL2, a GAM336152 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336152 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336152 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of HD. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336152 IGF1 A A CACTGCACTCCAGCC TGGGCAA A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336152 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of IGF1, a GAM336152 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336152 IL1A A A CACTGCACTCCAGCC TGGGCAA A Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336152 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of IL1A, a GAM336152 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336152 NGB A A CACTGCACTCCAGCC TGGGCAA A Neuroglobin (NGB, Accession NM_021257.2) is another GAM336152 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336152 is therefore inhibition of NGB, a GAM336152 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336152 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336152 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336153 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336153 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336153 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336153 is therefore inhibition of BCHE. Accordingly, utilities of GAM336153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336153 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336153 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336153 is therefore inhibition of CTSB. Accordingly, utilities of GAM336153 include diagnosis,

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GAM336153 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336153 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336153 is therefore inhibition of CTSK. Accordingly, utilities of GAM336153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336153 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336153 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336153 is therefore inhibition of FHL2, a GAM336153 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336153 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336153 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336153 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336153 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336153 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336153 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336153 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336154 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336154 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336154 is therefore inhibition of APPBP2, a GAM336154 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336154 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336154 target gene. A A

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GAM336154 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336154 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336154 is therefore inhibition of CTSB. Accordingly, utilities of GAM336154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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Another function of GAM336154 is therefore inhibition of CTSK. Accordingly, utilities of GAM336154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336154 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336154 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336154 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336154 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336154 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336154 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336154 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336154 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336155 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336155 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336155 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336155 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336155 is therefore inhibition of HD. Accordingly, utilities of GAM336155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336155 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336155 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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IGF1, a GAM336155 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336155 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A TGGGCAA GAM336155 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336155 is therefore inhibition of IL1A, a GAM336155 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336155 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336155 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336155 is therefore inhibition of NGB, a GAM336155 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336155 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336155 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336155 is therefore inhibition of PRND, a GAM336155 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336156 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336156 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336156 is therefore inhibition of APPBP2, a GAM336156 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336156 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336156 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336156 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336156 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336156 is therefore inhibition of BCHE. Accordingly, utilities of GAM336156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336156 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336156 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336156 is therefore inhibition of CTSB. Accordingly, utilities of GAM336156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336156 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336156 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336156 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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GAM336156 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336156 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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TGGGCAA NM_000618.2) is another GAM336156 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336156 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

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GAM336156 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336156 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336156 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

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GAM336157 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336157 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336157 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336157 target gene. A A

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A function of GAM336158 is therefore inhibition of APPBP2, a GAM336158 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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Another function of GAM336158 is therefore inhibition of BCHE. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336158 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147782.1) is another GAM336158 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336158 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336158 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336158 is therefore inhibition of CTSK. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336158 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336158 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336158 is therefore inhibition of FHL2, a GAM336158 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336158 HD A A TGGGCAA CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336158 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336158 IGF1 A A TGGGCAA CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336158 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336158 is therefore inhibition of IGF1, a GAM336158 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336158 IL1A A A TGGGCAA CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336158 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336158 is therefore inhibition of IL1A, a GAM336158 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336158 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336158 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336158 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336158 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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previous studies, as described hereinabove with reference to GAM44.

GAM336159 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336159 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336159 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336159 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336159 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336159 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336159 is therefore inhibition of BCHE. Accordingly, utilities of GAM336159 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336159 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336159 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336159 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336159 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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Another function of GAM336159 is therefore inhibition of FHL2, a GAM336159 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336159 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

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GAM336159 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336159 target gene.
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GAM336159 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
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Another function of GAM336159 is therefore inhibition of IGF1, a GAM336159 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336159 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

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GAM336159 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336159 A A
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Another function of GAM336159 is therefore inhibition of NGB, a GAM336159 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336159 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

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GAM336160 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
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untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336160 is therefore inhibition of APPBP2, a GAM336160 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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GAM336160 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
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Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of CTSB. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336161 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336161 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of CTSK. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336161 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336161 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of FHL2, a GAM336161 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336161 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336161 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336161

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of HD. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336161 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336161 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of IGF1, a GAM336161 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336161 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336161 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of IL1A, a GAM336161 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336161 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336161 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of NGB, a GAM336161 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336161 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336161 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336161 is therefore inhibition of PRND, a GAM336161 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336162 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336162 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336162 is therefore inhibition of APPBP2, a GAM336162 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336162 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336162 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of BACE2, a GAM336162 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336162 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336162 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of BCHE. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336162 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336162 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of CTSB. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336162 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336162 target gene. A A

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Another function of GAM336162 is therefore inhibition of CTSK. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336162 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336162 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of FHL2, a GAM336162 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336162 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336162 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of HD. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336162 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336162 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of IGF1, a GAM336162 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336162 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336162 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of IL1A, a GAM336162 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336162 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336162 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336162 is therefore inhibition of NGB, a GAM336162 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336162 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336162 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336162 is therefore inhibition of PRND, a GAM336162 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336163 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336163 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336163 is therefore inhibition of APPBP2, a GAM336163 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336163 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336163 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of BACE2, a GAM336163 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336163 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336163 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of BCHE. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336163 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336163 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of CTSB. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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Another function of GAM336163 is therefore inhibition of CTSK. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336163 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336163 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of FHL2, a GAM336163 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336163 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336163 target gene. HD A A

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TGGGCAA NM_000618.2) is another GAM336163 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of IGF1, a GAM336163 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336163 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336163 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of IL1A, a GAM336163 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336163 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336163 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of NGB, a GAM336163 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention

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GAM336163 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336163 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336163 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336163 is therefore inhibition of PRND, a GAM336163 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336163 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336164 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336164 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336164 is therefore inhibition of APPBP2, a GAM336164 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336164 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336164 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of BACE2, a GAM336164 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336164 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336164 target gene. A A

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Another function of GAM336164 is therefore inhibition of BCHE. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336164 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336164 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of CTSB. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336164 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336164 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of CTSK. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336164 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336164 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of FHL2, a GAM336164 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336164 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336164 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of HD. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336164 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336164 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of IGF1, a GAM336164 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336164 IL1A CACTGCACTCCAGCC A A TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336164 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of IL1A, a GAM336164 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336164 NGB CACTGCACTCCAGCC A A TGGGCAA Neuroglobin (NGB, Accession NM_021257.2) is another GAM336164 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of NGB, a GAM336164 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336164 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336164 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336164 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336164 is therefore inhibition of PRND, a GAM336164 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336164 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336165 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336165 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336165 is therefore inhibition of APPBP2, a GAM336165 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336165 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336165 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of BACE2, a GAM336165 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336165 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336165 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of BCHE. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336165 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336165 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of CTSB. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of CTSK. Accordingly, utilities of GAM336165 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336165 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336165 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of FHL2, a GAM336165 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336165 HD HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336165 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of HD. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336165 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336165 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of IGF1, a GAM336165 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336165 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336165 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of IL1A, a GAM336165 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336165 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336165 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of NGB, a GAM336165 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336165 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336165 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336165 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336165 is therefore inhibition of PRND, a GAM336165 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336165 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336166 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336166 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336166 is therefore inhibition of APPBP2, a GAM336166 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336166 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336166 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of BACE2, a GAM336166 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of

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GAM336166 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336166 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of BCHE. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336166 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336166 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of CTSB. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336166 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336166 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of CTSK. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336166 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336166 target gene. FHL2 BINDING SITE1 and FHL2 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of FHL2, a GAM336166 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336166 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336166 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336166 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336166 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of IGF1, a GAM336166 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

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GAM336166 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336166 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of IL1A, a GAM336166 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336166 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336166 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336166 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336166 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336166 is therefore inhibition of PRND, a GAM336166 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336167 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336167 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336167 is therefore inhibition of APPBP2, a GAM336167 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336167 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336167 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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Another function of GAM336167 is therefore inhibition of BCHE. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336167 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336167 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of CTSB. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336167 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336167 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of CTSK. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336167 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336167 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336167 is therefore inhibition of FHL2, a GAM336167 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336167 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336167 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of HD. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336167 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336167 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of IGF1, a GAM336167 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336167 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336167 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of IL1A, a GAM336167 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336167 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336167 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of NGB, a GAM336167 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336167 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336167 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336167 is therefore inhibition of PRND, a GAM336167 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336168 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336168 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336168 is therefore inhibition of APPBP2, a GAM336168 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336168 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336168 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of BACE2, a GAM336168 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336168 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336168 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of BCHE. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336168 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147780.1) is another GAM336168 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of CTSB. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336168 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336168 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of CTSK. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336168 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336168 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of FHL2, a GAM336168 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336168 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336168 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of HD. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336168 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336168 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of IGF1, a GAM336168 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336168 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336168 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of IL1A, a GAM336168 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336168 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336168 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of NGB, a GAM336168 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336168 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336168 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336168 is therefore inhibition of PRND, a GAM336168 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336169 BLMH ACATGATCTCCTCAC Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a A A

TCTAGGA GAM336169 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336169 is therefore inhibition of BLMH, a GAM336169 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM336169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM336169 GSK3B ACATGATCTCCTCAC Glycogen Synthase Kinase 3 Beta (GSK3B, Accession NM_002093.2) A A
TCTAGGA is another GAM336169 target gene. GSK3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GSK3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSK3B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336169 is therefore inhibition of GSK3B, a GAM336169 target gene which b subunit of glycogen synthase kinase 3 which phosphorylates regulatory proteins. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSK3B.The function of GSK3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2027.

GAM336169 MAPT ACATGATCTCCTCAC Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM336169 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336169 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A
TCTAGGA

Another function of GAM336169 is therefore inhibition of MAPT, a GAM336169 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336169 PSEN2 ACATGATCTCCTCAC PSEN2 (Accession NM_012486.1) is another GAM336169 target gene. A A

TCTAGGA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336169 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336170 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336170 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336170 is therefore inhibition of APPBP2, a GAM336170 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336170 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336170 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of

BACE2, a GAM336170 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336170 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336170 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of BCHE. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336170 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336170 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of CTSB. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336170 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336170 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of CTSK. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with CTSK.

GAM336170 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336170 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of FHL2, a GAM336170 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336170 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336170 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of HD. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336170 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336170 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of IGF1, a GAM336170 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336170 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336170 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of IL1A, a GAM336170 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336170 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336170 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of NGB, a GAM336170 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336170 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336170 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336170 is therefore inhibition of PRND, a GAM336170 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336171 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336171 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336171 is therefore inhibition of APPBP2, a GAM336171 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336171 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336171 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of BACE2, a GAM336171 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336171 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336171 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of BCHE. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336171 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336171 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of CTSB. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336171 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336171 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of CTSK. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336171 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336171 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of FHL2, a GAM336171 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336171 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336171 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of HD. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336171 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336171 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of IGF1, a GAM336171 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336171 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336171 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of IL1A, a GAM336171 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336171 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336171 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of NGB, a GAM336171 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336171 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336171 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336171 is therefore inhibition of PRND, a GAM336171 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336172 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336172 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336172 is therefore inhibition of APPBP2, a GAM336172 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336172 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336172 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of BACE2, a GAM336172 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336172 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336172 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of BCHE. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336172 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336172 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of CTSB. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336172 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336172 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of CTSK. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336172 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336172 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336172 is therefore inhibition of FHL2, a GAM336172 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336172 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336172 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of HD. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336172 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336172 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of IGF1, a GAM336172 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336172 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336172 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of IL1A, a GAM336172 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336172 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336172 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of NGB, a GAM336172 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336172 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336172 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336172 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336172 is therefore inhibition of PRND, a GAM336172 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336173 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336173 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336173 is therefore inhibition of APPBP2, a GAM336173 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336173 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336173 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of BACE2, a GAM336173 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336173 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336173 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of BCHE. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336173 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336173 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of CTSB. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336173 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336173 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of CTSK. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336173 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336173 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of FHL2, a GAM336173 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336173 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336173 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of HD. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336173 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336173 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of IGF1, a GAM336173 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336173 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336173 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of IL1A, a GAM336173 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336173 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336173 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of NGB, a GAM336173 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336173 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336173 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336173 is therefore inhibition of PRND, a GAM336173 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336174 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336174 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336174 is therefore inhibition of APPBP2, a GAM336174 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336174 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336174 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of BACE2, a GAM336174 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336174 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336174 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of BCHE. Accordingly, utilities of GAM336174 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336174 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336174 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of CTSB. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336174 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336174 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of CTSK. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336174 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336174 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of FHL2, a GAM336174 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336174 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336174 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of HD. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336174 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336174 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of IGF1, a GAM336174 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336174 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336174 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of IL1A, a GAM336174 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336174 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336174 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of NGB, a GAM336174 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336174 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336174 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336174 is therefore inhibition of PRND, a GAM336174 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336175 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336175 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336175 is therefore inhibition of APPBP2, a GAM336175 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336175 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336175 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of BACE2, a GAM336175 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336175 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336175 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of BCHE. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336175 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336175 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of CTSB. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336175 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336175 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of CTSK. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336175 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336175 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of FHL2, a GAM336175 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336175 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336175 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of HD. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336175 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
TGGGCAA NM_000618.2) is another GAM336175 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of IGF1, a GAM336175 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336175 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
A
TGGGCAA GAM336175 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of IL1A, a GAM336175 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336175 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336175 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of NGB, a GAM336175 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336175 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336175 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336175 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336175 is therefore inhibition of PRND, a GAM336175 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336175 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336176 AVP TCTTGTGAAATCTGT AVP (Accession NM_000490.2) is a GAM336176 target gene. AVP A A
GGACCCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336176 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336176 is therefore inhibition of AVP. Accordingly, utilities of GAM336176 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with AVP.

GAM336177 BLMH ACATGATCTCCTCAC Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a A A

TCTAGGA GAM336177 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336177 is therefore inhibition of BLMH, a GAM336177 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM336177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM336177 GSK3B ACATGATCTCCTCAC Glycogen Synthase Kinase 3 Beta (GSK3B, Accession NM_002093.2) A A

TCTAGGA is another GAM336177 target gene. GSK3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GSK3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSK3B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336177 is therefore inhibition of GSK3B, a GAM336177 target gene which b subunit of glycogen synthase kinase 3 which phosphorylates regulatory proteins. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSK3B.The function of GSK3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2027.

GAM336177 MAPT ACATGATCTCCTCAC Microtubule- associated Protein Tau (MAPT, Accession A A

TCTAGGA NM_173727.1) is another GAM336177 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336177 is therefore inhibition of MAPT, a GAM336177 target gene which Microtubule- associated protein

tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336177 PSEN2 ACATGATCTCCTCAC PSEN2 (Accession NM_012486.1) is another GAM336177 target gene. A A

TCTAGGA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336177 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336178 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336178 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336178 is therefore inhibition of APPBP2, a GAM336178 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336178 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336178 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336178 is therefore inhibition of BACE2, a GAM336178 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336178 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336178 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of BCHE. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336178 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336178 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of CTSB. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336178 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336178 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of CTSK. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336178 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336178 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of FHL2, a GAM336178 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336178 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336178 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of HD. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336178 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336178 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of IGF1, a GAM336178 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336178 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336178 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of IL1A, a GAM336178 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336178 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336178 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of NGB, a GAM336178 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336178 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336178 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336178 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336178 is therefore inhibition of PRND, a GAM336178 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336178 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336179 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336179 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336179 is therefore inhibition of APPBP2, a GAM336179 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336179 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336179 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336179 is therefore inhibition of BACE2, a GAM336179 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336179 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336179 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of BCHE. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336179 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336179 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of CTSB. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336179 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336179 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of CTSK. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336179 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336179 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of FHL2, a GAM336179 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336179 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336179 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of HD. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336179 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM336179 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of IGF1, a GAM336179 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM336179 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336179 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of IL1A, a GAM336179 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336179 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336179 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336179 is therefore inhibition of NGB, a GAM336179 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336179 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336179 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336179 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336179 is therefore inhibition of PRND, a GAM336179 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336180 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336180 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336180 is therefore inhibition of APPBP2, a GAM336180 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336180 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336180 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of BACE2, a GAM336180 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336180 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336180 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of BCHE. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336180 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336180 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of CTSB. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336180 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336180 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of CTSK. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336180 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336180 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of FHL2, a GAM336180 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336180 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336180 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of HD. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336180 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336180 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of IGF1, a GAM336180 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336180 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336180 target gene. IL1A BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of IL1A, a GAM336180 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336180 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336180 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of NGB, a GAM336180 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336180 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336180 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336180 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336180 is therefore inhibition of PRND, a GAM336180 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336181 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336181 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336181 is therefore inhibition of APPBP2, a GAM336181 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336181 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336181 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of BACE2, a GAM336181 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336181 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336181 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of BCHE. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336181 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147782.1) is another GAM336181 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of CTSB. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336181 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336181 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of CTSK. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336181 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336181 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of

FHL2, a GAM336181 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336181 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336181 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of HD. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336181 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336181 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of IGF1, a GAM336181 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336181 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336181 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and

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Another function of GAM336181 is therefore inhibition of IL1A, a GAM336181 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336181 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336181 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of NGB, a GAM336181 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336181 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336181 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336181 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336181 is therefore inhibition of PRND, a GAM336181 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336182 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336182 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336182 is therefore inhibition of APPBP2, a GAM336182 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336182 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336182 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of BACE2, a GAM336182 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336182 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336182 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of BCHE. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336182 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336182 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of CTSB. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336182 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336182 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of CTSK. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336182 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336182 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of FHL2, a GAM336182 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336182 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336182 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of HD. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336182 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336182 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of IGF1, a GAM336182 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336182 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336182 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of IL1A, a GAM336182 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation &

proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336182 NGB CACTGCACTCCAGCC TGGGCAA A A

Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of NGB, a GAM336182 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336182 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336182 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336182 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336182 is therefore inhibition of PRND, a GAM336182 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336182 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336183 APPBP2 CACTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336183 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336183 is therefore inhibition of APPBP2, a GAM336183 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336183 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336183 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of BACE2, a GAM336183 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336183 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336183 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of BCHE. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336183 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336183 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of CTSB. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336183 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336183 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of CTSK. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336183 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336183 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of FHL2, a GAM336183 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336183 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336183 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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Another function of GAM336183 is therefore inhibition of IGF1, a GAM336183 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336183 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
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Another function of GAM336183 is therefore inhibition of IL1A, a GAM336183 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as

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GAM336183 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336183 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336183 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336183 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336183 is therefore inhibition of PRND, a GAM336183 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336184 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336184 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336184 is therefore inhibition of APPBP2, a GAM336184 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336184 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336184 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of BACE2, a GAM336184 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336184 BCHE CACTGCACTCCAGCC TGGGCAA A A BCHE (Accession NM_000055.1) is another GAM336184 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of BCHE. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336184 CTSB CACTGCACTCCAGCC TGGGCAA A A CTSB (Accession NM_147782.1) is another GAM336184 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of CTSB. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336184 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336184 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of CTSK. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336184 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336184 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of FHL2, a GAM336184 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336184 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336184 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of HD. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336184 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336184 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of IGF1, a GAM336184 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336184 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336184 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of IL1A, a GAM336184 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336184 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336184 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of NGB, a GAM336184 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336184 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336184 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336184 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336184 is therefore inhibition of PRND, a GAM336184 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336185 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336185 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336185 is therefore inhibition of APPBP2, a GAM336185 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336185 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336185 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of BACE2, a GAM336185 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336185 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336185 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of BCHE. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336185 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336185 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of

CTSB. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336185 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336185 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of CTSK. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336185 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336185 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of FHL2, a GAM336185 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336185 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336185 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of HD. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336185 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336185 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of IGF1, a GAM336185 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336185 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336185 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of IL1A, a GAM336185 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336185 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336185 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of NGB, a GAM336185 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336185 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336185 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336185 is therefore inhibition of PRND, a GAM336185 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336186 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336186 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336186 is therefore inhibition of APPBP2, a GAM336186 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336186 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336186 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336186 is therefore inhibition of BACE2, a GAM336186 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336186 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336186 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336186 is therefore inhibition of FHL2, a GAM336186 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336186 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336186 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336186 is therefore inhibition of IGF1, a GAM336186 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336186 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336186 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336186 is therefore inhibition of MME, a GAM336186 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336186 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336186 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336186 is therefore inhibition of PRND, a GAM336186 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336187 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336187 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336187 is therefore inhibition of APPBP2, a GAM336187 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336187 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336187 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of BACE2, a GAM336187 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336187 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336187 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of BCHE. Accordingly, utilities of GAM336187 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336187 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336187 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of CTSB. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336187 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336187 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of CTSK. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336187 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336187 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of FHL2, a GAM336187 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336187 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336187 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of HD. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336187 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336187 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of IGF1, a GAM336187 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336187 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336187 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of IL1A, a GAM336187 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336187 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336187 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of NGB, a GAM336187 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336187 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336187 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336187 is therefore inhibition of PRND, a GAM336187 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336188 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336188 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336188 is therefore inhibition of APPBP2, a GAM336188 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336188 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336188 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of BACE2, a GAM336188 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336188 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336188 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of BCHE. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336188 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336188 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of CTSB. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336188 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336188 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of CTSK. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336188 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336188 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of FHL2, a GAM336188 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336188 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336188 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of HD. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336188 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
TGGGCAA NM_000618.2) is another GAM336188 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of IGF1, a GAM336188 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336188 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A
A
TGGGCAA GAM336188 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of IL1A, a GAM336188 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336188 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336188 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of NGB, a GAM336188 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336188 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336188 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336188 is therefore inhibition of PRND, a GAM336188 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336189 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336189 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336189 is therefore inhibition of APPBP2,

a GAM336189 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336189 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336189 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of BACE2, a GAM336189 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336189 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336189 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of BCHE. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336189 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336189 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of CTSB. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336189 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336189 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of CTSK. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336189 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336189 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of FHL2, a GAM336189 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336189 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336189 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of HD. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336189 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336189 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of IGF1, a GAM336189 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336189 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336189 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of IL1A, a GAM336189 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336189 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336189 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of NGB, a GAM336189 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336189 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336189 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336189 is therefore inhibition of PRND, a GAM336189 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336190 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336190 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336190 is therefore inhibition of APPBP2, a GAM336190 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336190 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336190 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of BACE2, a GAM336190 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336190 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336190 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of BCHE. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336190 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336190 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of CTSB. Accordingly, utilities of GAM336190 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336190 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336190 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of CTSK. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336190 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336190 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of FHL2, a GAM336190 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336190 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336190 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of HD. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336190 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336190 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336190 is therefore inhibition of IGF1, a GAM336190 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336190 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336190 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336190 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336190 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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NGB, a GAM336190 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336190 PRND CACTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336190 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336190 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

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GAM336191 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336191 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

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GAM336191 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336191 target gene. BACE2 BINDING SITE is A A

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GAM336191 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336191 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336191 is therefore inhibition of BCHE. Accordingly, utilities of GAM336191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336191 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336191 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336191 is therefore inhibition of CTSB. Accordingly, utilities of GAM336191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336191 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336191 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a

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Another function of GAM336191 is therefore inhibition of CTSK. Accordingly, utilities of GAM336191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336191 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336191 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336191 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336191 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336191 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336191 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336191 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

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GAM336191 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336191 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336191 is therefore inhibition of NGB, a GAM336191 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336191 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336191 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336191 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336192 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336192 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336192 is therefore inhibition of APPBP2, a GAM336192 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336192 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336192 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336192 is therefore inhibition of BACE2, a GAM336192 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336192 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336192 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336192 is therefore inhibition of BCHE. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336192 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336192 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336192 is therefore inhibition of CTSB. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336192 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336192 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336192 is therefore inhibition of CTSK. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336192 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336192 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336192 is therefore inhibition of FHL2, a GAM336192 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336192 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336192 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336192 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336193 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336193 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336193 is therefore inhibition of FHL2, a GAM336193 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336193 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336193 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336193 is therefore inhibition of HD. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336193 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336193 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336193 is therefore inhibition of IGF1, a GAM336193 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336193 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336193 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336193 is therefore inhibition of IL1A, a GAM336193 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336193 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336193 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336193 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336193 is therefore inhibition of NGB, a GAM336193 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336193 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336193 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING

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Another function of GAM336193 is therefore inhibition of PRND, a GAM336193 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336193 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336194 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336194 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336194 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336194 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336194 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336194 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336194 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336194 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336194 is therefore inhibition of CTSB. Accordingly, utilities of GAM336194 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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GAM336194 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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GAM336194 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336194 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336195 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336195 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336195 is therefore inhibition of APPBP2, a GAM336195 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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TGGGCAA NM_138991.1) is another GAM336195 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a

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GAM336195 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336195 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336195 is therefore inhibition of CTSB. Accordingly, utilities of GAM336195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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GAM336195 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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nucleotide sequence of GAM336195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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Another function of GAM336196 is therefore inhibition of CTSK. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336196 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336196 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336196 is therefore inhibition of FHL2, a GAM336196 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336196 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336196 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336196 is therefore inhibition of HD. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336196 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336196 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336196 is therefore inhibition of IGF1, a GAM336196 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336196 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336196 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336196 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336196 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336196 is therefore inhibition of NGB, a GAM336196 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336196 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
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Another function of GAM336196 is therefore inhibition of PRND, a GAM336196 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336197 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336197 target gene. APPBP2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336197 is therefore inhibition of APPBP2, a GAM336197 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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Another function of GAM336197 is therefore inhibition of BACE2, a GAM336197 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336197 BCHE CACTGCACTCCAGCC A A TGGGCAA BCHE (Accession NM_000055.1) is another GAM336197 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336197 is therefore inhibition of BCHE. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336197 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336197 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336197 is therefore inhibition of CTSB. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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GAM336197 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
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Another function of GAM336197 is therefore inhibition of FHL2, a GAM336197 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336197 is therefore inhibition of HD. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336197 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

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Another function of GAM336197 is therefore inhibition of IL1A, a GAM336197 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and

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GAM336197 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336197 A A
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GAM336198 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336198 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336198 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336198 is therefore inhibition of APPBP2, a GAM336198 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336198 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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Another function of GAM336198 is therefore inhibition of BCHE. Accordingly, utilities of GAM336198 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

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Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336198 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336198 is therefore inhibition of CTSB. Accordingly, utilities of GAM336198 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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Another function of GAM336199 is therefore inhibition of CTSB. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336199 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336199 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of CTSK. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336199 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336199 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of FHL2, a GAM336199 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336199 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336199 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of HD. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336199 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336199 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of IGF1, a GAM336199 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336199 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336199 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of IL1A, a GAM336199 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336199 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336199 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336199 is therefore inhibition of NGB, a GAM336199 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336199 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336199 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336199 is therefore inhibition of PRND, a GAM336199 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336200 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336200 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336200 is therefore inhibition of APPBP2, a GAM336200 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336200 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336200 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of BACE2, a GAM336200 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336200 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336200 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of BCHE. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336200 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336200 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of CTSB. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336200 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336200 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of CTSK. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336200 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336200 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of FHL2, a GAM336200 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336200 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336200 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of HD. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336200 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336200 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of IGF1, a GAM336200 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336200 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336200 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of IL1A, a GAM336200 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336200 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336200 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of NGB, a GAM336200 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336200 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336200 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336200 is therefore inhibition of PRND, a GAM336200 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336201 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336201 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336201 is therefore inhibition of APPBP2, a GAM336201 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336201 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336201 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of BACE2, a GAM336201 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336201 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336201 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of BCHE. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336201 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336201 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of CTSB. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336201 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336201 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of CTSK. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336201 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336201 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of FHL2, a GAM336201 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336201 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336201 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of HD. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336201 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336201 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of IGF1, a GAM336201 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336201 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336201 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of IL1A, a GAM336201 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336201 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336201 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of NGB, a GAM336201 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336201 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336201 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336201 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336201 is therefore inhibition of PRND, a GAM336201 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336201 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336202 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336202 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336202 is therefore inhibition of APPBP2, a GAM336202 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336202 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336202 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of BACE2, a GAM336202 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336202 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336202 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of BCHE. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336202 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336202 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of CTSB. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336202 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336202 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of CTSK. Accordingly, utilities of GAM336202 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336202 FHL2 A A CACTGCACTCCAGCC TGGGCAA A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336202 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of FHL2, a GAM336202 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336202 HD HD A A CACTGCACTCCAGCC TGGGCAA A HD (Accession NM_002111.3) is another GAM336202 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of HD. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336202 IGF1 A A CACTGCACTCCAGCC TGGGCAA A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336202 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of IGF1, a GAM336202 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336202 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336202 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of IL1A, a GAM336202 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336202 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336202 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of NGB, a GAM336202 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336202 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336202 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336202 is therefore inhibition of PRND, a GAM336202 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336203 APBB2 AGTGGGATGGAGTCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GCAGAAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336203 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336203 is therefore inhibition of APBB2, a GAM336203 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336203 GLUL AGTGGGATGGAGTCA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GCAGAAG NM_002065.3) is another GAM336203 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336203 is therefore inhibition of GLUL, a GAM336203 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function

of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336203 IL1A AGTGGGATGGAGTCA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

GCAGAAG GAM336203 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336203 is therefore inhibition of IL1A, a GAM336203 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336203 NGB AGTGGGATGGAGTCA Neuroglobin (NGB, Accession NM_021257.2) is another GAM336203 A A

GCAGAAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336203 is therefore inhibition of NGB, a GAM336203 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336203 PRND AGTGGGATGGAGTCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GCAGAAG another GAM336203 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336203 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336203 is therefore inhibition of PRND, a GAM336203 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336204 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336204 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336204 is therefore inhibition of APPBP2, a GAM336204 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336204 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336204 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of BACE2, a GAM336204 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336204 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336204 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of BCHE. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336204 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336204 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of CTSB. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336204 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336204 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of CTSK. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336204 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336204 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of FHL2, a GAM336204 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336204 HD A A TGGGCAA CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336204 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of HD. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336204 IGF1 A A TGGGCAA CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336204 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of IGF1, a GAM336204 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336204 IL1A A A TGGGCAA CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336204 target gene. IL1A BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of IL1A, a GAM336204 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336204 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336204 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of NGB, a GAM336204 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336204 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336204 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336204 is therefore inhibition of PRND, a GAM336204 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336205 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336205 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336205 is therefore inhibition of APPBP2, a GAM336205 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336205 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336205 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of BACE2, a GAM336205 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336205 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336205 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of BCHE. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336205 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336205 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of CTSB. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336205 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336205 target gene. A A
TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of CTSK. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336205 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336205 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of

FHL2, a GAM336205 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336205 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336205 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of HD. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336205 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336205 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of IGF1, a GAM336205 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336205 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336205 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of IL1A, a GAM336205 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336205 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336205 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of NGB, a GAM336205 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336205 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336205 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336205 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336205 is therefore inhibition of PRND, a GAM336205 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336205 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336206 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336206 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336206 is therefore inhibition of APPBP2, a GAM336206 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336206 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336206 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of BACE2, a GAM336206 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336206 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336206 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of BCHE. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336206 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336206 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of CTSB. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336206 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336206 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of CTSK. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336206 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336206 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of FHL2, a GAM336206 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336206 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336206 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of HD. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336206 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336206 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of IGF1, a GAM336206 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336206 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336206 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of IL1A, a GAM336206 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation &

proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336206 NGB CACTGCACTCCAGCC TGGGCAA A A

Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of NGB, a GAM336206 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336206 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336206 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336206 is therefore inhibition of PRND, a GAM336206 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336207 APPBP2 CACTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336207 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336207 is therefore inhibition of APPBP2, a GAM336207 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336207 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336207 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of BACE2, a GAM336207 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336207 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336207 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of BCHE. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336207 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336207 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of CTSB. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336207 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336207 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of CTSK. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336207 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336207 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of FHL2, a GAM336207 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336207 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336207 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of HD. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336207 IGF1 A CACTGCACTCCAGCC A TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336207 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of IGF1, a GAM336207 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336207 IL1A A CACTGCACTCCAGCC A TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336207 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of IL1A, a GAM336207 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM281.

GAM336207 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336207 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of NGB, a GAM336207 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336207 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336207 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336207 is therefore inhibition of PRND, a GAM336207 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336208 APBB2 AGTGGGATGGAGTCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GCAGAAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336208 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336208 is therefore inhibition of APBB2, a GAM336208 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336208 GLUL AGTGGGATGGAGTCA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GCAGAAG NM_002065.3) is another GAM336208 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336208 is therefore inhibition of GLUL, a GAM336208 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336208 IL1A AGTGGGATGGAGTCA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
GCAGAAG GAM336208 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336208 is therefore inhibition of IL1A, a GAM336208 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336208 NGB AGTGGGATGGAGTCA Neuroglobin (NGB, Accession NM_021257.2) is another GAM336208 A A

GCAGAAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336208 is therefore inhibition of NGB, a GAM336208 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336208 PRND AGTGGGATGGAGTCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GCAGAAG another GAM336208 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336208 is therefore inhibition of PRND, a GAM336208 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336209 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336209 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336209 is therefore inhibition of APPBP2, a GAM336209 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336209 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336209 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of BACE2, a GAM336209 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336209 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336209 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of BCHE. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336209 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336209 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of CTSB. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336209 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336209 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of CTSK. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336209 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336209 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of FHL2, a GAM336209 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336209 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336209 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of HD. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336209 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336209 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of IGF1, a GAM336209 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336209 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336209 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336209 is therefore inhibition of IL1A, a GAM336209 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336209 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336209 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336209 is therefore inhibition of NGB, a GAM336209 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336209 PRND CACTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336209 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336209 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336209 is therefore inhibition of PRND, a GAM336209 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336210 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336210 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336210 is therefore inhibition of APPBP2, a GAM336210 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336210 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336210 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of BACE2, a GAM336210 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336210 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336210 target gene. A A
TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of BCHE. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336210 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336210 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of CTSB. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336210 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336210 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of CTSK. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336210 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336210 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of FHL2, a GAM336210 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336210 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336210 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of HD. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336210 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336210 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of IGF1, a GAM336210 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336210 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336210 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of IL1A, a GAM336210 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336210 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336210 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of NGB, a GAM336210 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336210 PRND CACTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336210 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336210 is therefore inhibition of PRND, a GAM336210 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336211 APPBP2 CACTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336211 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336211 is therefore inhibition of APPBP2, a GAM336211 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336211 BACE2 CACTGCACTCCAGCC TGGGCAA A A

Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336211 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of BACE2, a GAM336211 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336211 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336211 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of BCHE. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336211 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336211 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of CTSB. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336211 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336211 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of CTSK. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336211 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336211 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of FHL2, a GAM336211 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336211 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336211 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of HD. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336211 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336211 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of IGF1, a GAM336211 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336211 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336211 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of IL1A, a GAM336211 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336211 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336211 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of NGB, a GAM336211 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336211 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336211 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336211 is therefore inhibition of PRND, a GAM336211 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336212 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336212 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336212 is therefore inhibition of APPBP2, a GAM336212 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336212 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336212 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of BACE2, a GAM336212 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336212 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336212 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of BCHE. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336212 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336212 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of CTSB. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336212 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336212 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of CTSK. Accordingly, utilities of GAM336212 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336212 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336212 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of FHL2, a GAM336212 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336212 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336212 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of HD. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336212 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336212 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of IGF1, a GAM336212 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336212 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A TGGGCAA GAM336212 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of IL1A, a GAM336212 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336212 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336212 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of NGB, a GAM336212 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336212 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336212 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336212 is therefore inhibition of PRND, a GAM336212 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336213 APPBP2 CACTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336213 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336213 is therefore inhibition of APPBP2, a GAM336213 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336213 BACE2 CACTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336213 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336213 is therefore inhibition of BACE2, a GAM336213 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336213 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336213 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of BCHE. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336213 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336213 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of CTSB. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336213 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336213 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of CTSK. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336213 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336213 target gene. FHL2 BINDING SITE1 and FHL2 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of FHL2, a GAM336213 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336213 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336213 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of HD. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336213 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336213 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of IGF1, a GAM336213 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM336213 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336213 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of IL1A, a GAM336213 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336213 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336213 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of NGB, a GAM336213 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336213 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336213 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336213 is therefore inhibition of PRND, a GAM336213 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336214 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336214 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336214 is therefore inhibition of APPBP2, a GAM336214 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336214 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336214 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of BACE2, a GAM336214 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336214 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336214 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of BCHE. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336214 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336214 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of CTSB. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336214 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336214 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of CTSK. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336214 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336214 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336214 is therefore inhibition of FHL2, a GAM336214 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336214 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336214 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of HD. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336214 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336214 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of IGF1, a GAM336214 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336214 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336214 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of IL1A, a GAM336214 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336214 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336214 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of NGB, a GAM336214 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336214 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336214 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336214 is therefore inhibition of PRND, a GAM336214 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336215 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336215 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336215 is therefore inhibition of APPBP2, a GAM336215 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336215 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336215 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336215 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336215 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of BCHE. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336215 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147782.1) is another GAM336215 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of CTSB. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336215 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336215 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of CTSK. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336215 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336215 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of FHL2, a GAM336215 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336215 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336215 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of HD. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336215 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336215 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of IGF1, a GAM336215 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336215 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336215 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of IL1A, a GAM336215 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336215 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336215 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of NGB, a GAM336215 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336215 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336215 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336215 is therefore inhibition of PRND, a GAM336215 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336216 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336216 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336216 is therefore inhibition of APPBP2, a GAM336216 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336216 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336216 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of BACE2, a GAM336216 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336216 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336216 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of BCHE. Accordingly, utilities of GAM336216 include diagnosis,

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GAM336216 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336216 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of CTSB. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336216 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336216 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336216 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336216 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of FHL2, a GAM336216 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336216 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336216 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of HD. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336216 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336216 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of IGF1, a GAM336216 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336216 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336216 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of IL1A, a GAM336216 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216

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GAM336216 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336216 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336216 is therefore inhibition of NGB, a GAM336216 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336216 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336216 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336217 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336217 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336217 is therefore inhibition of APPBP2, a GAM336217 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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Another function of GAM336217 is therefore inhibition of BCHE. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336217 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336217 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites

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Another function of GAM336217 is therefore inhibition of CTSB. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336217 is therefore inhibition of CTSK. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336217 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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Another function of GAM336217 is therefore inhibition of FHL2, a GAM336217 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336217 is therefore inhibition of IL1A, a GAM336217 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

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Another function of GAM336217 is therefore inhibition of PRND, a GAM336217 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336218 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336218 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336218 is therefore inhibition of APPBP2,

a GAM336218 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336218 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336218 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of BACE2, a GAM336218 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336218 BCHE CACTGCACTCCAGCC TGGGCAA A A BCHE (Accession NM_000055.1) is another GAM336218 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of BCHE. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336218 CTSB CACTGCACTCCAGCC TGGGCAA A A CTSB (Accession NM_147780.1) is another GAM336218 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of CTSB. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336218 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336218 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of CTSK. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336218 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336218 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of FHL2, a GAM336218 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336218 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336218 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of HD. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336218 IGF1 A CACTGCACTCCAGCC A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession TGGGCAA NM_000618.2) is another GAM336218 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of IGF1, a GAM336218 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336218 IL1A A CACTGCACTCCAGCC A Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another TGGGCAA GAM336218 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of IL1A, a GAM336218 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336218 NGB A CACTGCACTCCAGCC A Neuroglobin (NGB, Accession NM_021257.2) is another GAM336218 TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of NGB, a GAM336218 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336218 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336218 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336218 is therefore inhibition of PRND, a GAM336218 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336219 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336219 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336219 is therefore inhibition of APPBP2, a GAM336219 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336219 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336219 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of BACE2, a GAM336219 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336219 BCHE CACTGCACTCCAGCC TGGGCAA A A BCHE (Accession NM_000055.1) is another GAM336219 target gene. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of BCHE. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336219 CTSB CACTGCACTCCAGCC TGGGCAA A A CTSB (Accession NM_147780.1) is another GAM336219 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of CTSB. Accordingly, utilities of GAM336219 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336219 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336219 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of CTSK. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336219 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336219 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of FHL2, a GAM336219 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336219 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336219 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of HD. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336219 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336219 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of IGF1, a GAM336219 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336219 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336219 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of IL1A, a GAM336219 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336219 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336219 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of

NGB, a GAM336219 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336219 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336219 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336219 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336219 is therefore inhibition of PRND, a GAM336219 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336219 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336220 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336220 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336220 is therefore inhibition of APPBP2, a GAM336220 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336220 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336220 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of BACE2, a GAM336220 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336220 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336220 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of BCHE. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336220 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336220 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of CTSB. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336220 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336220 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of CTSK. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336220 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336220 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of FHL2, a GAM336220 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336220 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336220 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of HD. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336220 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336220 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of IGF1, a GAM336220 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336220 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336220 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of IL1A, a GAM336220 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336220 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336220 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of NGB, a GAM336220 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336220 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336220 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336220 is therefore inhibition of PRND, a GAM336220 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336221 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336221 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336221 is therefore inhibition of APPBP2, a GAM336221 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336221 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336221 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of BACE2, a GAM336221 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336221 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336221 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of BCHE. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336221 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336221 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of CTSB. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336221 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336221 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of CTSK. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336221 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336221 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of FHL2, a GAM336221 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336221 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336221 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of HD. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336221 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336221 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of

IGF1, a GAM336221 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336221 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336221 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of IL1A, a GAM336221 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336221 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336221 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336221 is therefore inhibition of NGB, a GAM336221 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336221 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336221 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336222 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336222 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336222 is therefore inhibition of APPBP2, a GAM336222 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336222 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336222 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of BACE2, a GAM336222 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336222 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336222 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of BCHE. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336222 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336222 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of CTSB. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336222 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336222 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of CTSK. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336222 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336222 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of FHL2, a GAM336222 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336222 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336222 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of HD. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336222 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336222 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of IGF1, a GAM336222 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336222 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336222 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of IL1A, a GAM336222 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336222 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336222 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336222 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336222 is therefore inhibition of NGB, a GAM336222 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336222 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336222 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING

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Another function of GAM336222 is therefore inhibition of PRND, a GAM336222 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336222 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336223 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336223 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336223 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336223 is therefore inhibition of APPBP2, a GAM336223 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

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GAM336223 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336223 target gene. A A

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Another function of GAM336223 is therefore inhibition of BCHE. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336223 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336223 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336223 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336223 is therefore inhibition of CTSB. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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Another function of GAM336223 is therefore inhibition of CTSK. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336223 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

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Another function of GAM336223 is therefore inhibition of FHL2, a GAM336223 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336223 is therefore inhibition of IGF1, a GAM336223 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

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Another function of GAM336223 is therefore inhibition of IL1A, a GAM336223 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336223 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336223 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336223 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336223 is therefore inhibition of NGB, a GAM336223 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336223 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336223 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336223 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336223 is therefore inhibition of PRND, a GAM336223 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336223 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336224 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336224 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336224 is therefore inhibition of APPBP2, a GAM336224 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336224 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336224 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of BACE2, a GAM336224 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336224 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336224 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of BCHE. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336224 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147780.1) is another GAM336224 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of CTSB. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336224 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336224 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of CTSK. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336224 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336224 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of FHL2, a GAM336224 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336224 HD A A TGGGCAA CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336224 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of HD. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336224 IGF1 A A TGGGCAA CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336224 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of IGF1, a GAM336224 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336224 IL1A A A TGGGCAA CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336224 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of IL1A, a GAM336224 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336224 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336224 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of NGB, a GAM336224 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336224 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336224 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336224 is therefore inhibition of PRND, a GAM336224 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM336225 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336225 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336225 is therefore inhibition of APPBP2, a GAM336225 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336225 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336225 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of BACE2, a GAM336225 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336225 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336225 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of BCHE. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336225 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336225 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of CTSB. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336225 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336225 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of CTSK. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336225 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336225 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of FHL2, a GAM336225 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336225 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336225 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of HD. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336225 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336225 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of IGF1, a GAM336225 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336225 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336225 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of IL1A, a GAM336225 target gene which stimulates thymocyte

proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336225 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336225 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of NGB, a GAM336225 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336225 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336225 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336225 is therefore inhibition of PRND, a GAM336225 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336226 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336226 target gene. APPBP2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336226 is therefore inhibition of APPBP2, a GAM336226 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336226 BACE2 CACTGCACTCCAGCC A A TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336226 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336226 is therefore inhibition of BACE2, a GAM336226 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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Another function of GAM336226 is therefore inhibition of BCHE. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336226 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336226 target gene. A A
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Another function of GAM336226 is therefore inhibition of CTSB. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

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GAM336226 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
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Another function of GAM336226 is therefore inhibition of FHL2, a GAM336226 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

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GAM336226 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336226 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336226 is therefore inhibition of IL1A, a GAM336226 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336226 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336226 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336226 is therefore inhibition of NGB, a GAM336226 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336226 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336226 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336226 is therefore inhibition of PRND, a GAM336226 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336227 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336227 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336227 is therefore inhibition of APPBP2, a GAM336227 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336227 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336227 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of BACE2, a GAM336227 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336227 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336227 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of BCHE. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336227 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336227 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of CTSB. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336227 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336227 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of CTSK. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336227 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336227 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of FHL2, a GAM336227 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336227 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336227 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of HD. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336227 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336227 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of IGF1, a GAM336227 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336227 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336227 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of IL1A, a GAM336227 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336227 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336227 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of NGB, a GAM336227 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336227 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336227 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336227 is therefore inhibition of PRND, a GAM336227 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336228 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336228 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336228 is therefore inhibition of APPBP2, a GAM336228 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336228 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336228 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A TGGGCAA

Another function of GAM336228 is therefore inhibition of BACE2, a GAM336228 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336228 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336228 target gene. A A TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of BCHE. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336228 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336228 target gene. A A TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of CTSB. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336228 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336228 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of CTSK. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336228 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336228 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of FHL2, a GAM336228 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336228 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336228 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of HD. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336228 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336228 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of IGF1, a GAM336228 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336228 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGGGCAA GAM336228 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of IL1A, a GAM336228 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336228 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336228 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336228 is therefore inhibition of NGB, a GAM336228 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336228 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336228 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336228 is therefore inhibition of PRND, a GAM336228 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336229 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336229 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336229 is therefore inhibition of APPBP2, a GAM336229 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336229 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138991.1) is another GAM336229 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of BACE2, a GAM336229 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336229 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336229 target gene. A A
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Another function of GAM336229 is therefore inhibition of BCHE. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336229 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336229 target gene. A A
TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of CTSB. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336229 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336229 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of CTSK. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336229 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336229 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of FHL2, a GAM336229 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336229 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336229 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of HD. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336229 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

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target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of IGF1, a GAM336229 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336229 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336229 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of IL1A, a GAM336229 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336229 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336229 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of NGB, a GAM336229 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336229 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336229 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336229 is therefore inhibition of PRND, a GAM336229 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336230 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336230 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336230 is therefore inhibition of APPBP2, a GAM336230 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336230 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336230 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of BACE2, a GAM336230 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336230 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336230 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of BCHE. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336230 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336230 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of CTSB. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336230 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336230 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of CTSK. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336230 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336230 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of FHL2, a GAM336230 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336230 HD HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336230 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of HD. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336230 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336230 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of IGF1, a GAM336230 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336230 IL1A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A GAM336230 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of IL1A, a GAM336230 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336230 NGB CACTGCACTCCAGCC TGGGCAA Neuroglobin (NGB, Accession NM_021257.2) is another GAM336230 A A target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of NGB, a GAM336230 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336230 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336230 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336230 is therefore inhibition of PRND, a GAM336230 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336231 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336231 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336231 is therefore inhibition of APPBP2, a GAM336231 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336231 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336231 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of BACE2, a GAM336231 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336231 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336231 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of BCHE. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336231 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336231 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of CTSB. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336231 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336231 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of CTSK. Accordingly, utilities of GAM336231 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336231 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336231 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of FHL2, a GAM336231 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336231 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336231 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of HD. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336231 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336231 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of IGF1, a GAM336231 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336231 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336231 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of IL1A, a GAM336231 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336231 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336231 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of NGB, a GAM336231 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336231 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336231 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336231 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336231 is therefore inhibition of PRND, a GAM336231 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336231 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336232 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336232 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336232 is therefore inhibition of APPBP2, a GAM336232 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336232 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336232 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of BACE2, a GAM336232 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336232 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336232 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of BCHE. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336232 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336232 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of CTSB. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336232 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336232 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of CTSK. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336232 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336232 target gene. FHL2 BINDING SITE1 and FHL2 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of FHL2, a GAM336232 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336232 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336232 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of HD. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336232 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336232 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of IGF1, a GAM336232 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM336232 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336232 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of IL1A, a GAM336232 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336232 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336232 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of NGB, a GAM336232 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336232 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336232 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336232 is therefore inhibition of PRND, a GAM336232 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336233 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336233 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336233 is therefore inhibition of APPBP2, a GAM336233 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336233 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336233 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of BACE2, a GAM336233 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336233 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336233 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of BCHE. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336233 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336233 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of CTSB. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336233 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336233 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of CTSK. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336233 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336233 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336233 is therefore inhibition of FHL2, a GAM336233 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336233 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336233 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of HD. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336233 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336233 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of IGF1, a GAM336233 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336233 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336233 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of IL1A, a GAM336233 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336233 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336233 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of NGB, a GAM336233 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336233 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336233 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336233 is therefore inhibition of PRND, a GAM336233 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336234 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336234 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336234 is therefore inhibition of APPBP2, a GAM336234 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336234 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336234 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of BACE2, a GAM336234 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336234 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336234 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of BCHE. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336234 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336234 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of CTSB. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336234 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336234 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of CTSK. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336234 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336234 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of FHL2, a GAM336234 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336234 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336234 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of HD. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336234 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336234 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of IGF1, a GAM336234 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336234 IL1A A A CACTGCACTCCAGCC TGGGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336234 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of IL1A, a GAM336234 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336234 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336234 A A TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of NGB, a GAM336234 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336234 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM336234 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336234 is therefore inhibition of PRND, a GAM336234 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336235 AVP TCTTGTGAAATCTGT AVP (Accession NM_000490.2) is a GAM336235 target gene. AVP A A

GGACCCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336235 is therefore inhibition of AVP. Accordingly, utilities of GAM336235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336236 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336236 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336236 is therefore inhibition of APPBP2, a GAM336236 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336236 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336236 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of BACE2, a GAM336236 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM336236 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336236 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of BCHE. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336236 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336236 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of CTSB. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336236 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336236 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of CTSK. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336236 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336236 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of FHL2, a GAM336236 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336236 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336236 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of HD. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336236 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336236 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of IGF1, a GAM336236 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336236 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336236 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of IL1A, a GAM336236 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336236 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336236 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of NGB, a GAM336236 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336236 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336236 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336236 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336236 is therefore inhibition of PRND, a GAM336236 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336236 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336237 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336237 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336237 is therefore inhibition of APPBP2, a GAM336237 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336237 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336237 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of BACE2, a GAM336237 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336237 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336237 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of BCHE. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336237 CTSB CACTGCACTCCAGCC A A TGGGCAA CTSB (Accession NM_147780.1) is another GAM336237 target gene. CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of CTSB. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336237 CTSK CACTGCACTCCAGCC A A TGGGCAA CTSK (Accession NM_000396.2) is another GAM336237 target gene. CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of CTSK. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336237 FHL2 CACTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336237 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of FHL2, a GAM336237 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336237 HD A A TGGGCAA CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336237 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of HD. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336237 IGF1 A A TGGGCAA CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336237 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of IGF1, a GAM336237 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336237 IL1A A A TGGGCAA CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336237 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of IL1A, a GAM336237 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336237 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336237 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of NGB, a GAM336237 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336237 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336237 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336237 is therefore inhibition of PRND, a GAM336237 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM336238 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336238 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336238 is therefore inhibition of APPBP2, a GAM336238 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336238 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336238 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336238 is therefore inhibition of BACE2, a GAM336238 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336238 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336238 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence A A

of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336238 is therefore inhibition of FHL2, a GAM336238 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336238 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336238 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336238 is therefore inhibition of IGF1, a GAM336238 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336238 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336238 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336238 is therefore inhibition of MME, a GAM336238 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM336238 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336238 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336238 is therefore inhibition of PRND, a GAM336238 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336239 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336239 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336239 is therefore inhibition of APPBP2, a GAM336239 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336239 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336239 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336239 is therefore inhibition of BACE2, a GAM336239 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336239 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336239 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336239 is therefore inhibition of FHL2, a GAM336239 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336239 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336239 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336239 is therefore inhibition of HD. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336239 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336239 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336239 is therefore inhibition of IGF1, a GAM336239 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336239 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336239 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336239 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336239 is therefore inhibition of PRND, a GAM336239 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336239 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336240 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336240 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336240 is therefore inhibition of APPBP2, a GAM336240 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336240 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336240 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of BACE2, a GAM336240 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336240 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336240 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of BCHE. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336240 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336240 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of CTSB. Accordingly, utilities of GAM336240 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336240 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336240 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of CTSK. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336240 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336240 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of FHL2, a GAM336240 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336240 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336240 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of HD. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336240 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336240 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of IGF1, a GAM336240 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336240 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336240 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of IL1A, a GAM336240 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336240 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336240 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of

NGB, a GAM336240 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336240 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336240 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336240 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336240 is therefore inhibition of PRND, a GAM336240 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336240 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336241 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336241 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336241 is therefore inhibition of APPBP2, a GAM336241 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336241 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336241 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of BACE2, a GAM336241 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336241 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336241 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of BCHE. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336241 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336241 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of CTSB. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336241 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336241 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of CTSK. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336241 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336241 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of FHL2, a GAM336241 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336241 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336241 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of HD. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336241 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336241 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of IGF1, a GAM336241 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336241 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336241 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of IL1A, a GAM336241 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336241 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336241 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of NGB, a GAM336241 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336241 PRND CACTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336241 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336241 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336241 is therefore inhibition of PRND, a GAM336241 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336241 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336242 APPBP2 CACTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336242 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336242 is therefore inhibition of APPBP2, a GAM336242 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336242 BACE2 CACTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM336242 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of BACE2, a GAM336242 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336242 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336242 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of BCHE. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336242 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336242 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of CTSB. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336242 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336242 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of CTSK. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336242 FHL2 A A CACTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336242 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of FHL2, a GAM336242 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336242 HD A A CACTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336242 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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GAM336242 IGF1 A A CACTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336242 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

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Another function of GAM336242 is therefore inhibition of IL1A, a GAM336242 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336242 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336242 A A

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Another function of GAM336242 is therefore inhibition of NGB, a GAM336242 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336242 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336242 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336242 is therefore inhibition of PRND, a GAM336242 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336243 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336243 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336243 is therefore inhibition of APPBP2, a GAM336243 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336243 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336243 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of BACE2, a GAM336243 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336243 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336243 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of BCHE. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336243 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147780.1) is another GAM336243 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of CTSB. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336243 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336243 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of CTSK. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336243 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336243 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of FHL2, a GAM336243 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336243 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336243 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of HD. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336243 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336243 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of IGF1, a GAM336243 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336243 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336243 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of IL1A, a GAM336243 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336243 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336243 A A

TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of NGB, a GAM336243 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336243 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336243 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336243 is therefore inhibition of PRND, a GAM336243 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336244 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336244 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336244 is therefore inhibition of APPBP2, a GAM336244 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336244 BACE2 CACTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138991.1) is another GAM336244 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of BACE2, a GAM336244 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336244 BCHE CACTGCACTCCAGCC BCHE (Accession NM_000055.1) is another GAM336244 target gene. A A

TGGGCAA BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of BCHE. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336244 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336244 target gene. A A

TGGGCAA CTSB BINDING SITE1 and CTSB BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CTSB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE1 and CTSB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of CTSB. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336244 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336244 target gene. A A

TGGGCAA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of CTSK. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336244 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336244 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of FHL2, a GAM336244 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336244 HD CACTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336244 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of HD. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336244 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336244 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of IGF1, a GAM336244 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336244 IL1A CACTGCACTCCAGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TGGGCAA GAM336244 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of IL1A, a GAM336244 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336244 NGB CACTGCACTCCAGCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336244 A A
TGGGCAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of NGB, a GAM336244 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336244 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336244 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336244 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336244 is therefore inhibition of PRND, a GAM336244 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336244 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336245 APPBP2 ATGGGAGACTGAGGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GCGGACG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336245 target gene. APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336245 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336245 is therefore inhibition of APPBP2, a GAM336245 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336245 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336245 BACE2 ATGGGAGACTGAGGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GCGGACG NM_138992.1) is another GAM336245 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336245 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336245 is therefore inhibition of BACE2, a GAM336245 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336245 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336245 HD ATGGGAGACTGAGGG HD (Accession NM_002111.3) is another GAM336245 target gene. HD A A

GCGGACG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336245 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336245 is therefore inhibition of HD. Accordingly, utilities of GAM336245 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336246 NGB TGGGATGATGTTAAA Neuroglobin (NGB, Accession NM_021257.2) is a GAM336246 target A A
CGTACTC gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336246 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336246 is therefore inhibition of NGB, a GAM336246 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336246 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336247 APPBP2 ACCCGAGAGGTGGAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GTTGCAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336247 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336247 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336247 is therefore inhibition of APPBP2, a GAM336247 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336247 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336247 IGF1 ACCCGAGAGGTGGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GTTGCAG NM_000618.2) is another GAM336247 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336247 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336247 is therefore inhibition of IGF1, a GAM336247 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336247 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336251 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336251 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336251 is therefore inhibition of APPBP2, a GAM336251 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336251 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336251 target gene. A A

TGGGCGA CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336251 is therefore inhibition of CTSB. Accordingly, utilities of GAM336251 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336251 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336251 target gene. A A

TGGGCGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336251 is therefore inhibition of CTSK. Accordingly, utilities of GAM336251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336251 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCGA another GAM336251 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336251 is therefore inhibition of FHL2, a GAM336251 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336251 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCGA NM_000618.2) is another GAM336251 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336251 is therefore inhibition of IGF1, a GAM336251 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336251 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336251 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCGA another GAM336251 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336251 is therefore inhibition of PRND, a GAM336251 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336252 GLUL GGTTCAATTCACCGG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

AGTCTCA NM_002065.3) is a GAM336252 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336252 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336252 is therefore inhibition of GLUL, a GAM336252 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336252 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336252 IGF1 GGTTCAATTCACCGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGTCTCA NM_000618.2) is another GAM336252 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336252 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336252 is therefore inhibition of IGF1, a GAM336252 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336252 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336255 APPBP2 TTCATTAGGCCAGGT GCGGTGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336255 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336255 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336255 is therefore inhibition of APPBP2, a GAM336255 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336256 APPBP2 TTCATTAGGCCAGGT GCGGTGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336256 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336256 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336256 is therefore inhibition of APPBP2, a GAM336256 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM336257 CLU GTCTGGAGGCTGGAA CCTGGTG — Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is a GAM336257 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336257 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336257 is therefore inhibition of CLU, a GAM336257 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336257 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM336257 OLR1 GTCTGGAGGCTGGAA CCTGGTG — Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM336257 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336257 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336257 is therefore inhibition of OLR1, a GAM336257 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336257 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336259 ACE GAGCAGGTTTGGAAT GGCTCCA — Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM336259 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336259 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336259 is therefore inhibition of ACE, a GAM336259 target gene which Angiotensin I- converting enzyme

(dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336259 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336259 B2M GAGCAGGTTTGGAAT Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A

GGCTCCA GAM336259 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336259 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336259 is therefore inhibition of B2M, a GAM336259 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336259 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336259 DSCR1 GAGCAGGTTTGGAAT Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

GGCTCCA NM_004414.3) is another GAM336259 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336259 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336259 is therefore inhibition of DSCR1, a GAM336259 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336259 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336259 IGF1 GAGCAGGTTTGGAAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGCTCCA NM_000618.2) is another GAM336259 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336259 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336259 is therefore inhibition of IGF1, a GAM336259 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336259 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336260 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336260 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336260 is therefore inhibition of APPBP2, a GAM336260 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336260 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336260 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336260 is therefore inhibition of BACE2, a GAM336260 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336260

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336260 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336260 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336260 is therefore inhibition of FHL2, a GAM336260 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336260 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336260 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336260 is therefore inhibition of HD. Accordingly, utilities of GAM336260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336260 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336260 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336260 is therefore inhibition of

IGF1, a GAM336260 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336260 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336260 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336260 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336260 is therefore inhibition of PRND, a GAM336260 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336260 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336261 GFAP GATGGCAGCTGGAGG GFAP (Accession NM_002055.2) is a GAM336261 target gene. GFAP A A

TGGAGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336261 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336261 is therefore inhibition of GFAP. Accordingly, utilities of GAM336261 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336261 HD GATGGCAGCTGGAGG HD (Accession NM_002111.3) is another GAM336261 target gene. HD A A

TGGAGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336261 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336261 is therefore inhibition of HD. Accordingly, utilities of GAM336261 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336261 MAPT GATGGCAGCTGGAGG TGGAGCA A A

Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM336261 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336261 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336261 is therefore inhibition of MAPT, a GAM336261 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336261 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336261 MT3 GATGGCAGCTGGAGG TGGAGCA A A

Metallothionein 3 (MT3, Accession NM_005954.1) is another GAM336261 target gene. MT3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MT3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336261 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336261 is therefore inhibition of MT3, a GAM336261 target gene which inhibits survival and neurite formation of cortical neurons in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336261 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MT3.The function of MT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3890.

GAM336264 DHCR24 CTGCCCTGAACTCTG GCCATCC A A

24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM336264 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336264 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336264 is therefore inhibition of DHCR24, a GAM336264 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336264 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336267 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGCGACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336267 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336267 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336267 is therefore inhibition of APPBP2, a GAM336267 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336267 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336267 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGCGACA another GAM336267 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336267 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336267 is therefore inhibition of FHL2, a GAM336267 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336267 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336267 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGCGACA NM_000618.2) is another GAM336267 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336267 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336267 is therefore inhibition of IGF1, a GAM336267 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336267 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336267 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGCGACA another GAM336267 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336267 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336267 is therefore inhibition of PRND, a GAM336267 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336267 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336270 APBB2 TCTCTAAGACAAAGG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AGAAGTC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336270 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336270 is therefore inhibition of APBB2, a GAM336270 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336271 HD AAGGCTTTTCTGGGA HD (Accession NM_002111.3) is a GAM336271 target gene. HD A A

AGAGCTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336271 is therefore inhibition of HD. Accordingly, utilities of GAM336271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336272 APBA2 CAGAATCTTTTGTCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

CTGAGAA 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM336272 target gene. APBA2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336272 is therefore inhibition of APBA2, a GAM336272 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336272 HTR2A CAGAATCTTTTGTCT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

CTGAGAA NM_000621.1) is another GAM336272 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336272 is therefore inhibition of HTR2A, a GAM336272 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336272 IGF1 CAGAATCTTTTGTCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTGAGAA NM_000618.2) is another GAM336272 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336272 is therefore inhibition of IGF1, a GAM336272 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336272 PSEN2 CAGAATCTTTTGTCT PSEN2 (Accession NM_012486.1) is another GAM336272 target gene. A A

CTGAGAA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336272 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336272 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336272 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336275 PSEN1 TAACTGGCCTTGGAA PSEN1 (Accession NM_007318.1) is a GAM336275 target gene. PSEN1 A A

CCTGTAG BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336275 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336275 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336275 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336279 CNTF GTAACAAAATGAATA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A
ATACCTG GAM336279 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336279 is therefore inhibition of CNTF, a GAM336279 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336279 DSCR1 GTAACAAAATGAATA Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A
ATACCTG NM_004414.3) is another GAM336279 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336279 is therefore inhibition of DSCR1, a GAM336279 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336279 HD GTAACAAAATGAATA HD (Accession NM_002111.3) is another GAM336279 target gene. HD A A

ATACCTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336279 is therefore inhibition of HD. Accordingly, utilities of GAM336279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336279 MME GTAACAAAATGAATA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

ATACCTG enkephalinase, (MME, Accession NM_007289.1) is another GAM336279 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336279 is therefore inhibition of MME, a GAM336279 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336281 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336281 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336281 is therefore inhibition of APP. Accordingly, utilities of GAM336281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336282 ACE TTGCTCAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGCAGTG (ACE, Accession NM_152831.1) is a GAM336282 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE,

and secondary structure complementarity to the nucleotide sequence of GAM336282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336282 is therefore inhibition of ACE, a GAM336282 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336282 ACT TTGCTCAGGCTGGAG Activator of CAMP- responsive Element Modulator (CR (ACT, A A
TGCAGTG Accession NM_020482.3) is another GAM336282 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336282 is therefore inhibition of ACT, a GAM336282 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336282 ADAM17 TTGCTCAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TGCAGTG factor, (ADAM17, Accession NM_021832.1) is another GAM336282 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336282 is therefore inhibition of ADAM17, a GAM336282 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM317.

GAM336282 IAPP TTGCTCAGGCTGGAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TGCAGTG another GAM336282 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336282 is therefore inhibition of IAPP, a GAM336282 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336282 TGFB1 TTGCTCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM336282 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336282 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336283 ACE TTGCTCAGGCTGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGCAGTG (ACE, Accession NM_152831.1) is a GAM336283 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336283 is therefore inhibition of ACE, a GAM336283 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336283 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336283 ACT TTGCTCAGGCTGGAG A Activator of CAMP- responsive Element Modulator (CR (ACT, A A TGCAGTG Accession NM_020482.3) is another GAM336283 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336283 is therefore inhibition of ACT, a GAM336283 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336283 ADAM17 TTGCTCAGGCTGGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A TGCAGTG factor, (ADAM17, Accession NM_021832.1) is another GAM336283 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336283 is therefore inhibition of ADAM17, a GAM336283 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336283 IAPP TTGCTCAGGCTGGAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A TGCAGTG another GAM336283 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336283 is therefore inhibition of IAPP, a GAM336283 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336283 TGFB1 TTGCTCAGGCTGGAG TGFB1 (Accession NM_000660.1) is another GAM336283 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336283 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336284 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336284 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336284 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336284 is therefore inhibition of APP. Accordingly, utilities of GAM336284 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336285 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336285 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336285 is therefore inhibition of APP.

Accordingly, utilities of GAM336285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336289 FHL2 GGAATGGATGGAAGT A A GTGTGAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM336289 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336289 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336289 is therefore inhibition of FHL2, a GAM336289 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336289 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336289 HTR2C GGAATGGATGGAAGT A A GTGTGAG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336289 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336289 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336289 is therefore inhibition of HTR2C, a GAM336289 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336289 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336290 FHL2 GGAATGGATGGAAGT A A GTGTGAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM336290 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336290 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336290 is therefore inhibition of FHL2, a GAM336290 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336290 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336290 HTR2C GGAATGGATGGAAGT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
GTGTGAG NM_000868.1) is another GAM336290 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336290 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336290 is therefore inhibition of HTR2C, a GAM336290 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336290 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336291 ACE TCCAGTGATTCTCGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GGGCAGA (ACE, Accession NM_152831.1) is a GAM336291 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336291 is therefore inhibition of ACE, a GAM336291 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336292 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336292 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336292 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336292 is therefore inhibition of APP. Accordingly, utilities of GAM336292 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336293 DLST CAGGTGGTGCTGTTA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

AGAAGCA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336293 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336293 is therefore inhibition of DLST, a GAM336293 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336293 HTR2A CAGGTGGTGCTGTTA 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

AGAAGCA NM_000621.1) is another GAM336293 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336293 is therefore inhibition of HTR2A, a GAM336293 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336294 APBA2 GAGATGGAGTTTTAC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
TATGTTG 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM336294 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336294 is therefore inhibition of APBA2, a GAM336294 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336294 IGF1 GAGATGGAGTTTTAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TATGTTG NM_000618.2) is another GAM336294 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336294 is therefore inhibition of IGF1, a GAM336294 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336294 TGFB1 GAGATGGAGTTTTAC TGFB1 (Accession NM_000660.1) is another GAM336294 target gene. A A
TATGTTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336294 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336297 DLST ACAACCTCTGCCTCC TGGGTTC Dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336297 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336297 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336297 is therefore inhibition of DLST, a GAM336297 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336297 IAPP ACAACCTCTGCCTCC TGGGTTC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM336297 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336297 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336297 is therefore inhibition of IAPP, a GAM336297 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336297 MTNR1A ACAACCTCTGCCTCC TGGGTTC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM336297 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide A A

sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336297 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336297 is therefore inhibition of MTNR1A, a GAM336297 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336298 DLST ACAACCTCTGCCTCC TGGGTTC A A Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336298 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336298 is therefore inhibition of DLST, a GAM336298 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336298 IAPP ACAACCTCTGCCTCC TGGGTTC A A Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM336298 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336298 is therefore inhibition of IAPP, a GAM336298 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336298 MTNR1A ACAACCTCTGCCTCC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

TGGGTTC another GAM336298 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336298 is therefore inhibition of MTNR1A, a GAM336298 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336299 THOP1 GGTCCAGACTGGAGT Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is a A A

ATAGTGC GAM336299 target gene. THOP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336299 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336299 is therefore inhibition of THOP1, a GAM336299 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336299 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM336300 THOP1 GGTCCAGACTGGAGT Thimet Oligopeptidase 1 (THOP1, Accession NM_003249.2) is a A A

ATAGTGC GAM336300 target gene. THOP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of THOP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336300 is therefore inhibition of THOP1, a GAM336300 target gene which involves in the metabolism of neuropeptide and in cytoplasmic peptide degradation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with THOP1.The function of THOP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM520.

GAM336303 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336303 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336303 is therefore inhibition of APPBP2, a GAM336303 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336303 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336303 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336303 is therefore inhibition of BACE2, a GAM336303 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336303 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336303 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336303 is therefore inhibition of FHL2, a GAM336303 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336303 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336303 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336303 is therefore inhibition of IGF1, a GAM336303 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336303 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336303 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336303 is therefore inhibition of MME, a GAM336303 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336303 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336303 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336303 is therefore inhibition of PRND, a GAM336303 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336304 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is a GAM336304 target gene. CTSB A A TAGGCAA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336304 is therefore inhibition of CTSB. Accordingly, utilities of GAM336304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336304 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A TAGGCAA another GAM336304 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336304 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336304 is therefore inhibition of FHL2, a GAM336304 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336304 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
TAGGCAA NM_000618.2) is another GAM336304 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336304 is therefore inhibition of IGF1, a GAM336304 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336304 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
TAGGCAA another GAM336304 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336304 is therefore inhibition of PRND, a GAM336304 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336306 APPBP2 TTCCAGTAGTTACTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CTCCCTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336306 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336306 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336306 is therefore inhibition of APPBP2, a GAM336306 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336307 APPBP2 TTCCAGTAGTTACTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CTCCCTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336307 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336307 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336307 is therefore inhibition of APPBP2, a GAM336307 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336307 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336308 APPBP2 AGCAGCACAGAAATA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TTGGCAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336308 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336308 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336308 is therefore inhibition of APPBP2,

a GAM336308 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336308 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336308 NCKAP1 AGCAGCACAGAAATA A A TTGGCAC NCKAP1 (Accession NM_013436.2) is another GAM336308 target gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336308 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336308 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM336308 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM336309 ACHE CTGGAAGACATGGTA A A GAGCTGA Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is a GAM336309 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336309 is therefore inhibition of ACHE, a GAM336309 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM336309 DLST CTGGAAGACATGGTA A A GAGCTGA Dihydrolipoamide S- succinyltransferase (E2 component of 2-oxo- glutarat (DLST, Accession NM_001933.2) is another GAM336309 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336309 is therefore inhibition of DLST, a GAM336309 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336309 IGF1 CTGGAAGACATGGTA A A GAGCTGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336309 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336309 is therefore inhibition of IGF1, a GAM336309 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336309 RAGE CTGGAAGACATGGTA A A GAGCTGA Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another GAM336309 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336309 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336309 is therefore inhibition of RAGE, a GAM336309 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM336309 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM1523.

GAM336311 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336311 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336311 is therefore inhibition of APPBP2, a GAM336311 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336311 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336311 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336311 is therefore inhibition of BACE2, a GAM336311 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336311 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336311 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence A A

of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336311 is therefore inhibition of FHL2, a GAM336311 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336311 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GGGCAAC NM_000618.2) is another GAM336311 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336311 is therefore inhibition of IGF1, a GAM336311 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336311 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336311 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336311 is therefore inhibition of MME, a GAM336311 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM336311 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336311 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336311 is therefore inhibition of PRND, a GAM336311 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336313 APLP1 CCACTGCACTCCAGC Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A

CTGGGTG NM_005166.2) is a GAM336313 target gene. APLP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336313 is therefore inhibition of APLP1, a GAM336313 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336313 APPBP2 CCACTGCACTCCAGC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CTGGGTG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336313 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336313 is therefore inhibition of

APPBP2, a GAM336313 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336313 CRAT CCACTGCACTCCAGC Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A

CTGGGTG another GAM336313 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336313 is therefore inhibition of CRAT, a GAM336313 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336313 CTSB CCACTGCACTCCAGC CTSB (Accession NM_147782.1) is another GAM336313 target gene. A A

CTGGGTG CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336313 is therefore inhibition of CTSB. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336313 FHL2 CCACTGCACTCCAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CTGGGTG another GAM336313 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336313 is therefore inhibition of FHL2, a GAM336313 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336313 IGF1 CCACTGCACTCCAGC CTGGGTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336313 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336313 is therefore inhibition of IGF1, a GAM336313 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336313 PRND CCACTGCACTCCAGC CTGGGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336313 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336313 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336313 is therefore inhibition of PRND, a GAM336313 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336315 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336315 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336315 is therefore inhibition of APPBP2, a GAM336315 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336315 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336315 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336315 is therefore inhibition of BACE2, a GAM336315 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336315 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336315 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336315 is therefore inhibition of FHL2, a GAM336315 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336315 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336315 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336315 is therefore inhibition of IGF1, a GAM336315 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336315 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336315 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336315 is therefore inhibition of MME, a GAM336315 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336315 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336315 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336315 is therefore inhibition of PRND, a GAM336315 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336316 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336316 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336316 is therefore inhibition of APPBP2, a GAM336316 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336316 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336316 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336316 is therefore inhibition of

BACE2, a GAM336316 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336316 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336316 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336316 is therefore inhibition of FHL2, a GAM336316 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336316 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336316 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336316 is therefore inhibition of IGF1, a GAM336316 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336316 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336316 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336316 is therefore inhibition of MME, a GAM336316 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336316 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336316 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336316 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336316 is therefore inhibition of PRND, a GAM336316 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336316 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336317 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336317 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336317 is therefore inhibition of APPBP2, a GAM336317 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336317 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336317 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336317 is therefore inhibition of BACE2, a GAM336317 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336317 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336317 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336317 is therefore inhibition of FHL2, a GAM336317 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336317 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336317 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336317 is therefore inhibition of IGF1, a GAM336317 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336317 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336317 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336317 is therefore inhibition of MME, a GAM336317 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336317 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336317 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336317 is therefore inhibition of PRND, a GAM336317 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336318 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336318 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336318 is therefore inhibition of APPBP2, a GAM336318 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336318 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336318 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336318 is therefore inhibition of BACE2, a GAM336318 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336318 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336318 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336318 is therefore inhibition of FHL2, a GAM336318 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336318 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336318 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336318 is therefore inhibition of IGF1, a GAM336318 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336318 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336318 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336318 is therefore inhibition of MME, a GAM336318 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336318 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336318 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336318 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336318 is therefore inhibition of PRND, a GAM336318 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336320 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336320 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336320 is therefore inhibition of APPBP2, a GAM336320 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336320 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336320 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a A A

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336320 is therefore inhibition of BACE2, a GAM336320 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336320 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336320 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336320 is therefore inhibition of FHL2, a GAM336320 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336320 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336320 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336320 is therefore inhibition of IGF1, a GAM336320 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336320 MME ACTGCACTCCAGCCT GGGCAAC A A

Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336320 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336320 is therefore inhibition of MME, a GAM336320 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336320 PRND ACTGCACTCCAGCCT GGGCAAC A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336320 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336320 is therefore inhibition of PRND, a GAM336320 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336321 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336321 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336321 is therefore inhibition of APPBP2, a GAM336321 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336321 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336321 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336321 is therefore inhibition of BACE2, a GAM336321 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336321 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336321 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336321 is therefore inhibition of FHL2, a GAM336321 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336321 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336321 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336321 is therefore inhibition of IGF1, a GAM336321 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336321 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336321 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336321 is therefore inhibition of MME, a GAM336321 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336321 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336321 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336321 is therefore inhibition of PRND, a GAM336321 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336322 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336322 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336322 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336322 is therefore inhibition of APP. Accordingly, utilities of GAM336322 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336323 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336323 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336323 is therefore inhibition of APPBP2, a GAM336323 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336323 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336323 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336323 is therefore inhibition of BACE2, a GAM336323 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336323 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336323 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336323 is therefore inhibition of FHL2, a GAM336323 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336323 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336323 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336323 is therefore inhibition of IGF1, a GAM336323 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336323 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336323 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336323 is therefore inhibition of MME, a GAM336323 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336323 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336323 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336323 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336323 is therefore inhibition of PRND, a GAM336323 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336323 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336324 BACE TCAGAGTGAGTCCCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
GGGACTA is a GAM336324 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336324 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336324 is therefore inhibition of BACE, a GAM336324 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336325 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336325 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336325 is therefore inhibition of APPBP2, a GAM336325 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336325 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336325 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336325 is therefore inhibition of BACE2, a GAM336325 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336325 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336325 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336325 is therefore inhibition of FHL2, a GAM336325 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336325 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336325 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336325 is therefore inhibition of IGF1, a GAM336325 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336325 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336325 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336325 is therefore inhibition of MME, a GAM336325 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336325 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336325 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336325 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336325 is therefore inhibition of PRND, a GAM336325 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336325 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336326 SNCA CTGGTCCCTGTGTCA SNCA (Accession NM_007308.1) is a GAM336326 target gene. SNCA A A GTCTTAA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336326 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336326 is therefore inhibition of SNCA. Accordingly, utilities of GAM336326 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM336329 MPO GCTCCCTTGTCTAGG Myeloperoxidase (MPO, Accession NM_000250.1) is a GAM336329 A A GCGTGGA target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336329 is therefore inhibition of MPO, a GAM336329 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM336330 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336330 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336330 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336330 is therefore inhibition of APP. Accordingly, utilities of GAM336330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336331 FOS GTCACTGCAATCAAC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

AATACTC Accession NM_005252.2) is a GAM336331 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336331 is therefore inhibition of FOS, a GAM336331 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336332 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336332 target

gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336332 is therefore inhibition of APPBP2, a GAM336332 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336332 BACE2 ACTGCACTCCAGCCT A A GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336332 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336332 is therefore inhibition of BACE2, a GAM336332 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336332 FHL2 ACTGCACTCCAGCCT A A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336332 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336332 is therefore inhibition of

FHL2, a GAM336332 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336332 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM336332 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336332 is therefore inhibition of IGF1, a GAM336332 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336332 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336332 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336332 is therefore inhibition of MME, a GAM336332 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336332 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336332 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336332 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336332 is therefore inhibition of PRND, a GAM336332 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336332 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336334 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336334 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336334 is therefore inhibition of APPBP2, a GAM336334 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336334 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336334 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336334 is therefore inhibition of BACE2, a GAM336334 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336334 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336334 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336334 is therefore inhibition of FHL2, a GAM336334 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336334 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336334 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336334 is therefore inhibition of HD. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336334 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336334 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336334 is therefore inhibition of IGF1, a GAM336334 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336334 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336334 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336334 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336334 is therefore inhibition of PRND, a GAM336334 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336335 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336335 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336335 is therefore inhibition of APPBP2, a GAM336335 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336335 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336335 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336335 is therefore inhibition of BACE2, a GAM336335 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336335 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336335 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336335 is therefore inhibition of FHL2, a GAM336335 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336335 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336335 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336335 is therefore inhibition of HD. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336335 IGF1 CATTGCACTCCAGCC TGGGCAA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336335 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336335 is therefore inhibition of IGF1, a GAM336335 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336335 PRND CATTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336335 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336335 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336335 is therefore inhibition of PRND, a GAM336335 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336335 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336336 APPBP2 CATTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336336 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM336336 is therefore inhibition of APPBP2, a GAM336336 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336336 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336336 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336336 is therefore inhibition of BACE2, a GAM336336 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336336 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336336 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336336 is therefore inhibition of FHL2, a GAM336336 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336336 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336336 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336336 is therefore inhibition of HD. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336336 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336336 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336336 is therefore inhibition of IGF1, a GAM336336 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336336 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336336 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336336 is therefore inhibition of PRND, a GAM336336 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336336 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336337 APPBP2 CATTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336337 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336337 is therefore inhibition of APPBP2, a GAM336337 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336337 BACE2 CATTGCACTCCAGCC TGGGCAA A A

Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336337 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336337 is therefore inhibition of BACE2, a GAM336337 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336337 FHL2 CATTGCACTCCAGCC TGGGCAA A A

Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336337 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336337 is therefore inhibition of FHL2, a GAM336337 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336337 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336337 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336337 is therefore inhibition of HD. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336337 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336337 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336337 is therefore inhibition of IGF1, a GAM336337 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336337 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336337 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336337 is therefore inhibition of PRND, a GAM336337 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336338 APBA1 AAACACAATGCAGTA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGAAGAG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM336338 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336338 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336338 is therefore inhibition of APBA1, a GAM336338 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336338 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336339 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336339 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336339 is therefore inhibition of APPBP2,

a GAM336339 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336339 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336339 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336339 is therefore inhibition of BACE2, a GAM336339 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336339 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336339 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336339 is therefore inhibition of FHL2, a GAM336339 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336339 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336339 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336339 is therefore inhibition of IGF1, a GAM336339 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336339 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336339 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336339 is therefore inhibition of MME, a GAM336339 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336339 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336339 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336339 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336339 is therefore inhibition of PRND, a GAM336339 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336339 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336340 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336340 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336340 is therefore inhibition of APPBP2, a GAM336340 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336340 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336340 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336340 is therefore inhibition of BACE2, a GAM336340 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336340 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336340 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336340 is therefore inhibition of FHL2, a GAM336340 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336340 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336340 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336340 is therefore inhibition of HD. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336340 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336340 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336340 is therefore inhibition of IGF1, a GAM336340 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336340 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336340 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336340 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336340 is therefore inhibition of PRND, a GAM336340 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336340 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336341 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336341 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336341 is therefore inhibition of APPBP2, a GAM336341 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336341 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336341 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336341 is therefore inhibition of BACE2, a GAM336341 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336341 FHL2 A ACTGCACTCCAGCCT A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336341 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

GGGCAAC

Another function of GAM336341 is therefore inhibition of FHL2, a GAM336341 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336341 IGF1 A ACTGCACTCCAGCCT A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336341 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

GGGCAAC

Another function of GAM336341 is therefore inhibition of IGF1, a GAM336341 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336341 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336341 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336341 is therefore inhibition of MME, a GAM336341 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336341 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336341 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336341 is therefore inhibition of PRND, a GAM336341 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336342 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336342 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336342 is therefore inhibition of APPBP2, a GAM336342 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336342 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336342 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336342 is therefore inhibition of BACE2, a GAM336342 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336342 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336342 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336342 is therefore inhibition of FHL2, a GAM336342 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336342 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336342 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336342 is therefore inhibition of IGF1, a GAM336342 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336342 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336342 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336342 is therefore inhibition of MME, a GAM336342 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336342 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336342 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336342 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336342 is therefore inhibition of PRND, a GAM336342 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336342 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336343 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336343 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336343 is therefore inhibition of APPBP2, a GAM336343 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336343 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336343 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336343 is therefore inhibition of BACE2, a GAM336343 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336343 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336343 target gene. FHL2 BINDING SITE1 and FHL2 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336343 is therefore inhibition of FHL2, a GAM336343 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336343 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336343 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336343 is therefore inhibition of IGF1, a GAM336343 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336343 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336343 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336343 is therefore inhibition of MME, a GAM336343 target gene which is thermolysin- like specificity.

and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336343 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336343 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336343 is therefore inhibition of PRND, a GAM336343 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336344 APP CAGGTACTTTTTGGT APP (Accession NM_000484.1) is a GAM336344 target gene. APP A A

TTACATG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336344 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336344 is therefore inhibition of APP. Accordingly, utilities of GAM336344 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336344 TNFSF5 CAGGTACTTTTTGGT TNFSF5 (Accession NM_000074.1) is another GAM336344 target A A

TTACATG gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336344 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336344 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336344 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336347 CHAT TCTGGCTCCTGAGTC Choline Acetyltransferase (CHAT, Accession NM_020549.2) is a A A
CTAGCTC GAM336347 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336347 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336347 is therefore inhibition of CHAT, a GAM336347 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336347 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336348 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336348 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336348 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336348 is therefore inhibition of APP. Accordingly, utilities of GAM336348 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336349 ACE TGACTTGTCTGGTTT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GGCATCT (ACE, Accession NM_152831.1) is a GAM336349 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336349 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336349 is therefore inhibition of ACE, a GAM336349 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336349 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336350 ACT CTTGCACTCCACAGC Activator of CAMP- responsive Element Modulator (CR (ACT, A A

CTGGGTG Accession NM_020482.3) is a GAM336350 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336350 is therefore inhibition of ACT, a GAM336350 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336350 APPBP2 CTTGCACTCCACAGC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CTGGGTG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336350 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336350 is therefore inhibition of APPBP2, a GAM336350 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336350 FHL2 CTTGCACTCCACAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CTGGGTG another GAM336350 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336350 is therefore inhibition of FHL2, a GAM336350 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336350 FOS A A CTTGCACTCCACAGC CTGGGTG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is another GAM336350 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336350 is therefore inhibition of FOS, a GAM336350 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336350 IGF1 A A CTTGCACTCCACAGC CTGGGTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336350 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336350 is therefore inhibition of IGF1, a GAM336350 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336350 PRND CTTGCACTCCACAGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CTGGGTG another GAM336350 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336350 is therefore inhibition of PRND, a GAM336350 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336352 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336352 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336352 is therefore inhibition of APP. Accordingly, utilities of GAM336352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336353 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336353 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336353 is therefore inhibition of APPBP2, a GAM336353 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336353 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336353 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336353 is therefore inhibition of BACE2, a GAM336353 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336353 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336353 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336353 is therefore inhibition of FHL2, a GAM336353 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336353 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336353 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336353 is therefore inhibition of IGF1, a GAM336353 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336353 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336353 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336353 is therefore inhibition of MME, a GAM336353 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336353 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336353 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336353 is therefore inhibition of PRND, a GAM336353 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM336354 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336354 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336354 is therefore inhibition of APPBP2, a GAM336354 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336354 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336354 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336354 is therefore inhibition of BACE2, a GAM336354 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336354 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336354 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336354 is therefore inhibition of FHL2, a GAM336354 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336354 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336354 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336354 is therefore inhibition of IGF1, a GAM336354 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336354 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336354 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336354 is therefore inhibition of MME, a GAM336354 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM336354 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336354 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336354 is therefore inhibition of PRND, a GAM336354 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336357 FLNB TTCCTTCTGCATTGT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GAGAAAA NM_001457.1) is a GAM336357 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336357 is therefore inhibition of FLNB, a GAM336357 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336359 IGF1 AGTGAGCCGAGATAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ATACATA NM_000618.2) is a GAM336359 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336359 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336359 is therefore inhibition of IGF1, a GAM336359 target gene which are structurally and functionally

related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336359 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336359 PRND AGTGAGCCGAGATAC ATACATA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336359 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336359 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336359 is therefore inhibition of PRND, a GAM336359 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336359 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336360 IGF1 AGTGAGCCGAGATAC ATACATA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM336360 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336360 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336360 is therefore inhibition of IGF1, a GAM336360 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336360 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336360 PRND AGTGAGCCGAGATAC ATACATA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336360 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences A A

of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336360 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336360 is therefore inhibition of PRND, a GAM336360 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336360 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336361 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336361 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336361 is therefore inhibition of APPBP2, a GAM336361 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336361 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336361 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336361 is therefore inhibition of BACE2, a GAM336361 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336361 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336361 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336361 is therefore inhibition of FHL2, a GAM336361 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336361 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336361 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336361 is therefore inhibition of IGF1, a GAM336361 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336361 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336361 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336361 is therefore inhibition of MME, a GAM336361 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336361 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336361 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336361 is therefore inhibition of PRND, a GAM336361 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336362 MME TGATCACAGGCAAAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A GAATAAA enkephalinase, (MME, Accession NM_000902.2) is a GAM336362 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336362 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336362 is therefore inhibition of MME, a GAM336362 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336362 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336362 TGFB1 TGATCACAGGCAAAG TGFB1 (Accession NM_000660.1) is another GAM336362 target gene. A A

GAATAAA TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336362 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336362 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336362 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336363 CNTF CACCCTCTGCCTGTG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

GTTGTCT GAM336363 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336363 is therefore inhibition of CNTF, a GAM336363 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336363 DHCR24 CACCCTCTGCCTGTG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GTTGTCT NM_014762.1) is another GAM336363 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336363 is therefore inhibition of DHCR24, a GAM336363 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM336364 APPBP2 ATTGCACTCCAGCCT GGGCAAT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336364 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336364 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336364 is therefore inhibition of APPBP2, a GAM336364 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336364 FHL2 ATTGCACTCCAGCCT GGGCAAT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336364 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336364 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336364 is therefore inhibition of FHL2, a GAM336364 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336364 IGF1 ATTGCACTCCAGCCT GGGCAAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336364 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336364 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336364 is therefore inhibition of IGF1, a GAM336364 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336364 PRND ATTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAT another GAM336364 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336364 is therefore inhibition of PRND, a GAM336364 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336365 ADAM17 ACAGTGTTACCCAGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
CTGGTCT factor, (ADAM17, Accession NM_003183.3) is a GAM336365 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336365 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336365 is therefore inhibition of ADAM17, a GAM336365 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336365 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336365 HTR2A ACAGTGTTACCCAGG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

CTGGTCT NM_000621.1) is another GAM336365 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336365 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336365 is therefore inhibition of HTR2A, a GAM336365 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336365 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336365 IAPP ACAGTGTTACCCAGG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

CTGGTCT another GAM336365 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336365 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336365 is therefore inhibition of IAPP, a GAM336365 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336365 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336365 RAGE ACAGTGTTACCCAGG Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A

CTGGTCT GAM336365 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336365 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336365 is therefore inhibition of RAGE, a GAM336365 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore

is associated with Alzheimer. Accordingly, utilities of GAM336365 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM336365 TGFB1 ACAGTGTTACCCAGG TGFB1 (Accession NM_000660.1) is another GAM336365 target gene. A A

CTGGTCT TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336365 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336365 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336365 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336368 ACE AGGTGAGAAAACTGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GGCTCAG (ACE, Accession NM_152831.1) is a GAM336368 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336368 is therefore inhibition of ACE, a GAM336368 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336368 BACE AGGTGAGAAAACTGA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

GGCTCAG is another GAM336368 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336368 is therefore inhibition of BACE, a GAM336368 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336368 IGF1 AGGTGAGAAAACTGA A A GGCTCAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336368 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336368 is therefore inhibition of IGF1, a GAM336368 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336368 IL1A AGGTGAGAAAACTGA A A GGCTCAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336368 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336368 is therefore inhibition of IL1A, a GAM336368 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336368 IL1B AGGTGAGAAAACTGA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A

GGCTCAG GAM336368 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336368 is therefore inhibition of IL1B, a GAM336368 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336368 MME AGGTGAGAAAACTGA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGCTCAG enkephalinase, (MME, Accession NM_007287.1) is another GAM336368 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336368 is therefore inhibition of MME, a GAM336368 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336368 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336369 GAL TAAGGACGCAAAGAG Galanin (GAL, Accession NM_015973.2) is a GAM336369 target A A

GGCAAGG gene. GAL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GAL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336369 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336369 is therefore inhibition of GAL, a GAM336369 target gene which stimulates LH secretion and enhances

LHRH- induced LH release from dispersed anterior pituitary cells in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336369 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GAL.The function of GAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3293.

GAM336372 APPBP2 ATGGAGCTGTTTTCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TCAGAGC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336372 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336372 is therefore inhibition of APPBP2, a GAM336372 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336373 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336373 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336373 is therefore inhibition of APPBP2, a GAM336373 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336373 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM336373 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336373 is therefore inhibition of BACE2, a GAM336373 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336373 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336373 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336373 is therefore inhibition of FHL2, a GAM336373 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336373 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336373 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336373 is therefore inhibition of HD. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336373 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336373 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336373 is therefore inhibition of IGF1, a GAM336373 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336373 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336373 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336373 is therefore inhibition of PRND, a GAM336373 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336374 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336374 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336374 is therefore inhibition of APPBP2, a GAM336374 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336374 BACE2 CATTGCACTCCAGCC A A TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336374 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336374 is therefore inhibition of BACE2, a GAM336374 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336374 FHL2 CATTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336374 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336374 is therefore inhibition of FHL2, a GAM336374 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336374 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336374 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336374 is therefore inhibition of HD. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336374 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336374 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336374 is therefore inhibition of IGF1, a GAM336374 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336374 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336374 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336374 is therefore inhibition of PRND, a GAM336374 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336375 CNTF TCCCGTGTGAAAATT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

TGTATGC GAM336375 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336375 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336375 is therefore inhibition of CNTF, a GAM336375 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336376 ARHA TGAAGTAGTTAGGTT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GTAGCTC is a GAM336376 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336376 is therefore inhibition of ARHA, a GAM336376 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336377 ARHA TGAAGTAGTTAGGTT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GTAGCTC is a GAM336377 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336377 is therefore inhibition of ARHA, a GAM336377 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336378 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336378 target gene. APP
A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336378 is therefore inhibition of APP. Accordingly, utilities of GAM336378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336380 CRAT GAGGTGAAGATCTTG Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is a
A A

GAGTCTG GAM336380 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336380 is therefore inhibition of CRAT, a GAM336380 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336380 MAPK10 GAGGTGAAGATCTTG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A
A

GAGTCTG NM_138980.1) is another GAM336380 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336380 is therefore inhibition of MAPK10, a GAM336380 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336381 CRAT GAGGTGAAGATCTTG A A GAGTCTG Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is a GAM336381 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336381 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336381 is therefore inhibition of CRAT, a GAM336381 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336381 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336381 MAPK10 GAGGTGAAGATCTTG A A GAGTCTG Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM336381 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336381 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336381 is therefore inhibition of MAPK10, a GAM336381 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336381 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336382 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAC a GAM336382 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336382 is therefore inhibition of FHL2, a GAM336382 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336382 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAC NM_000618.2) is another GAM336382 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336382 is therefore inhibition of IGF1, a GAM336382 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336382 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTGAC another GAM336382 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336382 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336382 is therefore inhibition of PRND, a GAM336382 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336382 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336384 HD TCCCAGTCATCTGGG HD (Accession NM_002111.3) is a GAM336384 target gene. HD A A

ATGTGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336384 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336384 is therefore inhibition of HD. Accordingly, utilities of GAM336384 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336385 HD TCCCAGTCATCTGGG HD (Accession NM_002111.3) is a GAM336385 target gene. HD A A

ATGTGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336385 is therefore inhibition of HD. Accordingly, utilities of GAM336385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336386 ADAM10 AGAGCTAGGAAGATA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

CAGGGTT Accession NM_001110.1) is a GAM336386 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336386 is therefore inhibition of ADAM10, a GAM336386 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336386 BAX AGAGCTAGGAAGATA BCL2- associated X Protein (BAX, Accession NM_004324.2) is A A CAGGGTT another GAM336386 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of BAX, a GAM336386 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM336386 GLUL AGAGCTAGGAAGATA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A CAGGGTT NM_002065.3) is another GAM336386 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of GLUL, a GAM336386 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336386 HD AGAGCTAGGAAGATA HD (Accession NM_002111.3) is another GAM336386 target gene. HD A A CAGGGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of HD. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336386 MAPK10 AGAGCTAGGAAGATA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
CAGGGTT NM_002753.2) is another GAM336386 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of MAPK10, a GAM336386 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336386 MAPT AGAGCTAGGAAGATA Microtubule- associated Protein Tau (MAPT, Accession A A
CAGGGTT NM_016841.1) is another GAM336386 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of MAPT, a GAM336386 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336386 TRPM2 AGAGCTAGGAAGATA TRPM2 (Accession NM_003307.1) is another GAM336386 target gene. A A
CAGGGTT TRPM2 BINDING SITE is a target binding site found in the 5`

untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336386 is therefore inhibition of TRPM2, a GAM336386 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336387 CTSB CACTGCACTGTAGCC CTSB (Accession NM_147782.1) is a GAM336387 target gene. CTSB A A
TCCTGGG BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336387 is therefore inhibition of CTSB. Accordingly, utilities of GAM336387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336387 FHL2 CACTGCACTGTAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TCCTGGG another GAM336387 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336387 is therefore inhibition of FHL2, a GAM336387 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336387 IAPP CACTGCACTGTAGCC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TCCTGGG another GAM336387 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336387 is therefore inhibition of IAPP, a GAM336387 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336387 IGF1 CACTGCACTGTAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TCCTGGG NM_000618.2) is another GAM336387 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336387 is therefore inhibition of IGF1, a GAM336387 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336387 PRND CACTGCACTGTAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TCCTGGG another GAM336387 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336387 is therefore inhibition of PRND, a GAM336387 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336388 ACT TGGCAGGTAAGCCAC Activator of CAMP- responsive Element Modulator (CR (ACT, A A CAGCATC Accession NM_020482.3) is a GAM336388 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336388 is therefore inhibition of ACT, a GAM336388 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336389 ACT TGGCAGGTAAGCCAC Activator of CAMP- responsive Element Modulator (CR (ACT, A A CAGCATC Accession NM_020482.3) is a GAM336389 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336389 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336389 is therefore inhibition of ACT, a GAM336389 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336389 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336390 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336390 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336390 is therefore inhibition of APPBP2, a GAM336390 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336390 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336390 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336390 is therefore inhibition of BACE2, a GAM336390 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336390 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336390 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336390 is therefore inhibition of FHL2, a GAM336390 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336390 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336390 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336390 is therefore inhibition of IGF1, a GAM336390 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336390 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336390 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336390 is therefore inhibition of MME, a GAM336390 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336390 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336390 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING A A

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336390 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336390 is therefore inhibition of PRND, a GAM336390 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336391 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336391 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336391 is therefore inhibition of APPBP2, a GAM336391 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336391 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336391 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336391 is therefore inhibition of BACE2, a GAM336391 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336391 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336391 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336391 is therefore inhibition of FHL2, a GAM336391 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336391 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336391 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336391 is therefore inhibition of IGF1, a GAM336391 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336391 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336391 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336391 is therefore inhibition of MME, a GAM336391 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336391 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336391 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336391 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336391 is therefore inhibition of PRND, a GAM336391 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336392 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336392 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336392 is therefore inhibition of APPBP2, a GAM336392 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336392 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336392 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336392 is therefore inhibition of BACE2, a GAM336392 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336392 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336392 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336392 is therefore inhibition of FHL2, a GAM336392 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336392 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336392 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336392 is therefore inhibition of IGF1, a GAM336392 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336392 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336392 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336392 is therefore inhibition of MME, a GAM336392 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336392 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336392 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336392 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336392 is therefore inhibition of PRND, a GAM336392 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336392 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336393 CLU GGAGCTGTAACAGAT CTGTTCT Clusterin (complement lysis inhibitor, SP- 40,40, sulfated glycoprotein (CLU, Accession NM_001831.1) is a GAM336393 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336393 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336393 is therefore inhibition of CLU, a GAM336393 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM336394 FLNB GTGTTTTTCCAAATG ACATCCA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM336394 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336394 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336394 is therefore inhibition of FLNB, a GAM336394 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336395 FLNB GTGTTTTTCCAAATG ACATCCA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM336395 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336395 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336395 is therefore inhibition of FLNB, a GAM336395 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336395 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336397 CAV1 GAGGAAGGTAATGAT CTTGATC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM336397 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336397 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336397 is therefore inhibition of CAV1, a GAM336397 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336399 ACE TAATGCTCAGCTGGA CCAGTGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_000789.2) is a GAM336399 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336399 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336399 is therefore inhibition of ACE, a GAM336399 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336399 APPBP2 TAATGCTCAGCTGGA CCAGTGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336399 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING A A

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336399 is therefore inhibition of APPBP2, a GAM336399 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336400 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336400 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336400 is therefore inhibition of APP. Accordingly, utilities of GAM336400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336403 HTR2C TTGCTTCATTAGGGC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

AAGCAAG NM_000868.1) is a GAM336403 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336403 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336403 is therefore inhibition of HTR2C, a GAM336403 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336403 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336404 IGF1 TATGAGTGTGATGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GTTTGAG NM_000618.2) is a GAM336404 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336404 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336404 is therefore inhibition of IGF1, a GAM336404 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336404 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336404 PSEN1 TATGAGTGTGATGGT PSEN1 (Accession NM_000021.2) is another GAM336404 target gene. A A

GTTTGAG PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336404 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336404 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336404 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336405 MAPK10 TCTCACACTCTGATT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

TCTTGCT NM_138980.1) is a GAM336405 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336405 is therefore inhibition of MAPK10, a GAM336405 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336405 PRND TCTCACACTCTGATT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TCTTGCT another GAM336405 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336405 is therefore inhibition of PRND, a GAM336405 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336406 APBB2 CAGAGCATTTGTGAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAGTGTT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336406 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336406 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336406 is therefore inhibition of APBB2, a GAM336406 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336406 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336406 BACE2 CAGAGCATTTGTGAG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GAGTGTT NM_138991.1) is another GAM336406 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336406 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336406 is therefore inhibition of BACE2, a GAM336406 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM336406 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336407 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A GAM336407 target

A function of GAM336407 is therefore inhibition of APPBP2, a GAM336407 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336407 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336407 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336407 is therefore inhibition of BACE2, a GAM336407 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336407 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336407 target gene. FHL2 BINDING SITE1 and FHL2 BINDING A A

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336407 is therefore inhibition of FHL2, a GAM336407 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336407 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336407 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336407 is therefore inhibition of IGF1, a GAM336407 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336407 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336407 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336407 is therefore inhibition of MME, a GAM336407 target gene which is thermolysin- like specificity.

and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336407 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336407 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336407 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336407 is therefore inhibition of PRND, a GAM336407 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336408 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336408 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336408 is therefore inhibition of APPBP2, a GAM336408 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336408 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336408 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336408 is therefore inhibition of BACE2, a GAM336408 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336408 FHL2 A ACTGCACTCCAGCCT A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336408 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336408 is therefore inhibition of FHL2, a GAM336408 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336408 IGF1 A ACTGCACTCCAGCCT A GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336408 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336408 is therefore inhibition of IGF1, a GAM336408 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336408 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336408 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336408 is therefore inhibition of MME, a GAM336408 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336408 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336408 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336408 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336408 is therefore inhibition of PRND, a GAM336408 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336409 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336409 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE A A

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336409 is therefore inhibition of APPBP2, a GAM336409 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336409 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336409 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336409 is therefore inhibition of BACE2, a GAM336409 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336409 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336409 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336409 is therefore inhibition of FHL2, a GAM336409 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336409 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336409 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336409 is therefore inhibition of IGF1, a GAM336409 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336409 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336409 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336409 is therefore inhibition of MME, a GAM336409 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336409 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336409 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336409 is therefore inhibition of PRND, a GAM336409 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336412 IAPP CTGCCTCCTGGGTTC AAGCAAT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM336412 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336412 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336412 is therefore inhibition of IAPP, a GAM336412 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336412 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336413 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336413 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336413 is therefore inhibition of APPBP2, a GAM336413 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336413 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336413 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336413 is therefore inhibition of BACE2, a GAM336413 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336413 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336413 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336413 is therefore inhibition of FHL2, a GAM336413 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336413 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336413 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336413 is therefore inhibition of IGF1, a GAM336413 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336413 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336413 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336413 is therefore inhibition of MME, a GAM336413 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336413 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336413 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336413 is therefore inhibition of PRND, a GAM336413 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM336414 CASP3 ATTGTAAATTAACAA TTTGCTC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM336414 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336414 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336414 is therefore inhibition of CASP3, a GAM336414 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336414 IAPP ATTGTAAATTAACAA TTTGCTC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM336414 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336414 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336414 is therefore inhibition of IAPP, a GAM336414 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336420 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM336420 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336420 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336420 is therefore inhibition of APP. Accordingly, utilities of GAM336420 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336422 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336422 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336422 is therefore inhibition of APPBP2, a GAM336422 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336422 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336422 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336422 is therefore inhibition of BACE2, a GAM336422 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336422 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336422 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336422 is therefore inhibition of FHL2, a GAM336422 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336422 HD A A TGGGCAA CATTGCACTCCAGCC

HD (Accession NM_002111.3) is another GAM336422 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336422 is therefore inhibition of HD. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336422 IGF1 A A TGGGCAA CATTGCACTCCAGCC

Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336422 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336422 is therefore inhibition of IGF1, a GAM336422 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336422 PRND A A TGGGCAA CATTGCACTCCAGCC

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336422 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336422 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336422 is therefore inhibition of PRND, a GAM336422 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336422 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336424 GLUL AGGTGGGGTTTCACC Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
ATGTTGG NM_002065.3) is a GAM336424 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336424 is therefore inhibition of GLUL, a GAM336424 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336424 IAPP AGGTGGGGTTTCACC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
ATGTTGG another GAM336424 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336424 is therefore inhibition of IAPP, a GAM336424 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The

function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336424 PSEN1 AGGTGGGGTTTCACC PSEN1 (Accession NM_007318.1) is another GAM336424 target gene. A A

ATGTTGG PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336424 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336424 TRPM2 AGGTGGGGTTTCACC TRPM2 (Accession NM_003307.1) is another GAM336424 target gene. A A

ATGTTGG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336424 is therefore inhibition of TRPM2, a GAM336424 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336426 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336426 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336426 is therefore inhibition of APP. Accordingly, utilities of GAM336426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336428 S100B GCACACACCTCCTTG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

CAGTGGC NM_006272.1) is a GAM336428 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336428 is therefore inhibition of S100B, a GAM336428 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336428 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336428 TGFB1 GCACACACCTCCTTG TGFB1 (Accession NM_000660.1) is another GAM336428 target gene. A A

CAGTGGC TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336428 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336428 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336429 ACE GTGCATCAGGATCTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A ACCAGAT (ACE, Accession NM_152831.1) is a GAM336429 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336429 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336429 is therefore inhibition of ACE, a GAM336429 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336429 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM44.

GAM336430 APPBP2 GTGCTTGACCATGTG GTGGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336430 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336430 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336430 is therefore inhibition of APPBP2, a GAM336430 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336430 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336430 PRND GTGCTTGACCATGTG GTGGCAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336430 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336430 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336430 is therefore inhibition of PRND, a GAM336430 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336430 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336431 APPBP2 GTGCTTGACCATGTG GTGGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336431 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336431 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336431 is therefore inhibition of APPBP2, a GAM336431 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336431 PRND GTGCTTGACCATGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GTGGCAG another GAM336431 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336431 is therefore inhibition of PRND, a GAM336431 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336432 APPBP2 GTGCTTGACCATGTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GTGGCAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336432 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336432 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336432 is therefore inhibition of APPBP2, a GAM336432 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336432 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336432 PRND GTGCTTGACCATGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GTGGCAG another GAM336432 target gene. PRND BINDING SITE is a target binding

site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336432 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336432 is therefore inhibition of PRND, a GAM336432 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336432 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336433 APPBP2 GTGCTTGACCATGTG GTGGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336433 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336433 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336433 is therefore inhibition of APPBP2, a GAM336433 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336433 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336433 PRND GTGCTTGACCATGTG GTGGCAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336433 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336433 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336433 is therefore inhibition of PRND, a GAM336433 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336433 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336434 GYPA TAGTGCAAGGTTTTG Glycophorin A (includes MN blood group) (GYPA, Accession A A

CCAACTT NM_002099.2) is a GAM336434 target gene. GYPA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336434 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336434 is therefore inhibition of GYPA, a GAM336434 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336434 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336434 MME TAGTGCAAGGTTTTG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

CCAACTT enkephalinase, (MME, Accession NM_000902.2) is another GAM336434 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336434 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336434 is therefore inhibition of MME, a GAM336434 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336434 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336435 IGF1 ACTGGGATATGAAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTGTGTG NM_000618.2) is a GAM336435 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336435 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336435 is therefore inhibition of IGF1, a GAM336435 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336435 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336435 PIN1 ACTGGGATATGAAGA CTGTGTG Protein (peptidyl- prolyl cis/trans isomerase) NIMA- interacting 1 (PIN1, Accession NM_006221.1) is another GAM336435 target gene. PIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336435 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336435 is therefore inhibition of PIN1, a GAM336435 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336435 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PIN1.The function of PIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM336439 CASP3 TGCATGATGCTGAGG TTTGGGA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM336439 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336439 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336439 is therefore inhibition of CASP3, a GAM336439 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336439 GFAP TGCATGATGCTGAGG GFAP (Accession NM_002055.2) is another GAM336439 target gene. A A

TTTGGGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336439 is therefore inhibition of GFAP. Accordingly, utilities of GAM336439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336439 NOTCH1 TGCATGATGCTGAGG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TTTGGGA (NOTCH1, Accession NM_017617.2) is another GAM336439 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336439 is therefore inhibition of NOTCH1, a GAM336439 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336439 NPY TGCATGATGCTGAGG Neuropeptide Y (NPY, Accession NM_000905.2) is another A A

TTTGGGA GAM336439 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336439 is therefore inhibition of NPY, a GAM336439 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM193.

GAM336440 CASP3 TGCATGATGCTGAGG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

TTTGGGA Accession NM_032991.1) is a GAM336440 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336440 is therefore inhibition of CASP3, a GAM336440 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336440 GFAP TGCATGATGCTGAGG GFAP (Accession NM_002055.2) is another GAM336440 target gene. A A

TTTGGGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336440 is therefore inhibition of GFAP. Accordingly, utilities of GAM336440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336440 NOTCH1 TGCATGATGCTGAGG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TTTGGGA (NOTCH1, Accession NM_017617.2) is another GAM336440 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336440 is therefore inhibition of NOTCH1, a GAM336440 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336440 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336440 NPY TGCATGATGCTGAGG Neuropeptide Y (NPY, Accession NM_000905.2) is another A A
TTTGGGA GAM336440 target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336440 is therefore inhibition of NPY, a GAM336440 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM336441 CTSB TGCACCACTACACTC CTSB (Accession NM_147782.1) is a GAM336441 target gene. CTSB A A
CTAGGCA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336441 is therefore inhibition of CTSB. Accordingly, utilities of GAM336441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336441 LRP1 TGCACCACTACACTC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
CTAGGCA macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM336441 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336441 is therefore inhibition of LRP1, a GAM336441 target gene which is a recycling lipoprotein

receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM336441 RAGE TGCACCACTACACTC CTAGGCA A A

Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another GAM336441 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336441 is therefore inhibition of RAGE, a GAM336441 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM336441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM336442 APPBP2 AAGCAGAACTGTTTT GTTTTCT A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336442 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336442 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336442 is therefore inhibition of APPBP2, a GAM336442 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336442 CAV1 AAGCAGAACTGTTTT GTTTTCT A A

Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM336442 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336442 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336442 is therefore inhibition of CAV1, a GAM336442 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336442 HTR2C AAGCAGAACTGTTTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

GTTTTCT NM_000868.1) is another GAM336442 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336442 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336442 is therefore inhibition of HTR2C, a GAM336442 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336442 NOTCH1 AAGCAGAACTGTTTT Notch (Drosophila) Homolog 1 (translocation- associated) A A

GTTTTCT (NOTCH1, Accession NM_017617.2) is another GAM336442 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336442 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336442 is therefore inhibition of NOTCH1, a GAM336442 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function

of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336445 MAPT GTGGCAAGTGACCAG Microtubule- associated Protein Tau (MAPT, Accession A A

ATGTCAC NM_173727.1) is a GAM336445 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336445 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336445 is therefore inhibition of MAPT, a GAM336445 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336445 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336447 ADAM17 TACAGTATCTGTAAA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AACTGTC factor, (ADAM17, Accession NM_021832.1) is a GAM336447 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336447 is therefore inhibition of ADAM17, a GAM336447 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336448 GLUL AGGTGGGGTTTCACC Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

ATGTTGG NM_002065.3) is a GAM336448 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336448 is therefore inhibition of GLUL, a GAM336448 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336448 IAPP AGGTGGGGTTTCACC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
ATGTTGG another GAM336448 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336448 is therefore inhibition of IAPP, a GAM336448 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336448 PSEN1 AGGTGGGGTTTCACC PSEN1 (Accession NM_007318.1) is another GAM336448 target gene. A A
ATGTTGG PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336448 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336448 TRPM2 AGGTGGGGTTTCACC TRPM2 (Accession NM_003307.1) is another GAM336448 target gene. A A
ATGTTGG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336448 is therefore inhibition of TRPM2, a GAM336448 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336450 IGF1 CTATTTTACATGGTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A ACTATCA NM_000618.2) is a GAM336450 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336450 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336450 is therefore inhibition of IGF1, a GAM336450 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336450 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336451 DSCR1 TAGCTGCCAGGCAAC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A AAGTACG NM_004414.3) is a GAM336451 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336451 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336451 is therefore inhibition of DSCR1, a GAM336451 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336451 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM1332.

GAM336451 MME TAGCTGCCAGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A

AAGTACG enkephalinase, (MME, Accession NM_007288.1) is another GAM336451 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336451 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336451 is therefore inhibition of MME, a GAM336451 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336451 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336452 DSCR1 TAGCTGCCAGGCAAC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

AAGTACG NM_004414.3) is a GAM336452 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336452 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336452 is therefore inhibition of DSCR1, a GAM336452 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336452 MME TAGCTGCCAGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A

AAGTACG enkephalinase, (MME, Accession NM_007288.1) is another GAM336452 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336452 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336452 is therefore inhibition of MME, a GAM336452 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336453 S100B TCCCTGGGACAACTT S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

TCTTATT NM_006272.1) is a GAM336453 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336453 is therefore inhibition of S100B, a GAM336453 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336454 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336454 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336454 is therefore inhibition of APPBP2, a GAM336454 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336454 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336454 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336454 is therefore inhibition of BACE2, a GAM336454 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336454 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336454 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336454 is therefore inhibition of FHL2, a GAM336454 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336454 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336454 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336454 is therefore inhibition of IGF1, a GAM336454 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336454 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336454 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336454 is therefore inhibition of MME, a GAM336454 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336454 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336454 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336454 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336454 is therefore inhibition of PRND, a GAM336454 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336455 PRND TTGCAATAGTGAAAA AACTGAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a GAM336455 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded A A

by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336455 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336455 is therefore inhibition of PRND, a GAM336455 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336455 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336455 TNFSF5 TTGCAATAGTGAAAA AACTGAA A A TNFSF5 (Accession NM_000074.1) is another GAM336455 target gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336455 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336455 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336455 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336456 APPBP2 CCAAAGTGCTAGGAA TACAGGT A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336456 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336456 is therefore inhibition of APPBP2, a GAM336456 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336456 HTR2A CCAAAGTGCTAGGAA A A 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession

TACAGGT NM_000621.1) is another GAM336456 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336456 is therefore inhibition of HTR2A, a GAM336456 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336456 IAPP CCAAAGTGCTAGGAA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TACAGGT another GAM336456 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336456 is therefore inhibition of IAPP, a GAM336456 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336456 MTNR1A CCAAAGTGCTAGGAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

TACAGGT another GAM336456 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336456 is therefore inhibition of MTNR1A, a GAM336456 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336456

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336456 TGFB1 CCAAAGTGCTAGGAA TGFB1 (Accession NM_000660.1) is another GAM336456 target gene. A A

TACAGGT TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336456 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336458 APBA1 GTACTCCAGCCTGCC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

TGGGTAA 1 (X11) (APBA1, Accession NM_001163.2) is a GAM336458 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336458 is therefore inhibition of APBA1, a GAM336458 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336458 APPBP2 GTACTCCAGCCTGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGTAA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336458 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336458 is therefore inhibition of APPBP2, a GAM336458 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336458 FHL2 GTACTCCAGCCTGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A TGGGTAA another GAM336458 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336458 is therefore inhibition of FHL2, a GAM336458 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336458 IGF1 GTACTCCAGCCTGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TGGGTAA NM_000618.2) is another GAM336458 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336458 is therefore inhibition of IGF1, a GAM336458 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336458 MAPT GTACTCCAGCCTGCC Microtubule- associated Protein Tau (MAPT, Accession A A

TGGGTAA NM_173727.1) is another GAM336458 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336458 is therefore inhibition of MAPT, a GAM336458 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336458 PRND GTACTCCAGCCTGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGTAA another GAM336458 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336458 is therefore inhibition of PRND, a GAM336458 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336460 DSCR1 TGTAGTGTGAAAGGC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

ATAGTGT NM_004414.3) is a GAM336460 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336460 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336460 is therefore inhibition of DSCR1, a GAM336460 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336460 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336461 CTNND2 GCAGTGAAGGAGGCA TGTGATC Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM336461 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336461 is therefore inhibition of CTNND2, a GAM336461 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336461 DHCR24 GCAGTGAAGGAGGCA TGTGATC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM336461 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336461 is therefore inhibition of DHCR24, a GAM336461 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336462 A2M TGGCAAGTGGGCACT TTTCAGG Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a GAM336462 target gene. A2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the A A

nucleotide sequence of GAM336462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336462 is therefore inhibition of A2M, a GAM336462 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM336462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM336465 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336465 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336465 is therefore inhibition of APPBP2, a GAM336465 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336465 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336465 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336465 is therefore inhibition of BACE2, a GAM336465 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336465 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336465 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336465 is therefore inhibition of FHL2, a GAM336465 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336465 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336465 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336465 is therefore inhibition of IGF1, a GAM336465 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336465 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336465 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336465 is therefore inhibition of MME, a GAM336465 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336465 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336465 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336465 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336465 is therefore inhibition of PRND, a GAM336465 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336468 CAV1 GCCTCCATTTCTACA TCTCTA Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM336468 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336468 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336468 is therefore inhibition of CAV1, a GAM336468 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336468 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336468 GFAP GCCTCCATTTCTACA GFAP (Accession NM_002055.2) is another GAM336468 target gene. A A

TCTCTA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336468 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336468 is therefore inhibition of GFAP. Accordingly, utilities of GAM336468 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336469 APBB2 TGCAGCCTTGAACTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTTCTGG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336469 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336469 is therefore inhibition of APBB2, a GAM336469 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336469 BACE2 TGCAGCCTTGAACTC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TTTCTGG NM_138991.1) is another GAM336469 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336469 is therefore inhibition of BACE2, a GAM336469 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336469 FPRL1 TGCAGCCTTGAACTC A A TTTCTGG FPRL1 (Accession NM_001462.1) is another GAM336469 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336469 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336469 HTR2A TGCAGCCTTGAACTC A A TTTCTGG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM336469 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336469 is therefore inhibition of HTR2A, a GAM336469 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336469 NCKAP1 TGCAGCCTTGAACTC A A TTTCTGG NCKAP1 (Accession NM_013436.2) is another GAM336469 target gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336469 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM336469 TNFRSF5 TGCAGCCTTGAACTC A A target TNFRSF5 (Accession NM_152854.1) is another GAM336469

TTTCTGG gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336469 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336470 APBB2 TGCAGCCTTGAACTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTTCTGG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336470 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336470 is therefore inhibition of APBB2, a GAM336470 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336470 BACE2 TGCAGCCTTGAACTC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TTTCTGG NM_138991.1) is another GAM336470 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336470 is therefore inhibition of BACE2, a GAM336470 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336470 FPRL1 TGCAGCCTTGAACTC A A TTTCTGG FPRL1 (Accession NM_001462.1) is another GAM336470 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336470 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336470 HTR2A TGCAGCCTTGAACTC A A TTTCTGG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM336470 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336470 is therefore inhibition of HTR2A, a GAM336470 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336470 NCKAP1 TGCAGCCTTGAACTC A A TTTCTGG NCKAP1 (Accession NM_013436.2) is another GAM336470 target gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336470 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM336470 TNFRSF5 TGCAGCCTTGAACTC A A target TNFRSF5 (Accession NM_152854.1) is another GAM336470

TTTCTGG gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336470 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336470 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336472 CTSK TTCAGGACTGTCTGG CTSK (Accession NM_000396.2) is a GAM336472 target gene. CTSK A A

ATTTATT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336472 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336472 is therefore inhibition of CTSK. Accordingly, utilities of GAM336472 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336472 FPRL1 TTCAGGACTGTCTGG FPRL1 (Accession NM_001462.1) is another GAM336472 target gene. A A

ATTTATT FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336472 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336472 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336472 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336474 FHL2 TGTCTGGAGGCGCAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TTTTCAG a GAM336474 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336474 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336474 is therefore inhibition of FHL2, a

GAM336474 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336474 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336474 GFAP TGTCTGGAGGCGCAG GFAP (Accession NM_002055.2) is another GAM336474 target gene. A A

TTTTCAG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336474 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336474 is therefore inhibition of GFAP. Accordingly, utilities of GAM336474 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336474 HD TGTCTGGAGGCGCAG HD (Accession NM_002111.3) is another GAM336474 target gene. HD A A

TTTTCAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336474 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336474 is therefore inhibition of HD. Accordingly, utilities of GAM336474 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336475 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336475 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336475 is therefore inhibition of APPBP2, a GAM336475 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336475 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336475 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336475 is therefore inhibition of BACE2, a GAM336475 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336475 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336475 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336475 is therefore inhibition of FHL2, a GAM336475 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336475 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336475 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336475 is therefore inhibition of IGF1, a GAM336475 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336475 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336475 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336475 is therefore inhibition of MME, a GAM336475 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336475 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336475 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336475 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336475 is therefore inhibition of PRND, a GAM336475 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336475 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336476 DHCR24 TCCCTTTGAAGCCAG GTTCCAG A A 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM336476 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336476 is therefore inhibition of DHCR24, a GAM336476 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336476 TGFB1 TCCCTTTGAAGCCAG GTTCCAG A A TGFB1 (Accession NM_000660.1) is another GAM336476 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336476 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336477 HTR2C GCACATTCCCGCAGG GTGTAAG A A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is a GAM336477 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336477 is therefore inhibition of HTR2C, a GAM336477 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336478 HTR2C GCACATTCCCGCAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A GTGTAAG NM_000868.1) is a GAM336478 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336478 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336478 is therefore inhibition of HTR2C, a GAM336478 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336478 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336479 HTR2C GCACATTCCCGCAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A GTGTAAG NM_000868.1) is a GAM336479 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336479 is therefore inhibition of HTR2C, a GAM336479 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336480 HTR2C GCACATTCCCGCAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A GTGTAAG NM_000868.1) is a GAM336480 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336480 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336480 is therefore inhibition of HTR2C, a GAM336480 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336480 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336483 CASP3 CTCTGAGTCTGAGAG AGTAGGT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM336483 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336483 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336483 is therefore inhibition of CASP3, a GAM336483 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336483 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336483 GLUL CTCTGAGTCTGAGAG AGTAGGT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM336483 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336483 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336483 is therefore inhibition of GLUL, a GAM336483 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336483 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336483 MAPT CTCTGAGTCTGAGAG Microtubule- associated Protein Tau (MAPT, Accession A A

AGTAGGT NM_173727.1) is another GAM336483 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336483 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336483 is therefore inhibition of MAPT, a GAM336483 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336483 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336483 OLR1 CTCTGAGTCTGAGAG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

AGTAGGT (OLR1, Accession NM_002543.1) is another GAM336483 target gene. OLR1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336483 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336483 is therefore inhibition of OLR1, a GAM336483 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336483 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336483 PRND CTCTGAGTCTGAGAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

AGTAGGT another GAM336483 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336483 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336483 is therefore inhibition of PRND, a GAM336483 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336483 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336484 CAV2 TAGGGAATGAACAAA Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM336484 target A A

TAGAGGC gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336484 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336484 is therefore inhibition of CAV2, a GAM336484 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336484 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336486 BAX TTACAAAATTTGGAG BCL2- associated X Protein (BAX, Accession NM_138765.1) is a A A

GGATTGT GAM336486 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336486 is therefore inhibition of BAX, a GAM336486 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM336486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM336486 TFCP2 TTACAAAATTTGGAG Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

GGATTGT another GAM336486 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336486 is therefore inhibition of TFCP2, a GAM336486 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM336487 CRYAB TGGCTAGGTAAGGGA CRYAB (Accession NM_001885.1) is a GAM336487 target gene. CRYAB A A
AG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CRYAB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRYAB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336487 is therefore inhibition of CRYAB. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRYAB.

GAM336487 CTSK TGGCTAGGTAAGGGA CTSK (Accession NM_000396.2) is another GAM336487 target gene. A A
AG CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of CTSK. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336487 DHCR24 TGGCTAGGTAAGGGA 24- dehydrocholesterol Reductase (DHCR24, Accession A A
AG NM_014762.1) is another GAM336487 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of DHCR24, a GAM336487 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336487 HTR2C TGGCTAGGTAAGGGA A A AG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336487 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of HTR2C, a GAM336487 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336487 IL1A TGGCTAGGTAAGGGA A A AG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336487 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of IL1A, a GAM336487 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336487 PSEN1 TGGCTAGGTAAGGGA PSEN1 (Accession NM_000021.2) is another GAM336487 target gene. A A

AG PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336487 SNCA TGGCTAGGTAAGGGA SNCA (Accession NM_000345.2) is another GAM336487 target gene. A A

AG SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336487 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336487 is therefore inhibition of SNCA. Accordingly, utilities of GAM336487 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM336488 ARHA GAACTGTACTGGACC Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

CATAGTT is a GAM336488 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336488 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336488 is therefore inhibition of ARHA, a GAM336488 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336488 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336489 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336489 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336489 is therefore inhibition of APP. Accordingly, utilities of GAM336489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336490 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336490 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336490 is therefore inhibition of APPBP2, a GAM336490 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336490 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336490 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336490 is therefore inhibition of BACE2, a GAM336490 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM336490 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336490 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336490 is therefore inhibition of FHL2, a GAM336490 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336490 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336490 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336490 is therefore inhibition of IGF1, a GAM336490 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336490 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336490 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336490 is therefore inhibition of MME, a GAM336490 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336490 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336490 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336490 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336490 is therefore inhibition of PRND, a GAM336490 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336491 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336491 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336491 is therefore inhibition of APPBP2, a GAM336491 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336491 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336491 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336491 is therefore inhibition of BACE2, a GAM336491 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336491 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336491 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336491 is therefore inhibition of FHL2, a GAM336491 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336491 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336491 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336491 is therefore inhibition of HD. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with HD.

GAM336491 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
TGGGCAA NM_000618.2) is another GAM336491 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336491 is therefore inhibition of IGF1, a GAM336491 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336491 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
TGGGCAA another GAM336491 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336491 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336491 is therefore inhibition of PRND, a GAM336491 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336491 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336492 CASP3 CTGGCTAATTTTCTT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A
A
GAGTTTT Accession NM_004346.2) is a GAM336492 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336492 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM336492 is therefore inhibition of CASP3, a GAM336492 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336492 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336492 HTR2C CTGGCTAATTTTCTT A A GAGTTTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336492 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336492 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336492 is therefore inhibition of HTR2C, a GAM336492 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336492 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336492 IDE CTGGCTAATTTTCTT A A GAGTTTT Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM336492 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336492 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336492 is therefore inhibition of IDE, a GAM336492 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336492 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336492 IGF1 CTGGCTAATTTTCTT A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession

GAGTTTT NM_000618.2) is another GAM336492 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336492 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336492 is therefore inhibition of IGF1, a GAM336492 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336492 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336493 FHL2 TAGTAGTTAGAGGCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GCAGTGA a GAM336493 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336493 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336493 is therefore inhibition of FHL2, a GAM336493 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336493 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336494 OLR1 TATCACGTGCAGCTT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

TGCTGAC (OLR1, Accession NM_002543.1) is a GAM336494 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336494 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336494 is therefore inhibition of OLR1, a GAM336494 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336494 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336495 CASP3 CTGGCTAATTTTCTT GAGTTTT A A Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is a GAM336495 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336495 is therefore inhibition of CASP3, a GAM336495 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336495 HTR2C CTGGCTAATTTTCTT GAGTTTT A A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336495 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336495 is therefore inhibition of HTR2C, a GAM336495 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336495 IDE CTGGCTAATTTTCTT GAGTTTT A A Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM336495 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336495 is therefore inhibition of IDE, a GAM336495 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336495 IGF1 CTGGCTAATTTTCTT GAGTTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336495 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336495 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336495 is therefore inhibition of IGF1, a GAM336495 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336496 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM336496 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336496 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336496 is therefore inhibition of APP. Accordingly, utilities of GAM336496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336497 ADAM17 GTGCATTTGTAGTTA AATGTGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is a GAM336497 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` A A

untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336497 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336497 is therefore inhibition of ADAM17, a GAM336497 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336497 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336497 FPRL1 GTGCATTTGTAGTTA FPRL1 (Accession NM_001462.1) is another GAM336497 target gene. A A

AATGTGT FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336497 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336497 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336497 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336497 GYPA GTGCATTTGTAGTTA Glycophorin A (includes MN blood group) (GYPA, Accession A A

AATGTGT NM_002099.2) is another GAM336497 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336497 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336497 is therefore inhibition of GYPA, a GAM336497 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336497 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336498 ADAM17 GTGCATTTGTAGTTA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AATGTGT factor, (ADAM17, Accession NM_003183.3) is a GAM336498 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336498 is therefore inhibition of ADAM17, a GAM336498 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336498 FPRL1 GTGCATTTGTAGTTA FPRL1 (Accession NM_001462.1) is another GAM336498 target gene. A A

AATGTGT FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336498 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336498 GYPA GTGCATTTGTAGTTA Glycophorin A (includes MN blood group) (GYPA, Accession A A

AATGTGT NM_002099.2) is another GAM336498 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336498 is therefore inhibition of GYPA, a GAM336498 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336499 HTR2A AGGGAGTGTCAGAAT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
GCCAGCA NM_000621.1) is a GAM336499 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336499 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336499 is therefore inhibition of HTR2A, a GAM336499 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336499 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336502 APBB2 AGCTGGATTGTTTAC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
CTGGGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336502 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336502 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336502 is therefore inhibition of APBB2, a GAM336502 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336502 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336502 NOTCH1 AGCTGGATTGTTTAC Notch (Drosophila) Homolog 1 (translocation- associated) A A
CTGGGGC (NOTCH1, Accession NM_017617.2) is another GAM336502 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336502 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336502 is therefore inhibition of NOTCH1, a GAM336502 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336502 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336503 HADH2 TTACTGGGCTCCTCT Hydroxyacyl- Coenzyme A Dehydrogenase, Type II (HADH2, A A
CAGTGTG Accession NM_004493.1) is a GAM336503 target gene. HADH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HADH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HADH2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336503 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336503 is therefore inhibition of HADH2, a GAM336503 target gene which catalyzes the reversible oxidation of L- 3- hydroxyacyl- CoAs to form 3- ketoacyl- CoAs and binds intracellular amyloid- beta. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336503 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HADH2.The function of HADH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1820.

GAM336504 ABCD1 AGTGGCCCTGGCCCT ABCD1 (Accession NM_000033.2) is a GAM336504 target gene. ABCD1 A A
GGGGCAT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336504 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336504 is therefore inhibition of ABCD1. Accordingly, utilities of GAM336504 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM336504 MAPT AGTGGCCCTGGCCCT Microtubule- associated Protein Tau (MAPT, Accession A A
GGGGCAT NM_173727.1) is another GAM336504 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336504 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336504 is therefore inhibition of MAPT, a GAM336504 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336504 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336505 BACE ATGGGCAGTTTCTTC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

CCTTTCC is a GAM336505 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336505 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336505 is therefore inhibition of BACE, a GAM336505 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336505 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336506 CASP3 CTGGCTAATTTTCTT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

GAGTTTT Accession NM_004346.2) is a GAM336506 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336506 is therefore inhibition of CASP3, a GAM336506 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM801.

GAM336506 HTR2C CTGGCTAATTTTCTT GAGTTTT A A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336506 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336506 is therefore inhibition of HTR2C, a GAM336506 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336506 IDE CTGGCTAATTTTCTT GAGTTTT A A Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM336506 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336506 is therefore inhibition of IDE, a GAM336506 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336506 IGF1 CTGGCTAATTTTCTT GAGTTTT A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336506 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336506 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336506 is therefore inhibition of

IGF1, a GAM336506 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336506 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336507 TNFRSF6 CTATTGGATTTTAAG TNFRSF6 (Accession NM_000043.3) is a GAM336507 target gene. A A

CATTGGG TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336507 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336507 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336508 TNFRSF6 CTATTGGATTTTAAG TNFRSF6 (Accession NM_000043.3) is a GAM336508 target gene. A A

CATTGGG TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336508 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336508 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336508 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336509 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336509 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336509 is therefore inhibition of APPBP2,

a GAM336509 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336509 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336509 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336509 is therefore inhibition of BACE2, a GAM336509 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336509 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336509 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336509 is therefore inhibition of FHL2, a GAM336509 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336509 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336509 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336509 is therefore inhibition of IGF1, a GAM336509 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336509 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336509 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336509 is therefore inhibition of MME, a GAM336509 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336509 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336509 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336509 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336509 is therefore inhibition of PRND, a GAM336509 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336509 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336510 CASP3 CTGGCTAATTTTCTT GAGTTTT A A Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is a GAM336510 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336510 is therefore inhibition of CASP3, a GAM336510 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336510 HTR2C CTGGCTAATTTTCTT GAGTTTT A A 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM336510 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336510 is therefore inhibition of HTR2C, a GAM336510 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336510 IDE CTGGCTAATTTTCTT GAGTTTT A A Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is another GAM336510 target gene. IDE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336510 is therefore inhibition of IDE, a GAM336510 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336510 IGF1 CTGGCTAATTTTCTT GAGTTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336510 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336510 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336510 is therefore inhibition of IGF1, a GAM336510 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336511 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM336511 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336511 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336511 is therefore inhibition of APP. Accordingly, utilities of GAM336511 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336512 CNTF GTAAAGAAATCATAA AAGTCCA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a GAM336512 target gene. CNTF BINDING SITE is a target binding site A A

found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336512 is therefore inhibition of CNTF, a GAM336512 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336512 CTNND2 GTAAAGAAATCATAA AAGTCCA Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM336512 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336512 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336512 is therefore inhibition of CTNND2, a GAM336512 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336512 LRP1 GTAAAGAAATCATAA AAGTCCA Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM336512 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336512 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336512 is therefore inhibition of LRP1, a GAM336512 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336512 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM336513 APBB2 TATGATTGTTTCATT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TGTTGGA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336513 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336513 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336513 is therefore inhibition of APBB2, a GAM336513 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336513 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336514 FHL2 CATTGCACTCCACCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TAGGCAA a GAM336514 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336514 is therefore inhibition of FHL2, a GAM336514 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336514 HD CATTGCACTCCACCC HD (Accession NM_002111.3) is another GAM336514 target gene. HD A A

TAGGCAA BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the

nucleotide sequence of GAM336514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336514 is therefore inhibition of HD. Accordingly, utilities of GAM336514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336514 IGF1 CATTGCACTCCACCC TAGGCAA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336514 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336514 is therefore inhibition of IGF1, a GAM336514 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336514 PRND CATTGCACTCCACCC TAGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336514 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336514 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336514 is therefore inhibition of PRND, a GAM336514 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336514 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336516 APPBP2 ACTGTACTCCAGCCT GGGCAAC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336516 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336516 is therefore inhibition of APPBP2, a GAM336516 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336516 FHL2 ACTGTACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336516 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336516 is therefore inhibition of FHL2, a GAM336516 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336516 IGF1 ACTGTACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336516 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336516 is therefore inhibition of IGF1, a GAM336516 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336516 PRND ACTGTACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336516 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336516 is therefore inhibition of PRND, a GAM336516 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336518 GFAP TGAGGTGATCAGCAA GFAP (Accession NM_002055.2) is a GAM336518 target gene. GFAP A A

GGTGGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336518 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336518 is therefore inhibition of GFAP. Accordingly, utilities of GAM336518 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336518 IGF1 TGAGGTGATCAGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGTGGAG NM_000618.2) is another GAM336518 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336518 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336518 is therefore inhibition of IGF1, a GAM336518 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336518 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336518 IL1A TGAGGTGATCAGCAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

GGTGGAG GAM336518 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336518 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336518 is therefore inhibition of IL1A, a GAM336518 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336518 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336519 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336519 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336519 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336519 is therefore inhibition of APP. Accordingly, utilities of GAM336519 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336520 BCHE TTCTGTGCAGGTTAA BCHE (Accession NM_000055.1) is a GAM336520 target gene. BCHE A A

CATTTCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336520 is therefore inhibition of BCHE. Accordingly, utilities of GAM336520 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336520 TNF TTCTGTGCAGGTTAA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A CATTTCT Accession NM_000594.2) is another GAM336520 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336520 is therefore inhibition of TNF, a GAM336520 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM336520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336522 APLP2 TTGAGAGCATAGAGC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession A A CAGGAAG NM_001642.1) is a GAM336522 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336522 is therefore inhibition of APLP2, a GAM336522 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336523 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336523 target gene. APP A A GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336523 is therefore inhibition of APP. Accordingly, utilities of GAM336523 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336524 BACE TGGTCTCCTATCCTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

GCTCACA is a GAM336524 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336524 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336524 is therefore inhibition of BACE, a GAM336524 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336526 B2M GACATGGAGACAACA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a A A

GCCAAAT GAM336526 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336526 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336526 is therefore inhibition of B2M, a GAM336526 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336526 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336527 B2M GACATGGAGACAACA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a A A

GCCAAAT GAM336527 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336527 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336527 is therefore inhibition of B2M, a GAM336527 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336527 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336528 ACE TCACAGTGATGGGTT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A CAGGAAT (ACE, Accession NM_152831.1) is a GAM336528 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336528 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336528 is therefore inhibition of ACE, a GAM336528 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336528 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336529 ACE TCACAGTGATGGGTT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A CAGGAAT (ACE, Accession NM_152831.1) is a GAM336529 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336529 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336529 is therefore inhibition of ACE, a GAM336529 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336529 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336532 ACT TTTGTACGTCAACTC Activator of CAMP- responsive Element Modulator (CR (ACT, A A AGCCTTA Accession NM_020482.3) is a GAM336532 target gene. ACT BINDING SITE

is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336532 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336532 is therefore inhibition of ACT, a GAM336532 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336532 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336533 ACT TTTGTACGTCAACTC Activator of CAMP- responsive Element Modulator (CR (ACT, A A

AGCCTTA Accession NM_020482.3) is a GAM336533 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336533 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336533 is therefore inhibition of ACT, a GAM336533 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336533 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336534 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336534 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336534 is therefore inhibition of APPBP2, a GAM336534 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336534 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336534 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336534 is therefore inhibition of BACE2, a GAM336534 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336534 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336534 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336534 is therefore inhibition of FHL2, a GAM336534 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336534 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336534 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336534 is therefore inhibition of IGF1, a GAM336534 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336534 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336534 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336534 is therefore inhibition of MME, a GAM336534 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336534 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336534 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336534 is therefore inhibition of PRND, a GAM336534 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336534 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336535 APLP2 GAGGAGGTGGGGCAG A A CAGCAGG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM336535 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336535 is therefore inhibition of APLP2, a GAM336535 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336535 BACE2 GAGGAGGTGGGGCAG A A CAGCAGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336535 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of BACE2, a GAM336535 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336535 FHL2 GAGGAGGTGGGGCAG A A CAGCAGG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336535 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of FHL2, a GAM336535 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336535 GFAP GAGGAGGTGGGGCAG GFAP (Accession NM_002055.2) is another GAM336535 target gene. A A

CAGCAGG GFAP BINDING SITE1 through GFAP BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 through GFAP BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of GFAP. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336535 MT3 GAGGAGGTGGGGCAG Metallothionein 3 (MT3, Accession NM_005954.1) is another A A

CAGCAGG GAM336535 target gene. MT3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MT3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of MT3, a GAM336535 target gene which inhibits survival and neurite formation of cortical neurons in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MT3.The function of MT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3890.

GAM336535 MTNR1A GAGGAGGTGGGGCAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CAGCAGG another GAM336535 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of MTNR1A, a GAM336535 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336535 OGDH GAGGAGGTGGGGCAG A A CAGCAGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM336535 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of OGDH, a GAM336535 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM336535 PSEN1 GAGGAGGTGGGGCAG A A CAGCAGG PSEN1 (Accession NM_007318.1) is another GAM336535 target gene. PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336535 SNCG GAGGAGGTGGGGCAG A A CAGCAGG SYNUCLEIN, GAMMA (SNCG, Accession NM_003087.1) is another GAM336535 target gene. SNCG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCG,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCG BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336535 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336535 is therefore inhibition of SNCG, a GAM336535 target gene which plays a role in neurofilament network integrity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336535 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCG.The function of SNCG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336536 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336536 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336536 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336536 is therefore inhibition of APP. Accordingly, utilities of GAM336536 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336537 BACE CCAGGGTACTCTGGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

ATCACTT is a GAM336537 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336537 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336537 is therefore inhibition of BACE, a GAM336537 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336537 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336537 FLNB CCAGGGTACTCTGGG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

ATCACTT NM_001457.1) is another GAM336537 target gene. FLNB BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336537 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336537 is therefore inhibition of FLNB, a GAM336537 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336537 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336537 IDE CCAGGGTACTCTGGG Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is A A

ATCACTT another GAM336537 target gene. IDE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336537 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336537 is therefore inhibition of IDE, a GAM336537 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336537 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336538 BACE CCAGGGTACTCTGGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

ATCACTT is a GAM336538 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336538 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336538 is therefore inhibition of BACE, a GAM336538 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336538 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336538 FLNB CCAGGGTACTCTGGG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
ATCACTT NM_001457.1) is another GAM336538 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336538 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336538 is therefore inhibition of FLNB, a GAM336538 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336538 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336538 IDE CCAGGGTACTCTGGG Insulin- degrading Enzyme (IDE, Accession NM_004969.1) is A A
ATCACTT another GAM336538 target gene. IDE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IDE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IDE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336538 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336538 is therefore inhibition of IDE, a GAM336538 target gene which may play a role in the cellular processing of insulin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336538 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IDE.The function of IDE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2770.

GAM336539 FOS TAGTGCAGTTGAATG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
AACATTT Accession NM_005252.2) is a GAM336539 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336539 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336539 is therefore inhibition of FOS, a GAM336539 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336539 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336540 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336540 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336540 is therefore inhibition of APPBP2, a GAM336540 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336540 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336540 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336540 is therefore inhibition of BACE2, a GAM336540 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336540 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336540 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336540 is therefore inhibition of FHL2, a GAM336540 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336540 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336540 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336540 is therefore inhibition of IGF1, a GAM336540 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336540 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336540 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336540 is therefore inhibition of MME, a GAM336540 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336540 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336540 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336540 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336540 is therefore inhibition of PRND, a GAM336540 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336540 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336541 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336541 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336541 is therefore inhibition of APPBP2, a GAM336541 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM336541 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336541 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336541 is therefore inhibition of BACE2, a GAM336541 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336541 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336541 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336541 is therefore inhibition of FHL2, a GAM336541 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336541 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336541 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336541 is therefore inhibition of IGF1, a GAM336541 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336541 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336541 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336541 is therefore inhibition of MME, a GAM336541 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336541 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336541 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336541 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336541 is therefore inhibition of PRND, a GAM336541 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336545 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336545 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336545 is therefore inhibition of APPBP2, a GAM336545 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336545 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336545 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336545 is therefore inhibition of BACE2, a GAM336545 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336545 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336545 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336545 is therefore inhibition of

FHL2, a GAM336545 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336545 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336545 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336545 is therefore inhibition of HD. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336545 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336545 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336545 is therefore inhibition of IGF1, a GAM336545 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336545 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336545 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide

sequence of GAM336545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336545 is therefore inhibition of PRND, a GAM336545 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336546 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336546 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336546 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336546 is therefore inhibition of APP. Accordingly, utilities of GAM336546 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336548 FLNB TCTGGTTTTAATCCT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A
GAAGGCA NM_001457.1) is a GAM336548 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336548 is therefore inhibition of FLNB, a GAM336548 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336548 LRP1 TCTGGTTTTAATCCT Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
GAAGGCA macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM336548 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336548 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336548 is therefore inhibition of LRP1, a GAM336548 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM336549 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336549 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336549 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336549 is therefore inhibition of APP. Accordingly, utilities of GAM336549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336550 ACE TCAGAGCAGTGCCGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

AGCCCAG (ACE, Accession NM_152831.1) is a GAM336550 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336550 is therefore inhibition of ACE, a GAM336550 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336550 AVP TCAGAGCAGTGCCGA AVP (Accession NM_000490.2) is another GAM336550 target gene. A A

AGCCCAG AVP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE,

and secondary structure complementarity to the nucleotide sequence of GAM336550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336550 is therefore inhibition of AVP. Accordingly, utilities of GAM336550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336550 BACE2 TCAGAGCAGTGCCGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A AGCCCAG NM_012105.3) is another GAM336550 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336550 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336550 is therefore inhibition of BACE2, a GAM336550 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336550 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336551 CTSK GAGTTAAGCAAAGAG CTSK (Accession NM_000396.2) is a GAM336551 target gene. CTSK A A AGGAAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336551 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336551 is therefore inhibition of CTSK. Accordingly, utilities of GAM336551 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336551 HTR2C GAGTTAAGCAAAGAG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A AGGAAGA NM_000868.1) is another GAM336551 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336551 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336551 is therefore inhibition of HTR2C, a GAM336551 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336551 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336552 ACE CAGCACCATCAGATG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A ACTGTAT (ACE, Accession NM_152831.1) is a GAM336552 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336552 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336552 is therefore inhibition of ACE, a GAM336552 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336553 ACE GCAGGATGGTTGGAC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TGAAGGG (ACE, Accession NM_152831.1) is a GAM336553 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336553 is therefore inhibition of ACE, a GAM336553 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336553 SERPINA GCAGGATGGTTGGAC Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 A A

3 TGAAGGG antiprotei (SERPINA3, Accession NM_001085.2) is another GAM336553 target gene. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336553 is therefore inhibition of SERPINA3, a GAM336553 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM336556 NGB GGGAGAAAAGGAGGG Neuroglobin (NGB, Accession NM_021257.2) is a GAM336556 target A A

GATACAG gene. NGB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336556 is therefore inhibition of NGB, a GAM336556 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336557 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336557 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336557 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336557 is therefore inhibition of APP. Accordingly, utilities of GAM336557 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336558 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336558 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336558 is therefore inhibition of APPBP2, a GAM336558 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336558 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336558 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336558 is therefore inhibition of BACE2, a GAM336558 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336558 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336558 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336558 is therefore inhibition of FHL2, a GAM336558 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336558 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336558 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336558 is therefore inhibition of IGF1, a GAM336558 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336558 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336558 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336558 is therefore inhibition of MME, a GAM336558 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336558 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336558 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336558 is therefore inhibition of PRND, a GAM336558 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336559 CRAT GAGAGGTGAAGCCAG Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is a A A

GCTTCTG GAM336559 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336559 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336559 is therefore inhibition of CRAT, a GAM336559 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336559 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336560 ADAM17 AAGTGCTGGTATTAC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AAGTGTG factor, (ADAM17, Accession NM_021832.1) is a GAM336560 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336560 is therefore inhibition of ADAM17,

a GAM336560 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336560 GLUL AAGTGCTGGTATTAC A A AAGTGTG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM336560 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336560 is therefore inhibition of GLUL, a GAM336560 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336560 MTNR1A AAGTGCTGGTATTAC A A AAGTGTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM336560 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336560 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336560 is therefore inhibition of MTNR1A, a GAM336560 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336560 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336561 APCS TGTAGCAGAACACTG a A A GGTCCAG Amyloid P Component, Serum (APCS, Accession NM_001639.2) is a GAM336561 target gene. APCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APCS,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336561 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336561 is therefore inhibition of APCS, a GAM336561 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336561 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM772.

GAM336561 APPBP2 TGTAGCAGAACACTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGTCCAG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336561 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336561 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336561 is therefore inhibition of APPBP2, a GAM336561 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336561 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336563 APPBP2 ACTGCACTTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336563 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336563 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336563 is therefore inhibition of APPBP2, a GAM336563 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336563 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336563 FHL2 ACTGCACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAT another GAM336563 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336563 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336563 is therefore inhibition of FHL2, a GAM336563 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336563 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336563 IGF1 ACTGCACTTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAT NM_000618.2) is another GAM336563 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336563 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336563 is therefore inhibition of IGF1, a GAM336563 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336563 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336563 PRND ACTGCACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAT another GAM336563 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336563 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336563 is therefore inhibition of PRND, a GAM336563 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336563 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336564 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336564 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336564 is therefore inhibition of APPBP2, a GAM336564 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336564 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336564 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336564 is therefore inhibition of BACE2, a GAM336564 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336564 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336564 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336564 is therefore inhibition of FHL2, a GAM336564 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336564 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336564 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336564 is therefore inhibition of HD. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336564 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336564 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336564 is therefore inhibition of IGF1, a GAM336564 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336564 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336564 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336564 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336564 is therefore inhibition of PRND, a GAM336564 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336564 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336565 CTSB TTCTGCCACTGCATT CTSB (Accession NM_147780.1) is a GAM336565 target gene. CTSB A A

CCAGCCT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336565 is therefore inhibition of CTSB. Accordingly, utilities of GAM336565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336565 FHL2 TTCTGCCACTGCATT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CCAGCCT another GAM336565 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336565 is therefore inhibition of FHL2, a GAM336565 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336565 IGF1 TTCTGCCACTGCATT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A CCAGCCT NM_000618.2) is another GAM336565 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336565 is therefore inhibition of IGF1, a GAM336565 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336565 PRND TTCTGCCACTGCATT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A CCAGCCT another GAM336565 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336565 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336565 is therefore inhibition of PRND, a GAM336565 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336565 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336567 TRPM2 AAGGAAGTGTCTCTT TRPM2 (Accession NM_003307.1) is a GAM336567 target gene. TRPM2 A A

GGCTGGC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336567 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336567 is therefore inhibition of TRPM2, a GAM336567 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336568 TRPM2 AAGGAAGTGTCTCTT TRPM2 (Accession NM_003307.1) is a GAM336568 target gene. TRPM2 A A

GGCTGGC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336568 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336568 is therefore inhibition of TRPM2, a GAM336568 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336568 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336569 TRPM2 AAGGAAGTGTCTCTT TRPM2 (Accession NM_003307.1) is a GAM336569 target gene. TRPM2 A A

GGCTGGC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336569 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336569 is therefore inhibition of TRPM2, a GAM336569 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336570 ARHA CTGGAGAGGAGCGGT Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

CACTGGT is a GAM336570 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336570 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336570 is therefore inhibition of ARHA, a GAM336570 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336570 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336570 FOS CTGGAGAGGAGCGGT V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

CACTGGT Accession NM_005252.2) is another GAM336570 target gene. FOS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336570 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336570 is therefore inhibition of FOS, a GAM336570 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336570 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336571 APBB2 GGCCTGGTGGCTGTT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GTTTTGG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336571 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336571 is therefore inhibition of APBB2, a GAM336571 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336571 APCS GGCCTGGTGGCTGTT Amyloid P Component, Serum (APCS, Accession NM_001639.2) is A A

GTTTTGG another GAM336571 target gene. APCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336571 is therefore inhibition of APCS, a GAM336571 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM772.

GAM336571 BACE2 GGCCTGGTGGCTGTT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GTTTTGG NM_138991.1) is another GAM336571 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336571 is therefore inhibition of BACE2, a GAM336571 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336571 PRND GGCCTGGTGGCTGTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GTTTTGG another GAM336571 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336571 is therefore inhibition of PRND, a GAM336571 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336572 ADAMTS5 AAGTTTTTTTAAATT A Disintegrin- like and Metalloprotease (reprolysin type) with A A AGCTAGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336572 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336572 is therefore inhibition of ADAMTS5, a GAM336572 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336572 S100B AAGTTTTTTTAAATT S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A AGCTAGG NM_006272.1) is another GAM336572 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336572 is therefore inhibition of S100B, a GAM336572 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function

of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336573 APPBP2 ATTGCACTCCAGCCT GGGTGAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336573 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336573 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336573 is therefore inhibition of APPBP2, a GAM336573 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336573 FHL2 ATTGCACTCCAGCCT GGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336573 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336573 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336573 is therefore inhibition of FHL2, a GAM336573 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336573 IGF1 ATTGCACTCCAGCCT GGGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336573 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336573 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336573 is therefore inhibition of IGF1, a GAM336573 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336573 PRND ATTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM336573 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336573 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336573 is therefore inhibition of PRND, a GAM336573 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336573 TNFRSF5 ATTGCACTCCAGCCT TNFRSF5 (Accession NM_152854.1) is another GAM336573 target A A
GGGTGAC gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336573 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336573 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336574 APBB2 GCAGCGCTGAGATGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
TTTGTTG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336574 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336574 is therefore inhibition of APBB2, a GAM336574 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336574 MAPT GCAGCGCTGAGATGA Microtubule- associated Protein Tau (MAPT, Accession A A
TTTGTTG NM_173727.1) is another GAM336574 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336574 is therefore inhibition of MAPT, a GAM336574 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336575 APPBP2 ATTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGTGAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336575 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336575 is therefore inhibition of APPBP2, a GAM336575 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336575 FHL2 ATTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAC another GAM336575 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336575 is therefore inhibition of FHL2, a GAM336575 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336575 IGF1 ATTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAC NM_000618.2) is another GAM336575 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336575 is therefore inhibition of IGF1, a GAM336575 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336575 PRND ATTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTGAC another GAM336575 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336575 is therefore inhibition of PRND, a GAM336575 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336575 TNFRSF5 ATTGCACTCCAGCCT TNFRSF5 (Accession NM_152854.1) is another GAM336575 target A A

GGGTGAC gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336575 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336578 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGCGACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336578 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336578 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336578 is therefore inhibition of APPBP2, a GAM336578 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336578 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336578 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGCGACA another GAM336578 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336578 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336578 is therefore inhibition of FHL2, a GAM336578 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336578 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336578 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGCGACA NM_000618.2) is another GAM336578 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336578 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336578 is therefore inhibition of IGF1, a GAM336578 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336578 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336578 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGCGACA another GAM336578 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336578 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336578 is therefore inhibition of PRND, a GAM336578 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336578 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336579 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGCGACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336579 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336579 is therefore inhibition of APPBP2, a GAM336579 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336579 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGCGACA another GAM336579 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336579 is therefore inhibition of FHL2, a GAM336579 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336579 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGCGACA NM_000618.2) is another GAM336579 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336579 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336579 is therefore inhibition of IGF1, a GAM336579 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336579 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGCGACA another GAM336579 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336579 is therefore inhibition of PRND, a GAM336579 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336580 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336580 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336580 is therefore inhibition of APPBP2, a GAM336580 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336580 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336580 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336580 is therefore inhibition of BACE2, a GAM336580 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336580 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336580 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336580 is therefore inhibition of FHL2, a GAM336580 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336580 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336580 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336580 is therefore inhibition of IGF1, a GAM336580 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336580 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336580 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336580 is therefore inhibition of MME, a GAM336580 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336580 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336580 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336580 is therefore inhibition of PRND, a GAM336580 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336581 BLMH GTCCTGGAGCTGTTG Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a A A
GAGAAAT GAM336581 target gene. BLMH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336581 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336581 is therefore inhibition of BLMH, a GAM336581 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM336581 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM336582 APPBP2 ATTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGTGAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336582 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336582 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336582 is therefore inhibition of APPBP2, a GAM336582 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336582 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336582 FHL2 ATTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGTGAC another GAM336582 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336582 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336582 is therefore inhibition of FHL2, a GAM336582 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336582 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336582 IGF1 ATTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTGAC NM_000618.2) is another GAM336582 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336582 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336582 is therefore inhibition of IGF1, a GAM336582 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336582 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336582 PRND ATTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM336582 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336582 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336582 is therefore inhibition of PRND, a GAM336582 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336582 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336582 TNFRSF5 ATTGCACTCCAGCCT TNFRSF5 (Accession NM_152854.1) is another GAM336582 target A A
GGGTGAC gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336582 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336582 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336582 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336583 APLP2 GAGGTAGAGGTTGCA GTGAGTG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM336583 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336583 is therefore inhibition of APLP2, a GAM336583 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336583 APPBP2 GAGGTAGAGGTTGCA GTGAGTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336583 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336583 is therefore inhibition of APPBP2, a GAM336583 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336583 BACE GAGGTAGAGGTTGCA GTGAGTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) is another GAM336583 target gene. BACE BINDING SITE is a target A A

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336583 is therefore inhibition of BACE, a GAM336583 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336583 FHL2 GAGGTAGAGGTTGCA A A GTGAGTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336583 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336583 is therefore inhibition of FHL2, a GAM336583 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336583 GYPA GAGGTAGAGGTTGCA A A GTGAGTG Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM336583 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336583 is therefore inhibition of GYPA, a GAM336583 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336583 IGF1 GAGGTAGAGGTTGCA GTGAGTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336583 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336583 is therefore inhibition of IGF1, a GAM336583 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336583 PRND GAGGTAGAGGTTGCA GTGAGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336583 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336583 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336583 is therefore inhibition of PRND, a GAM336583 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336583 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336584 APLP2 GAGGTAGAGGTTGCA GTGAGTG Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM336584 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure A A

complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336584 is therefore inhibition of APLP2, a GAM336584 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336584 APPBP2 GAGGTAGAGGTTGCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GTGAGTG Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336584 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of APPBP2, a GAM336584 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336584 BACE GAGGTAGAGGTTGCA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

GTGAGTG is another GAM336584 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of BACE, a GAM336584 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM99.

GAM336584 FHL2 GAGGTAGAGGTTGCA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GTGAGTG another GAM336584 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of FHL2, a GAM336584 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336584 GYPA GAGGTAGAGGTTGCA Glycophorin A (includes MN blood group) (GYPA, Accession A A

GTGAGTG NM_002099.2) is another GAM336584 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of GYPA, a GAM336584 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336584 IGF1 GAGGTAGAGGTTGCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GTGAGTG NM_000618.2) is another GAM336584 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of

IGF1, a GAM336584 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336584 PRND GAGGTAGAGGTTGCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GTGAGTG another GAM336584 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336584 is therefore inhibition of PRND, a GAM336584 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336585 APBB2 GTTACAGCTCTCAAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GAAGACA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336585 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336585 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336585 is therefore inhibition of APBB2, a GAM336585 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336585 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336585 GAL GTTACAGCTCTCAAA Galanin (GAL, Accession NM_015973.2) is another GAM336585 A A
GAAGACA target gene. GAL BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by GAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GAL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336585 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336585 is therefore inhibition of GAL, a GAM336585 target gene which stimulates LH secretion and enhances LHRH- induced LH release from dispersed anterior pituitary cells in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336585 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GAL.The function of GAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3293.

GAM336585 PSEN1 GTTACAGCTCTCAAA PSEN1 (Accession NM_000021.2) is another GAM336585 target gene. A A

GAAGACA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336585 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336585 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336585 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336586 ADAM10 CACTGCACTCCAGCC A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

CGGCAAC Accession NM_001110.1) is a GAM336586 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336586 is therefore inhibition of ADAM10, a GAM336586 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336586 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CGGCAAC another GAM336586 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336586 is therefore inhibition of FHL2, a GAM336586 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336586 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CGGCAAC NM_000618.2) is another GAM336586 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336586 is therefore inhibition of IGF1, a GAM336586 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336586 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CGGCAAC another GAM336586 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336586 is therefore inhibition of PRND, a GAM336586 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336587 NPY TAAGATGTTTGCATT Neuropeptide Y (NPY, Accession NM_000905.2) is a GAM336587 A A
TCAGCAC target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336587 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336587 is therefore inhibition of NPY, a GAM336587 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336587 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM336588 NPY TAAGATGTTTGCATT Neuropeptide Y (NPY, Accession NM_000905.2) is a GAM336588 A A
TCAGCAC target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336588 is therefore inhibition of NPY, a GAM336588 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM336589 TNF ATCTGCTGTCTTTTA Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A
GAAGTGG Accession NM_000594.2) is a GAM336589 target gene. TNF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336589 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336589 is therefore inhibition of TNF, a GAM336589 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM336589 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336590 APBB2 CAAGTGCTTGAACAT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GGCAGAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336590 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336590 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336590 is therefore inhibition of APBB2, a GAM336590 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336590 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336590 CAV1 CAAGTGCTTGAACAT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
GGCAGAG NM_001753.3) is another GAM336590 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336590 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336590 is therefore inhibition of CAV1, a GAM336590 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336590 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336590 PRND CAAGTGCTTGAACAT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGCAGAG another GAM336590 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336590 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336590 is therefore inhibition of PRND, a GAM336590 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336590 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336591 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336591 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336591 is therefore inhibition of APP. Accordingly, utilities of GAM336591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336592 DHCR24 TGAGAGAGGAAGGCC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GTAGGGA NM_014762.1) is a GAM336592 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336592 is therefore inhibition of DHCR24, a GAM336592 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336592 IL1A TGAGAGAGGAAGGCC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

GTAGGGA GAM336592 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336592 is therefore inhibition of IL1A, a GAM336592 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336592 TNF TGAGAGAGGAAGGCC Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

GTAGGGA Accession NM_000594.2) is another GAM336592 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336592 is therefore inhibition of TNF, a GAM336592 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM336592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336593 ADAM17 TTTGCACACTTTCCA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AGTTGCC factor, (ADAM17, Accession NM_003183.3) is a GAM336593 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336593 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336593 is therefore inhibition of ADAM17, a GAM336593 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336593 B2M TTTGCACACTTTCCA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A
AGTTGCC GAM336593 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336593 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336593 is therefore inhibition of B2M, a GAM336593 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336593 CTNND2 TTTGCACACTTTCCA Catenin (cadherin- associated protein), Delta 2 (neural A A
AGTTGCC plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM336593 target gene. CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTNND2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336593 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336593 is therefore inhibition of CTNND2, a GAM336593 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM550.

GAM336593 IGF1 TTTGCACACTTTCCA AGTTGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336593 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336593 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336593 is therefore inhibition of IGF1, a GAM336593 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336593 PRNP TTTGCACACTTTCCA AGTTGCC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM336593 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336593 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336593 is therefore inhibition of PRNP, a GAM336593 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336594 ADAM17 TTTGCACACTTTCCA AGTTGCC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_003183.3) is a GAM336594 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure A A

complementarity to the nucleotide sequence of GAM336594 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336594 is therefore inhibition of ADAM17, a GAM336594 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336594 B2M TTTGCACACTTTCCA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A
AGTTGCC GAM336594 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336594 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336594 is therefore inhibition of B2M, a GAM336594 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336594 CTNND2 TTTGCACACTTTCCA Catenin (cadherin- associated protein), Delta 2 (neural A A
AGTTGCC plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM336594 target gene. CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CTNND2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE1 and CTNND2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336594 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336594 is therefore inhibition of CTNND2, a GAM336594 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM550.

GAM336594 IGF1 TTTGCACACTTTCCA AGTTGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336594 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336594 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336594 is therefore inhibition of IGF1, a GAM336594 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336594 PRNP TTTGCACACTTTCCA AGTTGCC Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM336594 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336594 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336594 is therefore inhibition of PRNP, a GAM336594 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336595 APBB2 ATGGTGTAGGTGAAG AGAACAT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336595 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide A A

sequence of GAM336595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336595 is therefore inhibition of APBB2, a GAM336595 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336595 BACE ATGGTGTAGGTGAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

AGAACAT is another GAM336595 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336595 is therefore inhibition of BACE, a GAM336595 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336595 IL1A ATGGTGTAGGTGAAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

AGAACAT GAM336595 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336595 is therefore inhibition of IL1A, a GAM336595 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336595 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336596 APBB2 ATGGTGTAGGTGAAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
AGAACAT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336596 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336596 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336596 is therefore inhibition of APBB2, a GAM336596 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336596 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336596 BACE ATGGTGTAGGTGAAG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A
AGAACAT is another GAM336596 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336596 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336596 is therefore inhibition of BACE, a GAM336596 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336596 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336596 IL1A ATGGTGTAGGTGAAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
AGAACAT GAM336596 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336596 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336596 is therefore inhibition of IL1A, a GAM336596 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336596 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336597 ARHA CTGAATGTAATCTTA Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A GTTGTAA is a GAM336597 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336597 is therefore inhibition of ARHA, a GAM336597 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336597 CTNND2 CTGAATGTAATCTTA Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM336597 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336597 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A GTTGTAA

Another function of GAM336597 is therefore inhibition of CTNND2, a GAM336597 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336597 LRP1 CTGAATGTAATCTTA Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
GTTGTAA macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM336597 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336597 is therefore inhibition of LRP1, a GAM336597 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM336598 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336598 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336598 is therefore inhibition of APP. Accordingly, utilities of GAM336598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336599 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336599 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336599 is therefore inhibition of APPBP2, a GAM336599 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336599 BACE2 CATTGCACTCCAGCC A A TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336599 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336599 is therefore inhibition of BACE2, a GAM336599 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336599 FHL2 CATTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336599 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336599 is therefore inhibition of FHL2, a GAM336599 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336599 HD CATTGCACTCCAGCC A A TGGGCAA HD (Accession NM_002111.3) is another GAM336599 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336599 is therefore inhibition of HD. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336599 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336599 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336599 is therefore inhibition of IGF1, a GAM336599 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336599 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336599 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336599 is therefore inhibition of PRND, a GAM336599 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336600 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336600 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336600 is therefore inhibition of APPBP2, a GAM336600 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336600 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336600 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM336600 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336600 is therefore inhibition of BACE2, a GAM336600 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336600 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336600 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336600 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336600 is therefore inhibition of FHL2, a GAM336600 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336600 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336600 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336600 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336600 is therefore inhibition of HD. Accordingly, utilities of GAM336600 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336600 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336600 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336600 is therefore inhibition of IGF1, a GAM336600 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336600 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336600 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336600 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336600 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336600 is therefore inhibition of PRND, a GAM336600 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336600 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336601 ACE TGGAGTAAAATGTCA GGTGTTT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM336601 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336601 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336601 is therefore inhibition of ACE, a GAM336601 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336601 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336602 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336602 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336602 is therefore inhibition of APPBP2, a GAM336602 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336602 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336602 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336602 is therefore inhibition of BACE2, a GAM336602 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336602 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336602 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336602 is therefore inhibition of FHL2, a GAM336602 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336602 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336602 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336602 is therefore inhibition of IGF1, a GAM336602 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336602 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336602 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336602 is therefore inhibition of MME, a GAM336602 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336602 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336602 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336602 is therefore inhibition of PRND, a GAM336602 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336605 PRNP AGGCAGTCTTGATTA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A
GCTTCTA Strausler- (PRNP, Accession NM_000311.1) is a GAM336605 target gene. PRNP BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336605 is therefore inhibition of PRNP, a GAM336605 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336606 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336606 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336606 is therefore inhibition of APPBP2, a GAM336606 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336606 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336606 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336606 is therefore inhibition of

BACE2, a GAM336606 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336606 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336606 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336606 is therefore inhibition of FHL2, a GAM336606 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336606 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336606 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336606 is therefore inhibition of IGF1, a GAM336606 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336606 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336606 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336606 is therefore inhibition of MME, a GAM336606 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336606 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336606 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336606 is therefore inhibition of PRND, a GAM336606 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336607 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336607 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336607 is therefore inhibition of APPBP2, a GAM336607 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336607 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336607 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336607 is therefore inhibition of BACE2, a GAM336607 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336607 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336607 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336607 is therefore inhibition of FHL2, a GAM336607 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336607 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336607 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336607 is therefore inhibition of IGF1, a GAM336607 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336607 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336607 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336607 is therefore inhibition of MME, a GAM336607 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336607 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336607 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336607 is therefore inhibition of PRND, a GAM336607 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336608 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336608 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336608 is therefore inhibition of APPBP2, a GAM336608 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336608 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336608 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336608 is therefore inhibition of BACE2, a GAM336608 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336608 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336608 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336608 is therefore inhibition of FHL2, a GAM336608 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336608 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336608 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336608 is therefore inhibition of IGF1, a GAM336608 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336608 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336608 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336608 is therefore inhibition of MME, a GAM336608 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336608 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336608 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336608 is therefore inhibition of PRND, a GAM336608 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336609 BACE AACACGTTGCATCTG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

TGTCTCT is a GAM336609 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336609 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336609 is therefore inhibition of BACE, a GAM336609 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336609 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336610 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336610 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336610 is therefore inhibition of APPBP2, a GAM336610 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336610 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336610 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336610 is therefore inhibition of BACE2, a GAM336610 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336610 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336610 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336610 is therefore inhibition of FHL2, a GAM336610 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336610 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336610 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336610 is therefore inhibition of IGF1, a GAM336610 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336610 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336610 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336610 is therefore inhibition of MME, a GAM336610 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336610 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336610 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING A A

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336610 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336610 is therefore inhibition of PRND, a GAM336610 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336610 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336611 TNFRSF6 TGTGTTTGAACACCT TNFRSF6 (Accession NM_152876.1) is a GAM336611 target gene. A A

TGGTCAC TNFRSF6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336611 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336611 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336611 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336614 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336614 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336614 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336614 is therefore inhibition of APP. Accordingly, utilities of GAM336614 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336615 ADAMTS5 GTGTTATTAATAAAC A Disintegrin- like and Metalloprotease (reprolysin type) with A A

TCTTTTT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336615 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336615 is therefore inhibition of ADAMTS5, a GAM336615 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336615 IGF1 GTGTTATTAATAAAC TCTTTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336615 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336615 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336615 is therefore inhibition of IGF1, a GAM336615 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336617 APPBP2 ACTGCACTCCAGCCT GGCAACA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336617 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336617 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336617 is therefore inhibition of APPBP2, a GAM336617 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336617 HD ACTGCACTCCAGCCT HD (Accession NM_002111.3) is another GAM336617 target gene. HD A A

GGCAACA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336617 is therefore inhibition of HD. Accordingly, utilities of GAM336617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336617 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGCAACA NM_000618.2) is another GAM336617 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336617 is therefore inhibition of IGF1, a GAM336617 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336617 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGCAACA another GAM336617 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336617 is therefore inhibition of PRND, a GAM336617 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336618 DLST TTTGTGTCCTGACCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A
A
AGAGGAC oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336618 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336618 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336618 is therefore inhibition of DLST, a GAM336618 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336618 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336619 DLST TTTGTGTCCTGACCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A
A
AGAGGAC oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336619 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336619 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336619 is therefore inhibition of DLST, a GAM336619 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336619 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336620 DLST TTTGTGTCCTGACCC Dihydrolipoamide S- succinyltransferase (E2 component of 2- A
A
AGAGGAC oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336620 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336620 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336620 is therefore inhibition of DLST, a GAM336620 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336620 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336621 GFAP TAGCAGCAGGAGCAG GFAP (Accession NM_002055.2) is a GAM336621 target gene. GFAP A A

GTAACAT BINDING SITE1 through GFAP BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 through GFAP BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336621 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336621 is therefore inhibition of GFAP. Accordingly, utilities of GAM336621 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336621 MME TAGCAGCAGGAGCAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GTAACAT enkephalinase, (MME, Accession NM_007288.1) is another GAM336621 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336621 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336621 is therefore inhibition of MME, a GAM336621 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336621 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336621 PSEN1 TAGCAGCAGGAGCAG PSEN1 (Accession NM_007318.1) is another GAM336621 target gene. A A

GTAACAT PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336621 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336621 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336621 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336622 MAPT AAGAGGTAGTGTAAG Microtubule- associated Protein Tau (MAPT, Accession A A GAATTGT NM_016841.1) is a GAM336622 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336622 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336622 is therefore inhibition of MAPT, a GAM336622 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336622 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336626 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336626 target gene. APP A A GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336626 is therefore inhibition of APP. Accordingly, utilities of GAM336626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336628 IGF1 CCAGGCAACTGTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TTTTAAG NM_000618.2) is a GAM336628 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336628 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336628 is therefore inhibition of IGF1, a GAM336628 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336628 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336629 IGF1 CCAGGCAACTGTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTTTAAG NM_000618.2) is a GAM336629 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336629 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336629 is therefore inhibition of IGF1, a GAM336629 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336629 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336630 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336630 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336630 is therefore inhibition of APPBP2, a GAM336630 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336630 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336630 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336630 is therefore inhibition of BACE2, a GAM336630 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336630 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336630 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336630 is therefore inhibition of FHL2, a GAM336630 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336630 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336630 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336630 is therefore inhibition of IGF1, a GAM336630 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336630 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336630 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336630 is therefore inhibition of MME, a GAM336630 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336630 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336630 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336630 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336630 is therefore inhibition of PRND, a GAM336630 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336631 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336631 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target A A

binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336631 is therefore inhibition of APPBP2, a GAM336631 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336631 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336631 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336631 is therefore inhibition of BACE2, a GAM336631 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336631 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336631 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336631 is therefore inhibition of FHL2, a GAM336631 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336631 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336631 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336631 is therefore inhibition of IGF1, a GAM336631 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336631 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336631 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336631 is therefore inhibition of MME, a GAM336631 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336631 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336631 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336631 is therefore inhibition of PRND, a GAM336631 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336632 GSN TAATTTCCTGGTAGT GSN (Accession NM_000177.2) is a GAM336632 target gene. GSN A A

GATGACA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336632 is therefore inhibition of GSN. Accordingly, utilities of GAM336632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSN.

GAM336633 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336633 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336633 is therefore inhibition of APPBP2, a GAM336633 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336633 CTSB CACTGCACTCCAGCC CTSB (Accession NM_147782.1) is another GAM336633 target gene. A A

TGGGCGA CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336633 is therefore inhibition of CTSB. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336633 CTSK CACTGCACTCCAGCC CTSK (Accession NM_000396.2) is another GAM336633 target gene. A A

TGGGCGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336633 is therefore inhibition of CTSK. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336633 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCGA another GAM336633 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336633 is therefore inhibition of FHL2, a GAM336633 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336633 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCGA NM_000618.2) is another GAM336633 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336633 is therefore inhibition of IGF1, a GAM336633 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336633 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCGA another GAM336633 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336633 is therefore inhibition of PRND, a GAM336633 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336634 ACE TGGGCTCATTTTGCA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GTGATTT (ACE, Accession NM_152831.1) is a GAM336634 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336634 is therefore inhibition of ACE, a GAM336634 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336634 GSN TGGGCTCATTTTGCA GSN (Accession NM_000177.2) is another GAM336634 target gene. A A

GTGATTT GSN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GSN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336634 is therefore inhibition of GSN. Accordingly, utilities of GAM336634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GSN.

GAM336637 FPRL1 GGGCGTGATGTCAGC FPRL1 (Accession NM_001462.1) is a GAM336637 target gene. FPRL1 A A

CAGAGTC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336637 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336637 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336637 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336637 IL1A GGGCGTGATGTCAGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

CAGAGTC GAM336637 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336637 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336637 is therefore inhibition of IL1A, a GAM336637 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336637 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336638 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336638 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336638 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336638 is therefore inhibition of APP. Accordingly, utilities of GAM336638 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336639 ADAMTS5 ATTCAAGATAAGGGT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CTGGGAG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336639 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336639 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336639 is therefore inhibition of ADAMTS5, a GAM336639 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336639 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336639 BACE2 ATTCAAGATAAGGGT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

CTGGGAG NM_138992.1) is another GAM336639 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336639 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336639 is therefore inhibition of BACE2, a GAM336639 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336639 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336640 BACE TGGAATGAGGAAGGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TGTGGTC is a GAM336640 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336640 is therefore inhibition of BACE, a GAM336640 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336640 TNF TGGAATGAGGAAGGG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

TGTGGTC Accession NM_000594.2) is another GAM336640 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336640 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336640 is therefore inhibition of TNF, a GAM336640 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM336640 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336642 MAPT GTGAGGCAGGAACCC Microtubule- associated Protein Tau (MAPT, Accession A A

CAAAGCC NM_173727.1) is a GAM336642 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336642 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

A function of GAM336642 is therefore inhibition of MAPT, a GAM336642 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336642 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336642 PSEN2 GTGAGGCAGGAACCC PSEN2 (Accession NM_012486.1) is another GAM336642 target gene. A A

CAAAGCC PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336642 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336642 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336642 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336643 MAPT GTGAGGCAGGAACCC Microtubule- associated Protein Tau (MAPT, Accession A A

CAAAGCC NM_173727.1) is a GAM336643 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336643 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336643 is therefore inhibition of MAPT, a GAM336643 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336643 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336643 PSEN2 GTGAGGCAGGAACCC PSEN2 (Accession NM_012486.1) is another GAM336643 target gene. A A

CAAAGCC PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336643 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336643 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336643 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336646 DLST AGGCCTTTTTGGGAA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGACAG oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336646 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336646 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336646 is therefore inhibition of DLST, a GAM336646 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336646 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336646 GFAP AGGCCTTTTTGGGAA GFAP (Accession NM_002055.2) is another GAM336646 target gene. A A

GAGACAG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336646 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336646 is therefore inhibition of GFAP. Accordingly, utilities of GAM336646 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336646 HD AGGCCTTTTTGGGAA HD (Accession NM_002111.3) is another GAM336646 target gene. HD A A

GAGACAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336646

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336646 is therefore inhibition of HD. Accordingly, utilities of GAM336646 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336646 MME AGGCCTTTTTGGGAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GAGACAG enkephalinase, (MME, Accession NM_007288.1) is another GAM336646 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336646 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336646 is therefore inhibition of MME, a GAM336646 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336646 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336651 ABCD1 AGGCAGGTGGGTGTA ABCD1 (Accession NM_000033.2) is a GAM336651 target gene. ABCD1 A A
TGGGTCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336651 is therefore inhibition of ABCD1. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM336651 APBA2 AGGCAGGTGGGTGTA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
TGGGTCT 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM336651 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336651 is therefore inhibition of

APBA2, a GAM336651 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336651 DHCR24 AGGCAGGTGGGTGTA A A TGGGTCT 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM336651 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336651 is therefore inhibition of DHCR24, a GAM336651 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336651 FOS AGGCAGGTGGGTGTA A A TGGGTCT V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is another GAM336651 target gene. FOS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336651 is therefore inhibition of FOS, a GAM336651 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336651 GLUL AGGCAGGTGGGTGTA A A TGGGTCT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM336651 target gene. GLUL BINDING SITE is

a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336651 is therefore inhibition of GLUL, a GAM336651 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336651 HD AGGCAGGTGGGTGTA HD (Accession NM_002111.3) is another GAM336651 target gene. HD A A

TGGGTCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336651 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336651 is therefore inhibition of HD. Accordingly, utilities of GAM336651 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336652 ACE GAGGTTTGAGCCTTC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TCCTGCT (ACE, Accession NM_152831.1) is a GAM336652 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336652 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336652 is therefore inhibition of ACE, a GAM336652 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336652 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336652 CASP3 GAGGTTTGAGCCTTC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

TCCTGCT Accession NM_032991.1) is another GAM336652 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336652 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336652 is therefore inhibition of CASP3, a GAM336652 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336652 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336652 CRAT GAGGTTTGAGCCTTC Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A

TCCTGCT another GAM336652 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336652 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336652 is therefore inhibition of CRAT, a GAM336652 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336652 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336652 IAPP GAGGTTTGAGCCTTC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TCCTGCT another GAM336652 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336652 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336652 is therefore inhibition of IAPP, a GAM336652 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore

is associated with Alzheimer. Accordingly, utilities of GAM336652 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336652 NGB GAGGTTTGAGCCTTC TCCTGCT A A Neuroglobin (NGB, Accession NM_021257.2) is another GAM336652 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336652 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336652 is therefore inhibition of NGB, a GAM336652 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336652 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336653 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336653 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336653 is therefore inhibition of APPBP2, a GAM336653 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336653 BACE2 ACTGCACTCCAGCCT GGGCAAC A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336653 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336653 is therefore inhibition of BACE2, a GAM336653 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336653 FHL2 A ACTGCACTCCAGCCT A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336653 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336653 is therefore inhibition of FHL2, a GAM336653 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336653 IGF1 A ACTGCACTCCAGCCT A GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336653 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336653 is therefore inhibition of IGF1, a GAM336653 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336653 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336653 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336653 is therefore inhibition of MME, a GAM336653 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336653 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336653 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336653 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336653 is therefore inhibition of PRND, a GAM336653 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336653 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336656 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336656 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM336656 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336656 is therefore inhibition of APP. Accordingly, utilities of GAM336656 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336657 APBB2 CTAGCACAGTGCTTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A GCACACA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336657 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336657 is therefore inhibition of APBB2, a GAM336657 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336657 NGB CTAGCACAGTGCTTG Neuroglobin (NGB, Accession NM_021257.2) is another GAM336657 A A GCACACA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336657 is therefore inhibition of NGB, a GAM336657 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336657 PLAU CTAGCACAGTGCTTG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A GCACACA is another GAM336657 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336657 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336657 is therefore inhibition of PLAU, a GAM336657 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM336657 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336658 ADAMTS5 AGGGCACACGTCTCT A Disintegrin- like and Metalloprotease (reprolysin type) with A A
CTGAATT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336658 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336658 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336658 is therefore inhibition of ADAMTS5, a GAM336658 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336658 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336658 IGF1 AGGGCACACGTCTCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CTGAATT NM_000618.2) is another GAM336658 target gene. IGF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336658 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336658 is therefore inhibition of IGF1, a GAM336658 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336658 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336659 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336659 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336659 is therefore inhibition of APPBP2, a GAM336659 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336659 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336659 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336659 is therefore inhibition of BACE2, a GAM336659 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336659 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336659 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA A A

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336659 is therefore inhibition of FHL2, a GAM336659 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336659 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336659 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336659 is therefore inhibition of IGF1, a GAM336659 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336659 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336659 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336659 is therefore inhibition of MME, a GAM336659 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336659 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336659 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336659 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336659 is therefore inhibition of PRND, a GAM336659 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336659 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336660 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336660 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336660 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336660 is therefore inhibition of APP. Accordingly, utilities of GAM336660 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336661 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336661 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336661 is therefore inhibition of APPBP2, a GAM336661 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336661 BACE2 CATTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336661 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336661 is therefore inhibition of BACE2, a GAM336661 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336661 FHL2 CATTGCACTCCAGCC TGGGCAA A A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336661 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336661 is therefore inhibition of FHL2, a GAM336661 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336661 HD CATTGCACTCCAGCC HD A A TGGGCAA HD (Accession NM_002111.3) is another GAM336661 target gene. BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336661 is therefore inhibition of HD. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336661 IGF1 CATTGCACTCCAGCC A A TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336661 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336661 is therefore inhibition of IGF1, a GAM336661 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336661 PRND CATTGCACTCCAGCC A A TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336661 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336661 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336661 is therefore inhibition of PRND, a GAM336661 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336661 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336662 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336662 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336662 is therefore inhibition of APPBP2, a GAM336662 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336662 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336662 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336662 is therefore inhibition of BACE2, a GAM336662 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336662 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336662 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336662 is therefore inhibition of FHL2, a GAM336662 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336662 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336662 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336662 is therefore inhibition of HD. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336662 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336662 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336662 is therefore inhibition of IGF1, a GAM336662 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336662 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336662 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336662 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336662 is therefore inhibition of PRND, a GAM336662 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336662 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336663 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336663 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336663 is therefore inhibition of APPBP2, a GAM336663 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336663 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336663 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336663 is therefore inhibition of BACE2, a GAM336663 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336663 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336663 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336663 is therefore inhibition of FHL2, a GAM336663 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336663 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336663 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336663 is therefore inhibition of HD. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336663 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336663 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336663 is therefore inhibition of IGF1, a GAM336663 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336663 PRND CATTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336663 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336663 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336663 is therefore inhibition of PRND, a GAM336663 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336663 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336664 APPBP2 CATTGCACTCCAGCC TGGGCAA A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336664 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336664 is therefore inhibition of APPBP2, a GAM336664 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336664 BACE2 CATTGCACTCCAGCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336664 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336664 is therefore inhibition of BACE2, a GAM336664 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336664 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336664 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336664 is therefore inhibition of FHL2, a GAM336664 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336664 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336664 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336664 is therefore inhibition of HD. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336664 IGF1 A A CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession

TGGGCAA NM_000618.2) is another GAM336664 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336664 is therefore inhibition of IGF1, a GAM336664 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336664 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336664 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336664 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336664 is therefore inhibition of PRND, a GAM336664 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336664 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336665 BACE2 TGTGATAGTTCTTTT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGAGGC NM_138991.1) is a GAM336665 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336665 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336665 is therefore inhibition of BACE2,

a GAM336665 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336665 CAV1 TGTGATAGTTCTTTT GGAGGC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM336665 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336665 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336665 is therefore inhibition of CAV1, a GAM336665 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336665 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336669 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM336669 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336669 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336669 is therefore inhibition of APP. Accordingly, utilities of GAM336669 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336670 FPRL1 GTAAGGCTGGCATTA GGGTGAG FPRL1 (Accession NM_001462.1) is a GAM336670 target gene. FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336670 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336670 is therefore inhibition of FPRL1.

Accordingly, utilities of GAM336670 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336671 FPRL1 GTAAGGCTGGCATTA FPRL1 (Accession NM_001462.1) is a GAM336671 target gene. FPRL1 A A

GGGTGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336671 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336671 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336671 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336672 FPRL1 GTAAGGCTGGCATTA FPRL1 (Accession NM_001462.1) is a GAM336672 target gene. FPRL1 A A

GGGTGAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336672 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336672 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336672 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336673 ARHA GTTCTGGAGCCCATA Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

CTCACCA is a GAM336673 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336673 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336673 is therefore inhibition of ARHA, a GAM336673 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336673 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336673 AVP GTTCTGGAGCCCATA AVP (Accession NM_000490.2) is another GAM336673 target gene. A A

CTCACCA AVP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336673 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336673 is therefore inhibition of AVP. Accordingly, utilities of GAM336673 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336674 APOC1 TTCCAGTTCTCAGCA Apolipoprotein C- I (APOC1, Accession NM_001645.2) is a A A
CAGCGCT GAM336674 target gene. APOC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336674 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336674 is therefore inhibition of APOC1, a GAM336674 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM336674 IL1B TTCCAGTTCTCAGCA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A
CAGCGCT GAM336674 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336674 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336674 is therefore inhibition of IL1B, a GAM336674 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336674 PRNP TTCCAGTTCTCAGCA Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A
CAGCGCT Strausler- (PRNP, Accession NM_000311.1) is another GAM336674 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336674 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336674 is therefore inhibition of PRNP, a GAM336674 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336674 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336675 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGTGAC a GAM336675 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336675 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336675 is therefore inhibition of FHL2, a GAM336675 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336675 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336675 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTGAC NM_000618.2) is another GAM336675 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336675 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336675 is therefore inhibition of IGF1, a GAM336675 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336675 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336675 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM336675 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336675 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336675 is therefore inhibition of PRND, a GAM336675 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336675 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336676 ADAM17 CCAAAGTGCTGGCGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TACAGGT factor, (ADAM17, Accession NM_021832.1) is a GAM336676 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336676 is therefore inhibition of ADAM17, a GAM336676 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336676 APPBP2 CCAAAGTGCTGGCGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TACAGGT Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336676 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of APPBP2, a GAM336676 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336676 CTSK CCAAAGTGCTGGCGT CTSK (Accession NM_000396.2) is another GAM336676 target gene. A A

TACAGGT CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of CTSK. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336676 GFAP CCAAAGTGCTGGCGT GFAP (Accession NM_002055.2) is another GAM336676 target gene. A A

TACAGGT GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of GFAP. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336676 HTR2A CCAAAGTGCTGGCGT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

TACAGGT NM_000621.1) is another GAM336676 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of HTR2A, a GAM336676 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336676 IAPP CCAAAGTGCTGGCGT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A TACAGGT another GAM336676 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of IAPP, a GAM336676 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336676 MTNR1A CCAAAGTGCTGGCGT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A TACAGGT another GAM336676 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of MTNR1A, a GAM336676 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The

function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336676 PLAU CCAAAGTGCTGGCGT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1)
A A

TACAGGT is another GAM336676 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of PLAU, a GAM336676 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336676 TGFB1 CCAAAGTGCTGGCGT TGFB1 (Accession NM_000660.1) is another GAM336676 target gene. A A

TACAGGT TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336676 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336676 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336676 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336677 HTR2C ACACTTGTCTGCTTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A

CTACACT NM_000868.1) is a GAM336677 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336677 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336677 is therefore inhibition of HTR2C, a GAM336677 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336677 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336681 APBA2 ACTGCACTCCAGCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGGTGGC 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM336681 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336681 is therefore inhibition of APBA2, a GAM336681 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336681 APLP1 ACTGCACTCCAGCCT Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A

GGGTGGC NM_005166.2) is another GAM336681 target gene. APLP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of APLP1, a GAM336681 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336681 CRAT ACTGCACTCCAGCCT Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is A A

GGGTGGC another GAM336681 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of CRAT, a GAM336681 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336681 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGGC another GAM336681 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of FHL2, a GAM336681 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336681 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGGC NM_000618.2) is another GAM336681 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of IGF1, a GAM336681 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336681 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTGGC another GAM336681 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of PRND, a GAM336681 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336681 PSEN1 ACTGCACTCCAGCCT PSEN1 (Accession NM_007318.1) is another GAM336681 target gene. A A

GGGTGGC PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336681 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336681 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336681 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336683 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336683 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336683 is therefore inhibition of APPBP2, a GAM336683 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336683 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336683 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336683 is therefore inhibition of BACE2, a GAM336683 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336683 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336683 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336683 is therefore inhibition of FHL2, a GAM336683 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336683 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336683 target gene. IGF1 BINDING SITE is A A

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336683 is therefore inhibition of IGF1, a GAM336683 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336683 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336683 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336683 is therefore inhibition of MME, a GAM336683 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336683 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336683 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336683 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336683 is therefore inhibition of PRND, a GAM336683 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336683 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336685 CRH CTGAATAGAACAGAA Corticotropin Releasing Hormone (CRH, Accession NM_000756.1) is A A

GAGCAGC a GAM336685 target gene. CRH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336685 is therefore inhibition of CRH, a GAM336685 target gene which regulates the release of corticotropin from pituitary gland. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRH.The function of CRH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1976.

GAM336685 DLST CTGAATAGAACAGAA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGCAGC oxo- glutarat (DLST, Accession NM_001933.2) is another GAM336685 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336685 is therefore inhibition of DLST, a GAM336685 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336685 IL1B CTGAATAGAACAGAA Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A

GAGCAGC GAM336685 target gene. IL1B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336685 is therefore inhibition of IL1B, a GAM336685 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336685 TRPM2 CTGAATAGAACAGAA TRPM2 (Accession NM_003307.1) is another GAM336685 target gene. A A

GAGCAGC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336685 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336685 is therefore inhibition of TRPM2, a GAM336685 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336685 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336686 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336686 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336686 is therefore inhibition of APPBP2, a GAM336686 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM336686 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM336686 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336686 is therefore inhibition of BACE2, a GAM336686 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336686 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336686 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336686 is therefore inhibition of FHL2, a GAM336686 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336686 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336686 target gene. HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336686 is therefore inhibition of HD. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336686 IGF1 CATTGCACTCCAGCC A A TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336686 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336686 is therefore inhibition of IGF1, a GAM336686 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336686 PRND CATTGCACTCCAGCC A A TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336686 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336686 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336686 is therefore inhibition of PRND, a GAM336686 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336686 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336689 DSCR1 GGCACCATCTCAGCT A A CACTGGA Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM336689 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336689 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336689 is therefore inhibition of DSCR1, a GAM336689 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM336689 HD GGCACCATCTCAGCT HD (Accession NM_002111.3) is another GAM336689 target gene. HD A A

CACTGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336689 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336689 is therefore inhibition of HD. Accordingly, utilities of GAM336689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336689 MPO GGCACCATCTCAGCT Myeloperoxidase (MPO, Accession NM_000250.1) is another A A

CACTGGA GAM336689 target gene. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336689 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336689 is therefore inhibition of MPO, a GAM336689 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336689 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM336690 ACE TTGCCTAGGCCGGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGCAGTG (ACE, Accession NM_152831.1) is a GAM336690 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336690 is therefore inhibition of ACE, a GAM336690 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336690 IAPP TTGCCTAGGCCGGAG A A TGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM336690 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336690 is therefore inhibition of IAPP, a GAM336690 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336690 SNCB TTGCCTAGGCCGGAG A A TGCAGTG Synuclein, Beta (SNCB, Accession NM_003085.2) is another GAM336690 target gene. SNCB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336690 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336690 is therefore inhibition of SNCB, a GAM336690 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336690 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336691 IGF1 CAGAGAGGTTCAATG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCTTACT NM_000618.2) is a GAM336691 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336691 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336691 is therefore inhibition of IGF1, a GAM336691 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336691 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336697 FHL2 ACTGTACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGTGAC a GAM336697 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336697 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336697 is therefore inhibition of FHL2, a GAM336697 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336697 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336697 IGF1 ACTGTACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTGAC NM_000618.2) is another GAM336697 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336697 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336697 is therefore inhibition of IGF1, a GAM336697 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336697 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336697 PRND ACTGTACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM336697 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336697 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336697 is therefore inhibition of PRND, a GAM336697 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336697 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336699 CASP3 GCCTCAGTTGTGGCC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A
AGGGATT Accession NM_004346.2) is a GAM336699 target gene. CASP3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336699 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336699 is therefore inhibition of CASP3, a GAM336699 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336699 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336701 ADAMTS5 ATGGATATTTTTGAT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GCCCAGA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336701 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336701 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336701 is therefore inhibition of ADAMTS5, a GAM336701 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336701 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336701 TNFRSF6 ATGGATATTTTTGAT TNFRSF6 (Accession NM_152876.1) is another GAM336701 target A A

GCCCAGA gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336701 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336701 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336701 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336702 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336702 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336702 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336702 is therefore inhibition of APP. Accordingly, utilities of GAM336702 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336703 APPBP2 CACTGCACTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGTGAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336703 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336703 is therefore inhibition of APPBP2, a GAM336703 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336703 FHL2 CACTGCACTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAC another GAM336703 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336703 is therefore inhibition of FHL2, a GAM336703 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336703 IGF1 CACTGCACTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAC NM_000618.2) is another GAM336703 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336703 is therefore inhibition of IGF1, a GAM336703 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336703 PRND CACTGCACTCAGCCT GGGTGAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336703 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336703 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336703 is therefore inhibition of PRND, a GAM336703 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336703 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336704 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336704 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336704 is therefore inhibition of APPBP2, a GAM336704 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336704 BACE2 ACTGCACTCCAGCCT GGGCAAC A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336704 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336704 is therefore inhibition of BACE2, a GAM336704 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336704 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336704 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336704 is therefore inhibition of FHL2, a GAM336704 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336704 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336704 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336704 is therefore inhibition of IGF1, a GAM336704 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336704 MME ACTGCACTCCAGCCT GGGCAAC A A

Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336704 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336704 is therefore inhibition of MME, a GAM336704 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336704 PRND ACTGCACTCCAGCCT GGGCAAC A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336704 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336704 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336704 is therefore inhibition of PRND, a GAM336704 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336704 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336705 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336705 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and

secondary structure complementarity to the nucleotide sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336705 is therefore inhibition of APPBP2, a GAM336705 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336705 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A GGGCAAC NM_012105.3) is another GAM336705 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336705 is therefore inhibition of BACE2, a GAM336705 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336705 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGCAAC another GAM336705 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336705 is therefore inhibition of FHL2, a GAM336705 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336705 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336705 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336705 is therefore inhibition of IGF1, a GAM336705 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336705 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336705 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336705 is therefore inhibition of MME, a GAM336705 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336705 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336705 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide

sequence of GAM336705 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336705 is therefore inhibition of PRND, a GAM336705 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336705 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336706 NCSTN TCCAGTGATTCATTT NCSTN (Accession NM_015331.1) is a GAM336706 target gene. NCSTN A A

GGTTGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336706 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336706 is therefore inhibition of NCSTN, a GAM336706 target gene which has a central role in presenilin-mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp- 1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336706 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336707 AVP TGTGGCAGAAGGCTC AVP (Accession NM_000490.2) is a GAM336707 target gene. AVP A A

TGGATTA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336707 is therefore inhibition of AVP. Accordingly, utilities of GAM336707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336707 BACE TGTGGCAGAAGGCTC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

TGGATTA is another GAM336707 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and

secondary structure complementarity to the nucleotide sequence of GAM336707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336707 is therefore inhibition of BACE, a GAM336707 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336707 DHCR24 TGTGGCAGAAGGCTC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGATTA NM_014762.1) is another GAM336707 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336707 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336707 is therefore inhibition of DHCR24, a GAM336707 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336707 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336709 APBB2 ACAGCAGTCCAGCCT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGGTGAC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336709 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336709 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336709 is therefore inhibition of APBB2, a GAM336709 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336709 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM336709 FHL2 ACAGCAGTCCAGCCT GGGTGAC A A

Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336709 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336709 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336709 is therefore inhibition of FHL2, a GAM336709 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336709 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336709 IGF1 ACAGCAGTCCAGCCT GGGTGAC A A

Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336709 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336709 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336709 is therefore inhibition of IGF1, a GAM336709 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336709 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336710 CAV1 GGCAAAAAAATAGAG CAGAGGG A A

Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM336710 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336710 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336710 is therefore inhibition of CAV1, a GAM336710 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336710 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336710 IGF1 GGCAAAAAAATAGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CAGAGGG NM_000618.2) is another GAM336710 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336710 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336710 is therefore inhibition of IGF1, a GAM336710 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336710 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336713 MME TGGGAAACATCCAGC Membrane Metallo- endopeptidase (neutral endopeptidase, A A

ACATACT enkephalinase, (MME, Accession NM_000902.2) is a GAM336713 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336713 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336713 is therefore inhibition of MME, a GAM336713 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336713 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336713 PRND TGGGAAACATCCAGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

ACATACT another GAM336713 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336713 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336713 is therefore inhibition of PRND, a GAM336713 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336713 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336715 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336715 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336715 is therefore inhibition of APPBP2, a GAM336715 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336715 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336715 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336715 is therefore inhibition of

BACE2, a GAM336715 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336715 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336715 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336715 is therefore inhibition of FHL2, a GAM336715 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336715 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336715 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336715 is therefore inhibition of HD. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336715 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336715 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336715 is therefore inhibition of IGF1, a GAM336715 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336715 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336715 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336715 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336715 is therefore inhibition of PRND, a GAM336715 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336715 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336716 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336716 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336716 is therefore inhibition of APPBP2, a GAM336716 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM336716 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM336716 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336716 is therefore inhibition of BACE2, a GAM336716 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336716 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM336716 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336716 is therefore inhibition of FHL2, a GAM336716 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336716 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336716 target gene. HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336716 is therefore inhibition of HD. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336716 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336716 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336716 is therefore inhibition of IGF1, a GAM336716 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336716 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336716 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336716 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336716 is therefore inhibition of PRND, a GAM336716 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336716 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336717 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336717 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336717 is therefore inhibition of APPBP2, a GAM336717 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336717 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336717 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336717 is therefore inhibition of BACE2, a GAM336717 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336717 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336717 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336717 is therefore inhibition of FHL2, a GAM336717 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336717 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336717 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336717 is therefore inhibition of HD. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336717 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336717 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336717 is therefore inhibition of IGF1, a GAM336717 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336717 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336717 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336717 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336717 is therefore inhibition of

PRND, a GAM336717 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336717 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336718 ACE TGTGAAGGAGGAAGG GAGGAGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM336718 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336718 is therefore inhibition of ACE, a GAM336718 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336718 ACHE TGTGAAGGAGGAAGG GAGGAGC Acetylcholinesterase (YT blood group) (ACHE, Accession NM_015831.1) is another GAM336718 target gene. ACHE BINDING SITE1 and ACHE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ACHE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE1 and ACHE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336718 is therefore inhibition of ACHE, a GAM336718 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM336718 BLMH TGTGAAGGAGGAAGG GAGGAGC Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is another GAM336718 target gene. BLMH BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336718 is therefore inhibition of BLMH, a GAM336718 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM336718 CAV1 TGTGAAGGAGGAAGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
GAGGAGC NM_001753.3) is another GAM336718 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336718 is therefore inhibition of CAV1, a GAM336718 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336718 DHCR24 TGTGAAGGAGGAAGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A
GAGGAGC NM_014762.1) is another GAM336718 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336718 is therefore inhibition of DHCR24, a GAM336718 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336718 MME TGTGAAGGAGGAAGG GAGGAGC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336718 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336718 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336718 is therefore inhibition of MME, a GAM336718 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336718 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336719 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336719 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336719 is therefore inhibition of APPBP2, a GAM336719 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336719 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336719 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or A A

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336719 is therefore inhibition of BACE2, a GAM336719 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336719 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336719 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336719 is therefore inhibition of FHL2, a GAM336719 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336719 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336719 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336719 is therefore inhibition of HD. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336719 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336719 target gene. IGF1 BINDING SITE1

and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336719 is therefore inhibition of IGF1, a GAM336719 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336719 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336719 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336719 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336719 is therefore inhibition of PRND, a GAM336719 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336719 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336720 CTSB TGCACCACTGCACTC CTSB (Accession NM_147782.1) is a GAM336720 target gene. CTSB A A

TAACCTG BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336720 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336720 is therefore inhibition of CTSB. Accordingly, utilities of GAM336720 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with CTSB.

GAM336720 FHL2 TGCACCACTGCACTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TAACCTG another GAM336720 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336720 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336720 is therefore inhibition of FHL2, a GAM336720 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336720 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336720 IGF1 TGCACCACTGCACTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TAACCTG NM_000618.2) is another GAM336720 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336720 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336720 is therefore inhibition of IGF1, a GAM336720 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336720 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336720 PRND TGCACCACTGCACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TAACCTG another GAM336720 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336720 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336720 is therefore inhibition of PRND, a GAM336720 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336720 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336722 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336722 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336722 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336722 is therefore inhibition of APP. Accordingly, utilities of GAM336722 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336723 APPBP2 TTGCACTCCAGCCTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGTGACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336723 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336723 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336723 is therefore inhibition of APPBP2, a GAM336723 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336723 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336723 FHL2 TTGCACTCCAGCCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGTGACA another GAM336723 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336723 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336723 is therefore inhibition of FHL2, a GAM336723 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336723 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336723 IGF1 TTGCACTCCAGCCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGTGACA NM_000618.2) is another GAM336723 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336723 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336723 is therefore inhibition of IGF1, a GAM336723 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336723 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336723 PRND TTGCACTCCAGCCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGTGACA another GAM336723 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336723 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336723 is therefore inhibition of PRND, a GAM336723 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336723 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336723 TNFRSF5 TTGCACTCCAGCCTG TNFRSF5 (Accession NM_152854.1) is another GAM336723 target A A

GGTGACA gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336723 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336723 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336723 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336727 IL1B CTGGCTCTAATAACC TGAGCTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is a GAM336727 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336727 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336727 is therefore inhibition of IL1B, a GAM336727 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336727 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336727 NOTCH1 CTGGCTCTAATAACC TGAGCTT Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM336727 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336727 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336727 is therefore inhibition of NOTCH1, a GAM336727 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336727 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336728 ACE TCAAGCAATTCTCGT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GCCTCAG (ACE, Accession NM_152831.1) is a GAM336728 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336728 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336728 is therefore inhibition of ACE, a GAM336728 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336728 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336729 BACE2 GAGAGAGGTAGAGGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GAGCAGA NM_138992.1) is a GAM336729 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336729 is therefore inhibition of BACE2, a GAM336729 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336729 DLST GAGAGAGGTAGAGGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGCAGA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM336729 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336729 is therefore inhibition of

DLST, a GAM336729 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336729 GFAP GAGAGAGGTAGAGGG GFAP (Accession NM_002055.2) is another GAM336729 target gene. A A

GAGCAGA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336729 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336729 is therefore inhibition of GFAP. Accordingly, utilities of GAM336729 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336730 HD CATCTCAGTCTATGT HD (Accession NM_002111.3) is a GAM336730 target gene. HD A A

CCTTGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336730 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336730 is therefore inhibition of HD. Accordingly, utilities of GAM336730 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336730 PSEN2 CATCTCAGTCTATGT PSEN2 (Accession NM_012486.1) is another GAM336730 target gene. A A

CCTTGCT PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336730 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336730 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336730 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336731 IGF1 AGATGGAGAAGTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTCAGAT NM_000618.2) is a GAM336731 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336731 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336731 is therefore inhibition of IGF1, a GAM336731 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336731 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336731 S100B AGATGGAGAAGTGTT S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

TTCAGAT NM_006272.1) is another GAM336731 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336731 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336731 is therefore inhibition of S100B, a GAM336731 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336731 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336732 IGF1 AGATGGAGAAGTGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTCAGAT NM_000618.2) is a GAM336732 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336732 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336732 is therefore inhibition of IGF1, a GAM336732 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity

and therefore is associated with Alzheimer. Accordingly, utilities of GAM336732 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336732 S100B AGATGGAGAAGTGTT S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A TTCAGAT NM_006272.1) is another GAM336732 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336732 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336732 is therefore inhibition of S100B, a GAM336732 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336732 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336734 GYPA GGCAGATGGGACTCT Glycophorin A (includes MN blood group) (GYPA, Accession A A GTGCCCA NM_002099.2) is a GAM336734 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336734 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336734 is therefore inhibition of GYPA, a GAM336734 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336734 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336736 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336736 target gene. APP A A GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM336736 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336736 is therefore inhibition of APP. Accordingly, utilities of GAM336736 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336738 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336738 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336738 is therefore inhibition of APPBP2, a GAM336738 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336738 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336738 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336738 is therefore inhibition of BACE2, a GAM336738 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336738 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336738 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336738 is therefore inhibition of FHL2, a GAM336738 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336738 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336738 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336738 is therefore inhibition of IGF1, a GAM336738 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336738 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336738 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336738 is therefore inhibition of

MME, a GAM336738 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336738 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336738 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336738 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336738 is therefore inhibition of PRND, a GAM336738 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336738 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336739 IGF1 TAGCAGATCTGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TCCTATG NM_000618.2) is a GAM336739 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336739 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336739 is therefore inhibition of IGF1, a GAM336739 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336739 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336740 BACE2 GTTTTGTTGTCTCTG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGTTGTA NM_012105.3) is a GAM336740 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336740 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336740 is therefore inhibition of BACE2, a GAM336740 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336740 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336743 GYPA TATGAATGTAAGGAA TGTGGGA A A Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is a GAM336743 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336743 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336743 is therefore inhibition of GYPA, a GAM336743 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336743 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336743 IGF1 TATGAATGTAAGGAA TGTGGGA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336743 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336743 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336743 is therefore inhibition of IGF1, a GAM336743 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336743 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336743 MME TATGAATGTAAGGAA TGTGGGA A A Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is another GAM336743 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336743 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336743 is therefore inhibition of MME, a GAM336743 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336743 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336743 VLDLR TATGAATGTAAGGAA TGTGGGA A A Very Low Density Lipoprotein Receptor (VLDLR, Accession NM_003383.1) is another GAM336743 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336743 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336743 is therefore inhibition of VLDLR, a GAM336743 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM336743 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336744 GYPA TATGAATGTAAGGAA TGTGGGA A A Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is a GAM336744 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336744 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336744 is therefore inhibition of GYPA, a GAM336744 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336744 IGF1 TATGAATGTAAGGAA A
A
TGTGGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336744 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336744 is therefore inhibition of IGF1, a GAM336744 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336744 MME TATGAATGTAAGGAA A
A
TGTGGGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is another GAM336744 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336744 is therefore inhibition of MME, a GAM336744 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336744 VLDLR TATGAATGTAAGGAA Very Low Density Lipoprotein Receptor (VLDLR, Accession A A
TGTGGGA NM_003383.1) is another GAM336744 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336744 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336744 is therefore inhibition of VLDLR, a GAM336744 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM336744 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336745 GYPA TATGAATGTAAGGAA Glycophorin A (includes MN blood group) (GYPA, Accession A A
TGTGGGA NM_002099.2) is a GAM336745 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336745 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336745 is therefore inhibition of GYPA, a GAM336745 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336745 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336745 IGF1 TATGAATGTAAGGAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGTGGGA NM_000618.2) is another GAM336745 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336745 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336745 is therefore inhibition of IGF1, a GAM336745 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336745 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336745 MME TATGAATGTAAGGAA TGTGGGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is another GAM336745 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336745 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336745 is therefore inhibition of MME, a GAM336745 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336745 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336745 VLDLR TATGAATGTAAGGAA TGTGGGA Very Low Density Lipoprotein Receptor (VLDLR, Accession NM_003383.1) is another GAM336745 target gene. VLDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VLDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of VLDLR BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336745 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336745 is therefore inhibition of VLDLR, a GAM336745 target gene which may play a crucial role in triglyceride metabolism and therefore is associated with Alzheimer. Accordingly, utilities of GAM336745 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with VLDLR.The function of VLDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336746 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336746 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target A A

binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336746 is therefore inhibition of APPBP2, a GAM336746 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336746 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336746 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336746 is therefore inhibition of BACE2, a GAM336746 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336746 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336746 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336746 is therefore inhibition of FHL2, a GAM336746 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336746 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336746 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336746 is therefore inhibition of IGF1, a GAM336746 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336746 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336746 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336746 is therefore inhibition of MME, a GAM336746 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336746 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336746 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336746 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336746 is therefore inhibition of PRND, a GAM336746 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336746 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336747 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336747 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336747 is therefore inhibition of APPBP2, a GAM336747 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336747 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336747 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336747 is therefore inhibition of BACE2, a GAM336747 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336747 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336747 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336747 is therefore inhibition of FHL2, a GAM336747 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336747 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336747 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336747 is therefore inhibition of IGF1, a GAM336747 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336747 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336747 target gene. MME BINDING SITE is a target binding site found in the

5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336747 is therefore inhibition of MME, a GAM336747 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336747 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336747 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336747 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336747 is therefore inhibition of PRND, a GAM336747 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336747 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336749 APBB2 CATAAAATCAGAAAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
TATTACT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336749 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336749 is therefore inhibition of APBB2, a GAM336749 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336749 CNTF CATAAAATCAGAAAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

TATTACT another GAM336749 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336749 is therefore inhibition of CNTF, a GAM336749 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336749 NCKAP1 CATAAAATCAGAAAG NCKAP1 (Accession NM_013436.2) is another GAM336749 target A A

TATTACT gene. NCKAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336749 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336749 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM336749 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM336750 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336750 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336750 is therefore inhibition of APPBP2,

a GAM336750 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336750 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336750 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336750 is therefore inhibition of BACE2, a GAM336750 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336750 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336750 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336750 is therefore inhibition of FHL2, a GAM336750 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336750 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336750 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336750 is therefore inhibition of IGF1, a GAM336750 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336750 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336750 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336750 is therefore inhibition of MME, a GAM336750 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336750 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336750 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336750 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336750 is therefore inhibition of PRND, a GAM336750 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336750 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336751 DLST ACTGCACTCCAACCA GGCTGAC A A

Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336751 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336751 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336751 is therefore inhibition of DLST, a GAM336751 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336751 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336751 FHL2 ACTGCACTCCAACCA GGCTGAC A A

Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336751 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336751 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336751 is therefore inhibition of FHL2, a GAM336751 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336751 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336751 IGF1 ACTGCACTCCAACCA GGCTGAC A A

Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336751 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336751 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336751 is therefore inhibition of IGF1, a GAM336751 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336751 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336752 APBB2 TTCTGGGTTTTTGTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GGTTTGC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336752 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336752 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336752 is therefore inhibition of APBB2, a GAM336752 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336752 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336752 PIN1 TTCTGGGTTTTTGTG Protein (peptidyl- prolyl cis/trans isomerase) NIMA- A A
GGTTTGC interacting 1 (PIN1, Accession NM_006221.1) is another GAM336752 target gene. PIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PIN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336752 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336752 is therefore inhibition of PIN1, a GAM336752 target gene which intervenes in cell cycle regulation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336752 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PIN1.The function of PIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM336755 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336755 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336755 is therefore inhibition of APPBP2, a GAM336755 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336755 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336755 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336755 is therefore inhibition of BACE2, a GAM336755 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336755 FHL2 CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336755 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336755 is therefore inhibition of FHL2, a GAM336755 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336755 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336755 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336755 is therefore inhibition of HD. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336755 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336755 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336755 is therefore inhibition of IGF1, a GAM336755 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336755 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336755 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336755 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336755 is therefore inhibition of PRND, a GAM336755 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336755 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336756 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336756 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336756 is therefore inhibition of APPBP2, a GAM336756 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336756 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336756 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336756 is therefore inhibition of BACE2, a GAM336756 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336756 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336756 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336756 is therefore inhibition of FHL2, a GAM336756 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336756 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336756 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336756 is therefore inhibition of HD. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336756 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336756 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336756 is therefore inhibition of IGF1, a GAM336756 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336756 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336756 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336756 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336756 is therefore inhibition of PRND, a GAM336756 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336756 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336757 ACT GAGGTCTGTTGTTCA GAAAAAT Activator of CAMP- responsive Element Modulator (CR (ACT, Accession NM_020482.3) is a GAM336757 target gene. ACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336757 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336757 is therefore inhibition of ACT, a GAM336757 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336757 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336760 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336760 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336760 is therefore inhibition of APPBP2, a GAM336760 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336760 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336760 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336760 is therefore inhibition of BACE2, a GAM336760 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336760 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336760 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336760 is therefore inhibition of FHL2, a GAM336760 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336760 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336760 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336760 is therefore inhibition of IGF1, a GAM336760 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336760 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336760 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336760 is therefore inhibition of MME, a GAM336760 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336760 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336760 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336760 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336760 is therefore inhibition of PRND, a GAM336760 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336760 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336761 GLUL CAGAGAATGGCACAG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

CTGTCCT NM_002065.3) is a GAM336761 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336761 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336761 is therefore inhibition of GLUL, a GAM336761 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336761 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336761 TNFSF5 CAGAGAATGGCACAG TNFSF5 (Accession NM_000074.1) is another GAM336761 target A A

CTGTCCT gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336761 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336761 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336761 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336762 IAPP GTCTTGATCTCCTGA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a A A

CCTTGTG GAM336762 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336762 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336762 is therefore inhibition of IAPP, a GAM336762 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336762 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336762 IL1A GTCTTGATCTCCTGA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

CCTTGTG GAM336762 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336762 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336762 is therefore inhibition of IL1A, a GAM336762 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336762 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336763 ACE AGGGCTGTGGGTGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GCTGTGC (ACE, Accession NM_000789.2) is a GAM336763 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336763 is therefore inhibition of ACE, a GAM336763 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336763 APBB2 AGGGCTGTGGGTGTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GCTGTGC 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM336763 target gene. APBB2 BINDING SITE1 through APBB2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by APBB2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE1 through APBB2 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of APBB2, a GAM336763 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336763 ARHA AGGGCTGTGGGTGTG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

GCTGTGC is another GAM336763 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of ARHA, a GAM336763 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336763 CHAT AGGGCTGTGGGTGTG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is A A

GCTGTGC another GAM336763 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of CHAT, a GAM336763 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336763 FOS AGGGCTGTGGGTGTG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
GCTGTGC Accession NM_005252.2) is another GAM336763 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of FOS, a GAM336763 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336763 LRP1 AGGGCTGTGGGTGTG Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
GCTGTGC macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM336763 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of LRP1, a GAM336763 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM336763 SLC17A7 AGGGCTGTGGGTGTG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A
GCTGTGC NM_020309.1) is another GAM336763 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336763 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336763 is therefore inhibition of SLC17A7, a GAM336763 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM336763 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336764 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGTGAT a GAM336764 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336764 is therefore inhibition of FHL2, a GAM336764 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336764 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTGAT NM_000618.2) is another GAM336764 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM336764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336764 is therefore inhibition of IGF1, a GAM336764 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336764 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGTGAT another GAM336764 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336764 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336764 is therefore inhibition of PRND, a GAM336764 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336764 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336765 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGTGAT a GAM336765 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336765 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336765 is therefore inhibition of FHL2, a GAM336765 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336765 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336765 IGF1 ACTGCACTCCAGCCT A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
GGGTGAT NM_000618.2) is another GAM336765 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336765 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336765 is therefore inhibition of IGF1, a GAM336765 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336765 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336765 PRND ACTGCACTCCAGCCT A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
GGGTGAT another GAM336765 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336765 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336765 is therefore inhibition of PRND, a GAM336765 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336765 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336767 ADAMTS5 CTGAAATGCTGTTGA A Disintegrin- like and Metalloprotease (reprolysin type) with A
TTTTAGT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336767 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336767 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336767 is therefore inhibition of ADAMTS5, a GAM336767 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336767 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336768 FHL2 ACTGCACTCCAGCCT A A GGGTGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM336768 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336768 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336768 is therefore inhibition of FHL2, a GAM336768 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336768 IGF1 ACTGCACTCCAGCCT A A GGGTGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336768 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336768 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336768 is therefore inhibition of IGF1, a GAM336768 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336768 PRND ACTGCACTCCAGCCT A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is

GGGTGAC another GAM336768 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336768 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336768 is therefore inhibition of PRND, a GAM336768 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336768 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336770 ADAMTS5 TGTGGCTAGTTTGAA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CTGAGAT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336770 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336770 is therefore inhibition of ADAMTS5, a GAM336770 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336770 PLAU TGTGGCTAGTTTGAA Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

CTGAGAT is another GAM336770 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336770 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336770 is therefore inhibition of PLAU, a GAM336770 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with

Alzheimer. Accordingly, utilities of GAM336770 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336771 ADAMTS5 TGTGGCTAGTTTGAA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CTGAGAT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336771 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336771 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336771 is therefore inhibition of ADAMTS5, a GAM336771 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336771 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336771 PLAU TGTGGCTAGTTTGAA Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

CTGAGAT is another GAM336771 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336771 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336771 is therefore inhibition of PLAU, a GAM336771 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM336771 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336772 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336772 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by

APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336772 is therefore inhibition of APPBP2, a GAM336772 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336772 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336772 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336772 is therefore inhibition of BACE2, a GAM336772 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336772 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336772 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336772 is therefore inhibition of FHL2, a GAM336772 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336772 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336772 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336772 is therefore inhibition of IGF1, a GAM336772 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336772 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336772 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336772 is therefore inhibition of MME, a GAM336772 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336772 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336772 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336772 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336772 is therefore inhibition of PRND, a GAM336772 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336772 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336773 APBA2 TCTGTGACTGTATTT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

TCCCAAA 2 (X11- I (APBA2, Accession NM_005503.2) is a GAM336773 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336773 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336773 is therefore inhibition of APBA2, a GAM336773 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336773 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336775 AVP AGAGACACAGACACA AVP (Accession NM_000490.2) is a GAM336775 target gene. AVP A A

TGGGAGA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336775 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336775 is therefore inhibition of AVP. Accordingly, utilities of GAM336775 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336775 FOS AGAGACACAGACACA V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

TGGGAGA Accession NM_005252.2) is another GAM336775 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336775 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336775 is therefore inhibition of FOS, a GAM336775 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336775 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336775 HD AGAGACACAGACACA HD (Accession NM_002111.3) is another GAM336775 target gene. HD A A

TGGGAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336775 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336775 is therefore inhibition of HD. Accordingly, utilities of GAM336775 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336775 IGF1 AGAGACACAGACACA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGAGA NM_000618.2) is another GAM336775 target gene. IGF1 BINDING SITE1 through IGF1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 through IGF1 BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336775 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336775 is therefore inhibition of IGF1, a GAM336775 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336775 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM336775 MAPK10 AGAGACACAGACACA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A
TGGGAGA NM_138981.1) is another GAM336775 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336775 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336775 is therefore inhibition of MAPK10, a GAM336775 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336775 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336776 ADAM17 GCAAGTGCTGTCATA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TGGAAGA factor, (ADAM17, Accession NM_003183.3) is a GAM336776 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336776 is therefore inhibition of ADAM17, a GAM336776 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336776 APPBP2 GCAAGTGCTGTCATA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGAAGA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336776 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336776 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM336776 is therefore inhibition of APPBP2, a GAM336776 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336776 IGF1 GCAAGTGCTGTCATA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGAAGA NM_000618.2) is another GAM336776 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336776 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336776 is therefore inhibition of IGF1, a GAM336776 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336776 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336777 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336777 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336777 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336777 is therefore inhibition of APP. Accordingly, utilities of GAM336777 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336778 CAV1 ACAGGGCTAAGGATG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

TTTGCTG NM_001753.3) is a GAM336778 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336778 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336778 is therefore inhibition of CAV1, a GAM336778 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336778 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336780 HTR2A TAGCAACCTTAATAT A A TTTACAG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is a GAM336780 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336780 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336780 is therefore inhibition of HTR2A, a GAM336780 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336780 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336781 PRND TACCAGTGTCAGCTT A A CCTGTGT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a GAM336781 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336781 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336781 is therefore inhibition of PRND, a GAM336781 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336781 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to GAM44.

GAM336782 PRND TACCAGTGTCAGCTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

CCTGTGT GAM336782 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336782 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336782 is therefore inhibition of PRND, a GAM336782 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336782 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336783 MAPK10 AGCTACATTGTCTGC Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

TGGGTTT NM_138980.1) is a GAM336783 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336783 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336783 is therefore inhibition of MAPK10, a GAM336783 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336783 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336784 MAPK10 AGCTACATTGTCTGC Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

TGGGTTT NM_138980.1) is a GAM336784 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336784 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336784 is therefore inhibition of MAPK10, a GAM336784 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336784 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336785 CAV2 CCGTAAAATGTTCAA Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM336785 target A A

ATGTTTT gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336785 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336785 is therefore inhibition of CAV2, a GAM336785 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336785 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336785 PRND AAAGCTTTGTTCATT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

GTATCTG another GAM336785 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336785 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336785 is therefore inhibition of PRND, a GAM336785 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336785 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336786 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336786 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336786 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336786 is therefore inhibition of APP. Accordingly, utilities of GAM336786 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336787 IGF1 TCACTGTAAACTCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTCCTG NM_000618.2) is a GAM336787 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336787 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336787 is therefore inhibition of IGF1, a GAM336787 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336787 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336788 DHCR24 AAAGTGTGTTATCTA 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GGTAGTC NM_014762.1) is a GAM336788 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336788 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336788 is therefore inhibition of DHCR24, a GAM336788 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336788 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336789 FLNB ATGCCCTTCCTCTTC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

TGCCATG NM_001457.1) is a GAM336789 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336789 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336789 is therefore inhibition of FLNB, a GAM336789 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336789 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336789 GYPA ATGCCCTTCCTCTTC Glycophorin A (includes MN blood group) (GYPA, Accession A A

TGCCATG NM_002099.2) is another GAM336789 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336789 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336789 is therefore inhibition of GYPA, a GAM336789 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336789 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336790 PRND TATGGCAAAGTCACT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

GATTTCC GAM336790 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336790 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336790 is therefore inhibition of PRND, a GAM336790 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336790 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336792 APPBP2 TGAGGGGGAAGGTGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GTGTGTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336792 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336792 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336792 is therefore inhibition of APPBP2, a GAM336792 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336792 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336792 CTSB TGAGGGGGAAGGTGT CTSB (Accession NM_147783.1) is another GAM336792 target gene. A A

GTGTGTG CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336792 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336792 is therefore inhibition of CTSB. Accordingly, utilities of GAM336792 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336792 GYPA TGAGGGGGAAGGTGT Glycophorin A (includes MN blood group) (GYPA, Accession A A

GTGTGTG NM_002099.2) is another GAM336792 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336792 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336792 is therefore inhibition of GYPA, a GAM336792 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM336792 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336792 IL1A TGAGGGGGAAGGTGT GTGTGTG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336792 target gene. IL1A BINDING SITE1 and IL1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE1 and IL1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336792 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336792 is therefore inhibition of IL1A, a GAM336792 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336792 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336793 APPBP2 TGAGGGGGAAGGTGT GTGTGTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336793 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336793 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336793 is therefore inhibition of APPBP2, a GAM336793 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336793 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336793 CTSB TGAGGGGGAAGGTGT GTGTGTG CTSB (Accession NM_147783.1) is another GAM336793 target gene. A A

CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336793 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336793 is therefore inhibition of CTSB. Accordingly, utilities of GAM336793 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM336793 GYPA TGAGGGGGAAGGTGT GTGTGTG Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM336793 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336793 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336793 is therefore inhibition of GYPA, a GAM336793 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336793 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336793 IL1A TGAGGGGGAAGGTGT GTGTGTG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another GAM336793 target gene. IL1A BINDING SITE1 and IL1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE1 and IL1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336793 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336793 is therefore inhibition of IL1A, a GAM336793 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336793 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336794 APBA2 AACCTGTCATTCCAA Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGACAGT 2 (X11- I (APBA2, Accession NM_005503.2) is a GAM336794 target gene. APBA2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336794 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336794 is therefore inhibition of APBA2, a GAM336794 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336794 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336794 FLNB AACCTGTCATTCCAA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A GGACAGT NM_001457.1) is another GAM336794 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336794 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336794 is therefore inhibition of FLNB, a GAM336794 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336794 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336795 BCHE TGGCTCTGTGCTTCT BCHE (Accession NM_000055.1) is a GAM336795 target gene. BCHE A A AGTATCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336795 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336795 is therefore inhibition of BCHE. Accordingly, utilities of GAM336795 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM336795 PSEN2 TGGCTCTGTGCTTCT PSEN2 (Accession NM_000447.1) is another GAM336795 target gene. A A

AGTATCT PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336795 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336795 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336795 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336796 BACE GTTCACAGTTCAGCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

TGTAACA is a GAM336796 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336796 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336796 is therefore inhibition of BACE, a GAM336796 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336796 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336797 DHCR24 TGAGGGAGGAAGTTT 24- dehydrocholesterol Reductase (DHCR24, Accession A A

GGGATGA NM_014762.1) is a GAM336797 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336797 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336797 is therefore inhibition of DHCR24, a GAM336797 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336797 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM336797 FLNB TGAGGGAGGAAGTTT GGGATGA Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM336797 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336797 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336797 is therefore inhibition of FLNB, a GAM336797 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336797 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336798 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336798 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336798 is therefore inhibition of APPBP2, a GAM336798 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336798 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336798 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby A A

incorporated herein.

Another function of GAM336798 is therefore inhibition of BACE2, a GAM336798 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336798 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336798 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336798 is therefore inhibition of FHL2, a GAM336798 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336798 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336798 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336798 is therefore inhibition of HD. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336798 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336798 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336798 is therefore inhibition of IGF1, a GAM336798 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336798 PRND CATTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336798 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336798 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336798 is therefore inhibition of PRND, a GAM336798 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336798 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336799 APPBP2 CATTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336799 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336799 is therefore inhibition of APPBP2, a GAM336799 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336799 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336799 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336799 is therefore inhibition of BACE2, a GAM336799 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336799 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336799 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336799 is therefore inhibition of FHL2, a GAM336799 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336799 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336799 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336799 is therefore inhibition of HD. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336799 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM336799 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336799 is therefore inhibition of IGF1, a GAM336799 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336799 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336799 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336799 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336799 is therefore inhibition of PRND, a GAM336799 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336799 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336800 HTR2C GTTAGGAAATGTGCT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
TACTGGG NM_000868.1) is a GAM336800 target gene. HTR2C BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336800 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336800 is therefore inhibition of HTR2C, a GAM336800 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336800 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336801 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336801 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336801 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336801 is therefore inhibition of APP. Accordingly, utilities of GAM336801 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336804 IGF1 GAGTAACAGCACTCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTGGAGT NM_000618.2) is a GAM336804 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336804 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336804 is therefore inhibition of IGF1, a GAM336804 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336804 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336806 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336806 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336806 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336806 is therefore inhibition of APP. Accordingly, utilities of GAM336806 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336807 BACE GAAACCTACACATCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

CACTAAC is a GAM336807 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336807 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336807 is therefore inhibition of BACE, a GAM336807 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336807 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336809 APOC1 TAAGGCATTTTTATG Apolipoprotein C- I (APOC1, Accession NM_001645.2) is a A A

GT GAM336809 target gene. APOC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336809 is therefore inhibition of APOC1, a GAM336809 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM336809 BACE A A GT TAAGGCATTTTTATG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) is another GAM336809 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336809 is therefore inhibition of BACE, a GAM336809 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336809 CAV1 A A GT TAAGGCATTTTTATG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM336809 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336809 is therefore inhibition of CAV1, a GAM336809 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336809 CAV2 A A GT TAAGGCATTTTTATG Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM336809 target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336809 is therefore inhibition of

CAV2, a GAM336809 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336809 FLNB TAAGGCATTTTTATG GT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM336809 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336809 is therefore inhibition of FLNB, a GAM336809 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336809 HTR2A TAAGGCATTTTTATG GT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM336809 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336809 is therefore inhibition of HTR2A, a GAM336809 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336809 MAPK10 TAAGGCATTTTTATG GT Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is another GAM336809 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of A A

multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336809 is therefore inhibition of MAPK10, a GAM336809 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336809 SNCAIP TAAGGCATTTTTATG GT Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM336809 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336809 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336809 is therefore inhibition of SNCAIP, a GAM336809 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336809 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336810 APLP2 GTCTTGTTCCAGTTT CTCAGCC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM336810 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336810 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336810 is therefore inhibition of APLP2, a GAM336810 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336810 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336811 APLP2 GTCTTGTTCCAGTTT CTCAGCC Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is a GAM336811 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336811 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336811 is therefore inhibition of APLP2, a GAM336811 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336811 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336812 ACE TGTCTCAGTGTAGAG ACCCAGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM336812 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336812 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336812 is therefore inhibition of ACE, a GAM336812 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336812 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336814 A2M ACGCCGCTGTGGGAA AGCACTT Alpha- 2- macroglobulin (A2M, Accession NM_000014.3) is a GAM336814 target gene. A2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of A2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336814 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336814 is therefore inhibition of A2M, a GAM336814 target gene which inhibit all four classes of proteinases and therefore is associated with Alzheimer. Accordingly, utilities of GAM336814 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with A2M.The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.

GAM336815 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336815 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336815 is therefore inhibition of APPBP2, a GAM336815 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336815 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336815 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336815 is therefore inhibition of BACE2, a GAM336815 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336815 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336815 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336815 is therefore inhibition of FHL2, a GAM336815 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336815 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336815 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336815 is therefore inhibition of IGF1, a GAM336815 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336815 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336815 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336815 is therefore inhibition of

MME, a GAM336815 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336815 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336815 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336815 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336815 is therefore inhibition of PRND, a GAM336815 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336815 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336816 BACE CTGTGCATGTTGATA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

TCCTGGC is a GAM336816 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336816 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336816 is therefore inhibition of BACE, a GAM336816 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336816 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336816 TRPM2 CTGTGCATGTTGATA TRPM2 (Accession NM_003307.1) is another GAM336816 target gene. A A

TCCTGGC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336816 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336816 is therefore inhibition of TRPM2, a GAM336816 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336816 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336817 BACE CTGTGCATGTTGATA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

TCCTGGC is a GAM336817 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336817 is therefore inhibition of BACE, a GAM336817 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336817 TRPM2 CTGTGCATGTTGATA TRPM2 (Accession NM_003307.1) is another GAM336817 target gene. A A

TCCTGGC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336817 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336817 is therefore inhibition of TRPM2, a GAM336817 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336817 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336818 ADAM10 TGAGGTGGGATCCCG A Disintegrin and Metalloproteinase Domain 10 (ADAM10,
A A
AGGCC Accession NM_001110.1) is a GAM336818 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336818 is therefore inhibition of ADAM10, a GAM336818 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336818 APP TGAGGTGGGATCCCG APP (Accession NM_000484.1) is another GAM336818 target gene.
A A
AGGCC APP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336818 is therefore inhibition of APP. Accordingly, utilities of GAM336818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336818 BACE TGAGGTGGGATCCCG Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2)
A A
AGGCC is another GAM336818 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336818 is therefore inhibition of BACE, a GAM336818 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336818 TGFB1 TGAGGTGGGATCCCG TGFB1 (Accession NM_000660.1) is another GAM336818 target gene. A A

AGGCC TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336818 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336818 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336818 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336819 BACE ACTGGCCCACTCCAT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TTAGGGT is a GAM336819 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336819 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336819 is therefore inhibition of BACE, a GAM336819 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336819 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336820 APBA1 TGAGTTTAAGCTAAG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AAGTCTG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM336820 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336820 is therefore inhibition of APBA1, a GAM336820 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with

Alzheimer. Accordingly, utilities of GAM336820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336820 CNTF TGAGTTTAAGCTAAG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

AAGTCTG another GAM336820 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336820 is therefore inhibition of CNTF, a GAM336820 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336820 PSEN1 TGAGTTTAAGCTAAG PSEN1 (Accession NM_000021.2) is another GAM336820 target gene. A A

AAGTCTG PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336820 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336820 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336820 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336821 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336821 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336821 is therefore inhibition of APPBP2, a GAM336821 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336821 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336821 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336821 is therefore inhibition of BACE2, a GAM336821 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336821 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336821 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336821 is therefore inhibition of FHL2, a GAM336821 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336821 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM336821 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336821 is therefore inhibition of IGF1, a GAM336821 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336821 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336821 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336821 is therefore inhibition of MME, a GAM336821 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336821 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336821 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336821 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336821 is therefore inhibition of PRND, a GAM336821 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336821 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336822 SLC6A4 TCACATCCTCCCACT TCAAGTG Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is a GAM336822 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336822 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336822 is therefore inhibition of SLC6A4, a GAM336822 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336822 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM336823 IAPP TGGACAATGAAACCC TGACCTT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a GAM336823 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336823 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336823 is therefore inhibition of IAPP, a GAM336823 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336823 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336824 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336824 target A A

gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336824 is therefore inhibition of APPBP2, a GAM336824 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336824 BACE2 ACTGCACTCCAGCCT A A GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336824 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336824 is therefore inhibition of BACE2, a GAM336824 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336824 FHL2 ACTGCACTCCAGCCT A A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336824 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336824 is therefore inhibition of

FHL2, a GAM336824 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336824 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM336824 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336824 is therefore inhibition of IGF1, a GAM336824 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336824 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336824 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336824 is therefore inhibition of MME, a GAM336824 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336824 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336824 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336824 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336824 is therefore inhibition of PRND, a GAM336824 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336824 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336825 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336825 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336825 is therefore inhibition of APPBP2, a GAM336825 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336825 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336825 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336825 is therefore inhibition of BACE2, a GAM336825 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336825 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336825 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336825 is therefore inhibition of FHL2, a GAM336825 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336825 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336825 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336825 is therefore inhibition of IGF1, a GAM336825 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336825 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336825

target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336825 is therefore inhibition of MME, a GAM336825 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336825 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336825 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336825 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336825 is therefore inhibition of PRND, a GAM336825 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336825 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336826 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336826 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336826 is therefore inhibition of APPBP2, a GAM336826 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336826 BACE2 ACTGCACTCCAGCCT A A GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336826 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336826 is therefore inhibition of BACE2, a GAM336826 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336826 FHL2 ACTGCACTCCAGCCT A A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336826 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336826 is therefore inhibition of FHL2, a GAM336826 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336826 IGF1 ACTGCACTCCAGCCT A A GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336826 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336826 is therefore inhibition of IGF1, a GAM336826 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336826 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336826 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336826 is therefore inhibition of MME, a GAM336826 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336826 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336826 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336826 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336826 is therefore inhibition of PRND, a GAM336826 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336826 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336827 TGFB1 TCTTCCATTCCCCTC TGFB1 (Accession NM_000660.1) is a GAM336827 target gene. TGFB1 A A

CTACGCC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336827 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336827 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336827 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336828 TGFB1 TCTTCCATTCCCCTC TGFB1 (Accession NM_000660.1) is a GAM336828 target gene. TGFB1 A A

CTACGCC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336828 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336828 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336828 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336829 AVP GTACAGTGGGTGTAG AVP (Accession NM_000490.2) is a GAM336829 target gene. AVP A A

GGACCAG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336829 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336829 is therefore inhibition of AVP. Accordingly, utilities of GAM336829 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336829 FPRL1 GTACAGTGGGTGTAG FPRL1 (Accession NM_001462.1) is another GAM336829 target gene. A A

GGACCAG FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336829 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336829 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336829 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336829 MME GTACAGTGGGTGTAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGACCAG enkephalinase, (MME, Accession NM_007289.1) is another GAM336829 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336829 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336829 is therefore inhibition of MME, a GAM336829 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336829 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336830 IGF1 ATCTTTCTTAATTCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
AGGACTC NM_000618.2) is a GAM336830 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336830 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336830 is therefore inhibition of IGF1, a GAM336830 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336830 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336830 MME ATCTTTCTTAATTCC Membrane Metallo- endopeptidase (neutral endopeptidase, A A
AGGACTC enkephalinase, (MME, Accession NM_007287.1) is another GAM336830 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336830 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336830 is therefore inhibition of MME, a GAM336830 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336830 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336832 CRAT GTTGGGGTTTCAGTG A A GCAGTCA Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is a GAM336832 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336832 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336832 is therefore inhibition of CRAT, a GAM336832 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336832 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336832 OGDH GTTGGGGTTTCAGTG A A GCAGTCA Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM336832 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336832 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336832 is therefore inhibition of OGDH, a GAM336832 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336832 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM2014.

GAM336833 MME CTCAGTGGTTCAGAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A
ACTGTTT enkephalinase, (MME, Accession NM_007288.1) is a GAM336833 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336833 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336833 is therefore inhibition of MME, a GAM336833 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336833 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336833 TRPM2 CTCAGTGGTTCAGAC TRPM2 (Accession NM_003307.1) is another GAM336833 target gene. A A
ACTGTTT TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336833 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336833 is therefore inhibition of TRPM2, a GAM336833 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336833 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336834 MME CTCAGTGGTTCAGAC Membrane Metallo- endopeptidase (neutral endopeptidase, A A
ACTGTTT enkephalinase, (MME, Accession NM_007288.1) is a GAM336834 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336834 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336834 is therefore inhibition of MME, a

GAM336834 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336834 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336834 TRPM2 CTCAGTGGTTCAGAC TRPM2 (Accession NM_003307.1) is another GAM336834 target gene. A A

ACTGTTT TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336834 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336834 is therefore inhibition of TRPM2, a GAM336834 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336834 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336835 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336835 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336835 is therefore inhibition of APPBP2, a GAM336835 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336835 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336835 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336835 is therefore inhibition of BACE2, a GAM336835 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336835 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336835 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336835 is therefore inhibition of FHL2, a GAM336835 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336835 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336835 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336835 is therefore inhibition of IGF1, a GAM336835 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336835 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336835 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336835 is therefore inhibition of MME, a GAM336835 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336835 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336835 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336835 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336835 is therefore inhibition of PRND, a GAM336835 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336835 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336836 APBA2 GTGTCTCTGTTGTGG Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
CAGTCAT 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM336836 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336836 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336836 is therefore inhibition of APBA2, a GAM336836 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336836 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336837 ABCD1 GTTGGGTGTGAGGGG ABCD1 (Accession NM_000033.2) is a GAM336837 target gene. ABCD1 A A

GGTCCCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336837 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336837 is therefore inhibition of ABCD1. Accordingly, utilities of GAM336837 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM336837 MAPT GTTGGGTGTGAGGGG Microtubule- associated Protein Tau (MAPT, Accession A A

GGTCCCA NM_173727.1) is another GAM336837 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336837 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336837 is therefore inhibition of MAPT, a GAM336837 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336837 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336838 ADAM10 ATGGCCTTTTCTCTT A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A

ATCCTGG Accession NM_001110.1) is a GAM336838 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336838 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336838 is therefore inhibition of ADAM10, a GAM336838 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336838 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336838 ADAM17 ATGGCCTTTTCTCTT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

ATCCTGG factor, (ADAM17, Accession NM_021832.1) is another GAM336838 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336838 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336838 is therefore inhibition of ADAM17, a GAM336838 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336838 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336838 APBA1 ATGGCCTTTTCTCTT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

ATCCTGG 1 (X11) (APBA1, Accession NM_001163.2) is another GAM336838 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336838 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336838 is therefore inhibition of APBA1, a GAM336838 target gene which stabilises APP and inhibits

production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336838 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336838 FHL2 ATGGCCTTTTCTCTT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

ATCCTGG another GAM336838 target gene. FHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336838 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336838 is therefore inhibition of FHL2, a GAM336838 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336838 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336838 TNFSF5 ATGGCCTTTTCTCTT TNFSF5 (Accession NM_000074.1) is another GAM336838 target A A

ATCCTGG gene. TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336838 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336838 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336838 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336840 APBA2 GGAGGCAGTGGTTGC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

AGTGAGC 2 (X11- I (APBA2, Accession NM_005503.2) is a GAM336840 target gene. APBA2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336840 is therefore inhibition of APBA2, a GAM336840 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336840 APLP2 GGAGGCAGTGGTTGC AGTGAGC A A Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is another GAM336840 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of APLP2, a GAM336840 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM336840 APPBP2 GGAGGCAGTGGTTGC AGTGAGC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336840 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of APPBP2, a GAM336840 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336840 BACE GGAGGCAGTGGTTGC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1)
A A

AGTGAGC is another GAM336840 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of BACE, a GAM336840 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336840 CRAT GGAGGCAGTGGTTGC Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is
A A

AGTGAGC another GAM336840 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of CRAT, a GAM336840 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336840 FHL2 GGAGGCAGTGGTTGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A

AGTGAGC another GAM336840 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of

FHL2, a GAM336840 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336840 IGF1 GGAGGCAGTGGTTGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
AGTGAGC NM_000618.2) is another GAM336840 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of IGF1, a GAM336840 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336840 PRND GGAGGCAGTGGTTGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
AGTGAGC another GAM336840 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336840 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336840 is therefore inhibition of PRND, a GAM336840 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336840 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336841 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336841 target gene. APPBP2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336841 is therefore inhibition of APPBP2, a GAM336841 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336841 BACE2 CATTGCACTCCAGCC A A TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336841 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336841 is therefore inhibition of BACE2, a GAM336841 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336841 FHL2 CATTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336841 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336841 is therefore inhibition of FHL2, a GAM336841 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336841 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336841 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336841 is therefore inhibition of HD. Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336841 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336841 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336841 is therefore inhibition of IGF1, a GAM336841 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336841 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336841 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336841 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336841 is therefore inhibition of PRND, a GAM336841 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336841 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336842 B2M CTCAGATACTTGGGA GGTTGAG Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a GAM336842 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336842 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336842 is therefore inhibition of B2M, a GAM336842 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM336842 FHL2 CTCAGATACTTGGGA GGTTGAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336842 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336842 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336842 is therefore inhibition of FHL2, a GAM336842 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336842 IGF1 CTCAGATACTTGGGA GGTTGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336842 target gene. IGF1 BINDING SITE is A A

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336842 is therefore inhibition of IGF1, a GAM336842 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336842 PRND CTCAGATACTTGGGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGTTGAG another GAM336842 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336842 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336842 is therefore inhibition of PRND, a GAM336842 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336842 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336844 ACT AGATGGAGTTTGAGA Activator of CAMP- responsive Element Modulator (CR (ACT, A A

GGGAATA Accession NM_020482.3) is a GAM336844 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336844 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336844 is therefore inhibition of ACT, a GAM336844 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336844 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336844 IGF1 AGATGGAGTTTGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGAATA NM_000618.2) is another GAM336844 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336844 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336844 is therefore inhibition of IGF1, a GAM336844 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336844 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336845 ACT AGATGGAGTTTGAGA Activator of CAMP- responsive Element Modulator (CR (ACT, A A

GGGAATA Accession NM_020482.3) is a GAM336845 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336845 is therefore inhibition of ACT, a GAM336845 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM336845 IGF1 AGATGGAGTTTGAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGAATA NM_000618.2) is another GAM336845 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336845 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336845 is therefore inhibition of IGF1, a GAM336845 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336845 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336846 HD CATTGGGTATCACCT HD (Accession NM_002111.3) is a GAM336846 target gene. HD A A

ATACAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336846 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336846 is therefore inhibition of HD. Accordingly, utilities of GAM336846 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336847 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336847 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336847 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336847 is therefore inhibition of APP. Accordingly, utilities of GAM336847 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336848 FLNB GTATGTGTGGGTTTC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

TCAGCCT NM_001457.1) is a GAM336848 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336848 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336848 is therefore inhibition of FLNB, a GAM336848 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336848 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336849 FLNB GTATGTGTGGGTTTC TCAGCCT Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM336849 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336849 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336849 is therefore inhibition of FLNB, a GAM336849 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336849 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336852 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336852 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336852 is therefore inhibition of APPBP2, a GAM336852 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336852 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336852 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336852 is therefore inhibition of BACE2, a GAM336852 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336852 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336852 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336852 is therefore inhibition of FHL2, a GAM336852 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336852 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336852 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336852 is therefore inhibition of IGF1, a GAM336852 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336852 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336852 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336852 is therefore inhibition of MME, a GAM336852 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336852 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336852 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336852 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336852 is therefore inhibition of PRND, a GAM336852 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336852 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336853 SLC6A4 GTGTCACAGATGGCC Solute Carrier Family 6 (neurotransmitter transporter, A A
GGAAGAG serotonin), Mem (SLC6A4, Accession NM_001045.1) is a GAM336853 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336853 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336853 is therefore inhibition of SLC6A4, a GAM336853 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336853 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM336854 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336854 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336854 is therefore inhibition of APPBP2, a GAM336854 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336854 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM336854 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336854 is therefore inhibition of BACE2, a GAM336854 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336854 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336854 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336854 is therefore inhibition of FHL2, a GAM336854 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336854 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336854 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336854 is therefore inhibition of IGF1, a GAM336854 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336854 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336854

target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336854 is therefore inhibition of MME, a GAM336854 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336854 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM336854 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336854 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336854 is therefore inhibition of PRND, a GAM336854 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336854 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336855 HTR2C TAGAAAGTGTCTCAT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A TTTAATA NM_000868.1) is a GAM336855 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336855 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336855 is therefore inhibition of HTR2C, a GAM336855 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336855 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336857 TNFSF5 ACAGCTCACTACAGC TNFSF5 (Accession NM_000074.1) is a GAM336857 target gene. A A

CTGGATT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336857 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336857 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336857 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336860 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336860 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336860 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336860 is therefore inhibition of APP. Accordingly, utilities of GAM336860 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336861 APBB2 GTTATTGTCAGGGTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TCCCTTT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336861 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336861 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336861 is therefore inhibition of APBB2, a GAM336861 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336861 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM44.

GAM336862 APBB2 GTTATTGTCAGGGTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TCCCTTT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336862 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336862 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336862 is therefore inhibition of APBB2, a GAM336862 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336862 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336863 FHL2 ACTGCACTCCAGTCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGGTGAC a GAM336863 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336863 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336863 is therefore inhibition of FHL2, a GAM336863 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336863 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336863 IGF1 ACTGCACTCCAGTCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGGTGAC NM_000618.2) is another GAM336863 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336863 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336863 is therefore inhibition of IGF1, a GAM336863 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336863 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336863 PRND ACTGCACTCCAGTCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

AGGTGAC another GAM336863 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336863 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336863 is therefore inhibition of PRND, a GAM336863 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336863 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336864 APBB2 ATGATGCTGGAACTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GACAACA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336864 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336864 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336864 is therefore inhibition of APBB2, a GAM336864 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336864 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336864 FPRL1 ATGATGCTGGAACTG FPRL1 (Accession NM_001462.1) is another GAM336864 target gene. A A

GACAACA FPRL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336864 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336864 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336864 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336866 IL1A AGGAATATAATTAAA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a A A
ACTTTGC GAM336866 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336866 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336866 is therefore inhibition of IL1A, a GAM336866 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336866 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336867 HD ATTCCCTTTAGCTCT HD (Accession NM_002111.3) is a GAM336867 target gene. HD A A
GATGGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336867 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336867 is therefore inhibition of HD. Accordingly, utilities of GAM336867 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336867 MAPT ATTCCCTTTAGCTCT Microtubule- associated Protein Tau (MAPT, Accession A A
GATGGCA NM_173727.1) is another GAM336867 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336867 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336867 is therefore inhibition of MAPT, a GAM336867 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336867 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336868 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336868 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336868 is therefore inhibition of APPBP2, a GAM336868 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336868 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336868 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336868 is therefore inhibition of BACE2, a GAM336868 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336868 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336868 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336868 is therefore inhibition of FHL2, a GAM336868 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336868 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336868 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336868 is therefore inhibition of HD. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336868 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336868 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336868 is therefore inhibition of IGF1, a GAM336868 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336868 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336868 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336868 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336868 is therefore inhibition of PRND, a GAM336868 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336868 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336869 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336869 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336869 is therefore inhibition of APPBP2, a GAM336869 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336869 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336869 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336869 is therefore inhibition of BACE2, a GAM336869 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336869 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336869 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336869 is therefore inhibition of FHL2, a GAM336869 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336869 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336869 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336869 is therefore inhibition of IGF1, a GAM336869 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336869 MME ACTGCACTCCAGCCT GGGCAAC A A Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM336869 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336869 is therefore inhibition of MME, a GAM336869 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336869 PRND ACTGCACTCCAGCCT GGGCAAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336869 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336869 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336869 is therefore inhibition of PRND, a GAM336869 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336869 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336870 BACE TTGCACTCCAGTCTG GGTGACA A A Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) is a GAM336870 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336870 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336870 is therefore inhibition of BACE, a GAM336870 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336870 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336870 FHL2 TTGCACTCCAGTCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGTGACA another GAM336870 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336870 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336870 is therefore inhibition of FHL2, a GAM336870 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336870 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336870 IGF1 TTGCACTCCAGTCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGTGACA NM_000618.2) is another GAM336870 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336870 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336870 is therefore inhibition of IGF1, a GAM336870 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336870 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336870 PRND TTGCACTCCAGTCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGTGACA another GAM336870 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336870 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336870 is therefore inhibition of PRND, a GAM336870 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336870 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336870 TNFRSF5 TTGCACTCCAGTCTG TNFRSF5 (Accession NM_152854.1) is another GAM336870 target A A GGTGACA gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336870 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336870 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM336870 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM336871 ACE AGAGGCAGAGGTTAC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A AGTAGTG (ACE, Accession NM_152831.1) is a GAM336871 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336871 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336871 is therefore inhibition of ACE, a GAM336871 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with

Alzheimer. Accordingly, utilities of GAM336871 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336871 PRND AGAGGCAGAGGTTAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
AGTAGTG another GAM336871 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336871 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336871 is therefore inhibition of PRND, a GAM336871 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336871 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336872 APBB2 GGCTGCAGTGAACTA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
TGATCGT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336872 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336872 is therefore inhibition of APBB2, a GAM336872 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336872 CNTF GGCTGCAGTGAACTA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A
TGATCGT another GAM336872 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336872 is therefore inhibition of CNTF, a GAM336872 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336872 FHL2 GGCTGCAGTGAACTA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGATCGT another GAM336872 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336872 is therefore inhibition of FHL2, a GAM336872 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336872 IGF1 GGCTGCAGTGAACTA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGATCGT NM_000618.2) is another GAM336872 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336872 is therefore inhibition of IGF1, a GAM336872 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM336872 MME GGCTGCAGTGAACTA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGATCGT enkephalinase, (MME, Accession NM_007289.1) is another GAM336872 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336872 is therefore inhibition of MME, a GAM336872 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336872 PRND GGCTGCAGTGAACTA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGATCGT another GAM336872 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336872 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336872 is therefore inhibition of PRND, a GAM336872 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336872 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336873 ADAMTS5 TAGGAGTGAAAATAA A Disintegrin- like and Metalloprotease (reprolysin type) with A A

ACTCTGT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336873 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336873 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336873 is therefore inhibition of ADAMTS5, a GAM336873 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336873 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336873 CTNND2 TAGGAGTGAAAATAA ACTCTGT Catenin (cadherin- associated protein), Delta 2 (neural plakophilin- rel (CTNND2, Accession NM_001332.1) is another GAM336873 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336873 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336873 is therefore inhibition of CTNND2, a GAM336873 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336873 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336873 GYPA TAGGAGTGAAAATAA ACTCTGT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM336873 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336873 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336873 is therefore inhibition of GYPA, a GAM336873 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336873 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336873 PLAU TAGGAGTGAAAATAA ACTCTGT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) is another GAM336873 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A A

PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336873 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336873 is therefore inhibition of PLAU, a GAM336873 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM336873 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336873 PRND TAGGAGTGAAAATAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

ACTCTGT another GAM336873 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336873 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336873 is therefore inhibition of PRND, a GAM336873 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336873 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336874 MTNR1A TTCCCAGAAACCTGT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is a A A

GAGTGTG GAM336874 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336874 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336874 is therefore inhibition of MTNR1A, a GAM336874 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336874 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions,

has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336875 APBA1 GAGGCAGCAACTGGT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GAGGCAC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM336875 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336875 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336875 is therefore inhibition of APBA1, a GAM336875 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336875 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336875 TRPM2 GAGGCAGCAACTGGT TRPM2 (Accession NM_003307.1) is another GAM336875 target gene. A A

GAGGCAC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336875 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336875 is therefore inhibition of TRPM2, a GAM336875 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM336875 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336876 PSEN1 TGCATGCTCTTCATG PSEN1 (Accession NM_000021.2) is a GAM336876 target gene. PSEN1 A A

AGAATCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336876 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336876 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336876 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336877 PSEN1 TGCATGCTCTTCATG PSEN1 (Accession NM_000021.2) is a GAM336877 target gene. PSEN1 A A

AGAATCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336877 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336877 is therefore inhibition of PSEN1. Accordingly, utilities of GAM336877 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM336878 FHL2 ACTGCACTCTAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GAGCAAC a GAM336878 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336878 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336878 is therefore inhibition of FHL2, a GAM336878 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336878 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336878 IGF1 ACTGCACTCTAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAGCAAC NM_000618.2) is another GAM336878 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336878 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336878 is therefore inhibition of IGF1, a GAM336878 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336878 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336878 PRND ACTGCACTCTAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GAGCAAC another GAM336878 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336878 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336878 is therefore inhibition of PRND, a GAM336878 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336878 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336879 ADAM17 TTGCCCAGGCTAGAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TGCAGTG factor, (ADAM17, Accession NM_003183.3) is a GAM336879 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336879 is therefore inhibition of ADAM17, a GAM336879 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336879 CHAT TTGCCCAGGCTAGAG Choline Acetyltransferase (CHAT, Accession NM_020984.1) is A A
TGCAGTG another GAM336879 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of CHAT, a GAM336879 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM336879 HTR2A TTGCCCAGGCTAGAG A A TGCAGTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM336879 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of HTR2A, a GAM336879 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336879 IAPP TTGCCCAGGCTAGAG A A TGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM336879 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of IAPP, a GAM336879 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336879 TGFB1 TTGCCCAGGCTAGAG TGFB1 (Accession NM_000660.1) is another GAM336879 target gene. A A

TGCAGTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of TGFB1. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336879 HTR2C CACTGCAACCTCTGC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession B A

CTCCTGG NM_000868.1) is another GAM336879 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of HTR2C, a GAM336879 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336879 IAPP CACTGCAACCTCTGC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is B A

CTCCTGG another GAM336879 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of IAPP, a GAM336879 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM336879 MTNR1A CACTGCAACCTCTGC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is B A

CTCCTGG another GAM336879 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of MTNR1A, a GAM336879 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336879 OGDH CACTGCAACCTCTGC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession B A

CTCCTGG NM_002541.1) is another GAM336879 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of OGDH, a GAM336879 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM336879 PRND CACTGCAACCTCTGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is B A

CTCCTGG another GAM336879 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336879 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM336879 is therefore inhibition of PRND, a GAM336879 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336879 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336880 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336880 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336880 is therefore inhibition of APPBP2, a GAM336880 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336880 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM336880 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336880 is therefore inhibition of BACE2, a GAM336880 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336880 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336880 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336880 is therefore inhibition of FHL2, a GAM336880 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336880 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336880 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336880 is therefore inhibition of HD. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336880 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336880 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336880 is therefore inhibition of IGF1, a GAM336880 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336880 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM336880 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336880 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336880 is therefore inhibition of PRND, a GAM336880 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336880 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336882 IL1A AGAGTGTGTCTATGG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a A A
AAGGGGT GAM336882 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336882 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336882 is therefore inhibition of IL1A, a GAM336882 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336882 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336883 APBB2 TTGTGGTTTTCCCAG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GTGGTAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM336883 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336883 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336883 is therefore inhibition of APBB2, a GAM336883 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336883 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336886 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336886 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336886 is therefore inhibition of APPBP2, a GAM336886 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336886 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336886 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336886 is therefore inhibition of BACE2, a GAM336886 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336886 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336886 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336886 is therefore inhibition of FHL2, a GAM336886 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336886 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336886 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336886 is therefore inhibition of IGF1, a GAM336886 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336886 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336886 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336886 is therefore inhibition of MME, a GAM336886 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336886 PRND ACTGCACTCCAGCCT GGGCAAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336886 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336886 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336886 is therefore inhibition of PRND, a GAM336886 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336886 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336887 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336887 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336887 is therefore inhibition of APPBP2, a GAM336887 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336887 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336887 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336887 is therefore inhibition of BACE2, a GAM336887 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336887 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336887 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336887 is therefore inhibition of FHL2, a GAM336887 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336887 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336887 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336887 is therefore inhibition of IGF1, a GAM336887 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336887 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336887 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336887 is therefore inhibition of MME, a GAM336887 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336887 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM336887 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336887 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336887 is therefore inhibition of PRND, a GAM336887 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336887 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336888 TNFSF5 CTCTTTAGTAGGAAC TNFSF5 (Accession NM_000074.1) is a GAM336888 target gene. A A

TCTGGAT TNFSF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336888 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336888 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM336888 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM336889 DLST GTCACCAGGCAGAAT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TCAGATA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM336889 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336889 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336889 is therefore inhibition of DLST, a GAM336889 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336889 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336892 ACE GGCAGCTGTGCAGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGGGGGT (ACE, Accession NM_152831.1) is a GAM336892 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336892 is therefore inhibition of ACE, a GAM336892 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336892 ARHA GGCAGCTGTGCAGAG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

TGGGGGT is another GAM336892 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of ARHA, a GAM336892 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336892 DLST GGCAGCTGTGCAGAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TGGGGGT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM336892 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of DLST, a GAM336892 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336892 NOTCH1 GGCAGCTGTGCAGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGGGGGT (NOTCH1, Accession NM_017617.2) is another GAM336892 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of NOTCH1, a GAM336892 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336892 OLR1 GGCAGCTGTGCAGAG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A TGGGGGT (OLR1, Accession NM_002543.1) is another GAM336892 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of OLR1, a GAM336892 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336892 SNCA GGCAGCTGTGCAGAG SNCA (Accession NM_000345.2) is another GAM336892 target gene. A A TGGGGGT SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of SNCA. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM336892 UBB GGCAGCTGTGCAGAG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM336892 A A TGGGGGT target gene. UBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336892 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336892 is therefore inhibition of UBB, a GAM336892 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336892 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM336893 ACE GGCAGCTGTGCAGAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGGGGGT (ACE, Accession NM_152831.1) is a GAM336893 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336893 is therefore inhibition of ACE, a GAM336893 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336893 ARHA GGCAGCTGTGCAGAG Ras Homolog Gene Family, Member A (ARHA, Accession NM_001664.1) A A

TGGGGGT is another GAM336893 target gene. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ARHA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of ARHA, a GAM336893 target gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

ARHA.The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.

GAM336893 DLST GGCAGCTGTGCAGAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TGGGGGT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM336893 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of DLST, a GAM336893 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM336893 NOTCH1 GGCAGCTGTGCAGAG Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGGGGGT (NOTCH1, Accession NM_017617.2) is another GAM336893 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of NOTCH1, a GAM336893 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336893 OLR1 GGCAGCTGTGCAGAG Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

TGGGGGT (OLR1, Accession NM_002543.1) is another GAM336893 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of OLR1, a GAM336893 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336893 SNCA GGCAGCTGTGCAGAG SNCA (Accession NM_000345.2) is another GAM336893 target gene. A A

TGGGGGT SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of SNCA. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM336893 UBB GGCAGCTGTGCAGAG Ubiquitin B (UBB, Accession NM_018955.2) is another GAM336893 A A

TGGGGGT target gene. UBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336893 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336893 is therefore inhibition of UBB, a GAM336893 target gene which marks cellular proteins for degradation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336893 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM336894 BACE AGTATTTCTTGTTTT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

ATTGAGA is a GAM336894 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336894 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336894 is therefore inhibition of BACE, a GAM336894 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336894 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336894 GYPA AGTATTTCTTGTTTT ATTGAGA Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is another GAM336894 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336894 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336894 is therefore inhibition of GYPA, a GAM336894 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336894 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336894 NOTCH1 AGTATTTCTTGTTTT ATTGAGA Notch (Drosophila) Homolog 1 (translocation- associated) (NOTCH1, Accession NM_017617.2) is another GAM336894 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336894 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336894 is therefore inhibition of NOTCH1, a GAM336894 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336894 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM869.

GAM336895 BACE AGTATTTCTTGTTTT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138972.1) A A

ATTGAGA is a GAM336895 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336895 is therefore inhibition of BACE, a GAM336895 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336895 GYPA AGTATTTCTTGTTTT Glycophorin A (includes MN blood group) (GYPA, Accession A A

ATTGAGA NM_002099.2) is another GAM336895 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336895 is therefore inhibition of GYPA, a GAM336895 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336895 NOTCH1 AGTATTTCTTGTTTT Notch (Drosophila) Homolog 1 (translocation- associated) A A

ATTGAGA (NOTCH1, Accession NM_017617.2) is another GAM336895 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336895 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336895 is therefore inhibition of

NOTCH1, a GAM336895 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336895 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM336896 CAV1 GAAGCATTGTGAGAA A A ACAGGTT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM336896 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336896 is therefore inhibition of CAV1, a GAM336896 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336896 HD GAAGCATTGTGAGAA A A ACAGGTT HD (Accession NM_002111.3) is another GAM336896 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336896 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336896 is therefore inhibition of HD. Accordingly, utilities of GAM336896 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336897 ADAMTS5 TAGGCAGTCTCAGTT A A GTTGGGT A Disintegrin- like and Metalloprotease (reprolysin type) with Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM336897 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336897 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336897 is therefore inhibition of ADAMTS5, a GAM336897 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336897 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM336897 CAV1 TAGGCAGTCTCAGTT GTTGGGT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM336897 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336897 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336897 is therefore inhibition of CAV1, a GAM336897 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336897 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336897 MPO TAGGCAGTCTCAGTT GTTGGGT Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM336897 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336897 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336897 is therefore inhibition of MPO, a GAM336897 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336897 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM336898 APPBP2 AACCCTGGAGGCAGA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGTTGCG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336898 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336898 is therefore inhibition of APPBP2, a GAM336898 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336898 IGF1 AACCCTGGAGGCAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGTTGCG NM_000618.2) is another GAM336898 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336898 is therefore inhibition of IGF1, a GAM336898 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336898 MAPK10 AACCCTGGAGGCAGA Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

GGTTGCG NM_002753.2) is another GAM336898 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336898 is therefore inhibition of MAPK10, a GAM336898 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336898 MME AACCCTGGAGGCAGA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGTTGCG enkephalinase, (MME, Accession NM_007289.1) is another GAM336898 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336898 is therefore inhibition of MME, a GAM336898 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336898 PRND AACCCTGGAGGCAGA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGTTGCG another GAM336898 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336898 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336898 is therefore inhibition of PRND, a GAM336898 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336898 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336901 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336901 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336901 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336901 is therefore inhibition of APP. Accordingly, utilities of GAM336901 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336903 ACE TAGTGCAATGGCGCG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

ATCTCGG (ACE, Accession NM_152831.1) is a GAM336903 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336903 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336903 is therefore inhibition of ACE, a GAM336903 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336903 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336903 MTNR1A TAGTGCAATGGCGCG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

ATCTCGG another GAM336903 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336903 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336903 is therefore inhibition of MTNR1A, a GAM336903 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336903 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM336906 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336906 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336906 is therefore inhibition of APPBP2, a GAM336906 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336906 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336906 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336906 is therefore inhibition of BACE2, a GAM336906 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336906 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM336906 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336906 is therefore inhibition of

FHL2, a GAM336906 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336906 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM336906 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336906 is therefore inhibition of HD. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336906 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM336906 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336906 is therefore inhibition of IGF1, a GAM336906 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336906 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336906 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide

sequence of GAM336906 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336906 is therefore inhibition of PRND, a GAM336906 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336906 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336907 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336907 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336907 is therefore inhibition of APPBP2, a GAM336907 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336907 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336907 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM336907 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336907 is therefore inhibition of BACE2, a GAM336907 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336907 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM336907 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336907 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336907 is therefore inhibition of FHL2, a GAM336907 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336907 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336907 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM336907 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336907 is therefore inhibition of HD. Accordingly, utilities of GAM336907 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336907 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336907 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336907 is therefore inhibition of IGF1, a GAM336907 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336907 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336907 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM336907 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM336907 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336907 is therefore inhibition of PRND, a GAM336907 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336907 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336908 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336908 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336908 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336908 is therefore inhibition of APP. Accordingly, utilities of GAM336908 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336909 IGF1 CTGCTAAACATCCTA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CACTGC NM_000618.2) is a GAM336909 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336909 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336909 is therefore inhibition of IGF1, a GAM336909 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity

and therefore is associated with Alzheimer. Accordingly, utilities of GAM336909 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336911 GYPA AAGACACTTTCTAAA Glycophorin A (includes MN blood group) (GYPA, Accession A A
TAGAAGT NM_002099.2) is a GAM336911 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336911 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336911 is therefore inhibition of GYPA, a GAM336911 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336911 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336913 IGF1 ACAAAAAATACGAAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ATTAGCT NM_000618.2) is a GAM336913 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336913 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336913 is therefore inhibition of IGF1, a GAM336913 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336913 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336913 PRND ACAAAAAATACGAAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
ATTAGCT another GAM336913 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336913 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336913 is therefore inhibition of PRND, a GAM336913 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336913 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336914 IGF1 ACAAAAAATACGAAA ATTAGCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM336914 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336914 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336914 is therefore inhibition of IGF1, a GAM336914 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336914 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336914 PRND ACAAAAAATACGAAA ATTAGCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336914 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336914 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336914 is therefore inhibition of PRND, a GAM336914 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336914 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336916 FLNB CTTCTTTGGGGTGGG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

CTTGCTC NM_001457.1) is a GAM336916 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336916 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336916 is therefore inhibition of FLNB, a GAM336916 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336916 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM336917 GFAP TTTGGTCTAATCTTC GFAP (Accession NM_002055.2) is a GAM336917 target gene. GFAP A A

AAGAGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336917 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336917 is therefore inhibition of GFAP. Accordingly, utilities of GAM336917 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336917 HD TTTGGTCTAATCTTC HD (Accession NM_002111.3) is another GAM336917 target gene. HD A A

AAGAGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336917 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336917 is therefore inhibition of HD. Accordingly, utilities of GAM336917 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336918 GFAP TTTGGTCTAATCTTC GFAP (Accession NM_002055.2) is a GAM336918 target gene. GFAP A A

AAGAGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336918

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336918 is therefore inhibition of GFAP. Accordingly, utilities of GAM336918 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336918 HD TTTGGTCTAATCTTC HD (Accession NM_002111.3) is another GAM336918 target gene. HD A A

AAGAGGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336918 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336918 is therefore inhibition of HD. Accordingly, utilities of GAM336918 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336919 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336919 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336919 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336919 is therefore inhibition of APP. Accordingly, utilities of GAM336919 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336920 APPBP2 GCCTGTAATCCCAGC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TACTTGG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336920 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336920 is therefore inhibition of APPBP2, a GAM336920 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336920 CASP3 GCCTGTAATCCCAGC Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A
TACTTGG Accession NM_032991.1) is another GAM336920 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336920 is therefore inhibition of CASP3, a GAM336920 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336920 FHL2 GCCTGTAATCCCAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TACTTGG another GAM336920 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336920 is therefore inhibition of FHL2, a GAM336920 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336920 GFAP GCCTGTAATCCCAGC GFAP (Accession NM_002055.2) is another GAM336920 target gene. A A
TACTTGG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336920 is therefore inhibition of GFAP. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336920 IGF1 GCCTGTAATCCCAGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TACTTGG NM_000618.2) is another GAM336920 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336920 is therefore inhibition of IGF1, a GAM336920 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336920 PRND GCCTGTAATCCCAGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TACTTGG another GAM336920 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336920 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336920 is therefore inhibition of PRND, a GAM336920 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336920 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336921 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGTAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336921 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336921 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336921 is therefore inhibition of APPBP2, a GAM336921 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336921 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336921 FHL2 A A CACTGCACTCCAGCC TGGGTAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336921 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336921 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336921 is therefore inhibition of FHL2, a GAM336921 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336921 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336921 IGF1 A A CACTGCACTCCAGCC TGGGTAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336921 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336921 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336921 is therefore inhibition of IGF1, a GAM336921 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336921 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336921 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGTAA another GAM336921 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336921 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336921 is therefore inhibition of PRND, a GAM336921 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336921 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336922 APPBP2 CACTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGTAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336922 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336922 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336922 is therefore inhibition of APPBP2, a GAM336922 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336922 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336922 FHL2 CACTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGTAA another GAM336922 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM336922 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336922 is therefore inhibition of FHL2, a GAM336922 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336922 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336922 IGF1 CACTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TGGGTAA NM_000618.2) is another GAM336922 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336922 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336922 is therefore inhibition of IGF1, a GAM336922 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336922 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336922 PRND CACTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGTAA another GAM336922 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336922 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336922 is therefore inhibition of PRND, a GAM336922 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336922 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM336923 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336923 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336923 is therefore inhibition of APPBP2, a GAM336923 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336923 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336923 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336923 is therefore inhibition of BACE2, a GAM336923 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336923 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336923 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336923 is therefore inhibition of FHL2, a GAM336923 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336923 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GGGCAAC NM_000618.2) is another GAM336923 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336923 is therefore inhibition of IGF1, a GAM336923 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336923 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336923 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336923 is therefore inhibition of MME, a GAM336923 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM336923 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336923 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336923 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336923 is therefore inhibition of PRND, a GAM336923 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336923 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336924 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336924 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336924 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336924 is therefore inhibition of APP. Accordingly, utilities of GAM336924 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336925 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336925 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336925 is therefore inhibition of APPBP2, a GAM336925 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336925 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336925 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336925 is therefore inhibition of BACE2, a GAM336925 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336925 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336925 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336925 is therefore inhibition of FHL2, a GAM336925 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336925 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336925 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336925 is therefore inhibition of IGF1, a GAM336925 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336925 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336925 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336925 is therefore inhibition of MME, a GAM336925 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336925 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336925 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336925 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336925 is therefore inhibition of PRND, a GAM336925 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336925 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336926 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336926 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336926 is therefore inhibition of APPBP2, a GAM336926 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336926 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336926 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336926 is therefore inhibition of BACE2, a GAM336926 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336926 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336926 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336926 is therefore inhibition of FHL2, a GAM336926 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336926 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336926 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336926 is therefore inhibition of IGF1, a GAM336926 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336926 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336926 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336926 is therefore inhibition of MME, a GAM336926 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336926 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336926 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336926 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336926 is therefore inhibition of PRND, a GAM336926 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336926 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336927 FOS TTAGAAAGAATATTG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
CCAGTCC Accession NM_005252.2) is a GAM336927 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336927 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336927 is therefore inhibition of FOS, a GAM336927 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM336927 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM336931 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336931 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

A function of GAM336931 is therefore inhibition of APPBP2, a GAM336931 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336931 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336931 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336931 is therefore inhibition of BACE2, a GAM336931 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336931 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336931 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336931 is therefore inhibition of FHL2, a GAM336931 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM336931 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336931 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336931 is therefore inhibition of IGF1, a GAM336931 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336931 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336931 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336931 is therefore inhibition of MME, a GAM336931 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336931 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336931 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336931 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336931 is therefore inhibition of PRND, a GAM336931 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336931 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336932 ADAM17 GGCTGGAGAGTAAAT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

CAGGTCT factor, (ADAM17, Accession NM_021832.1) is a GAM336932 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336932 is therefore inhibition of ADAM17, a GAM336932 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336932 APPBP2 GGCTGGAGAGTAAAT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CAGGTCT Protein 2 (APPBP2, Accession NM_006380.2) is another GAM336932 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336932 is therefore inhibition of APPBP2, a GAM336932 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336932 GFAP GGCTGGAGAGTAAAT GFAP (Accession NM_002055.2) is another GAM336932 target gene. A A

CAGGTCT GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336932 is therefore inhibition of GFAP. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336932 GLUL GGCTGGAGAGTAAAT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

CAGGTCT NM_002065.3) is another GAM336932 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336932 is therefore inhibition of GLUL, a GAM336932 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336932 OGDH GGCTGGAGAGTAAAT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

CAGGTCT NM_002541.1) is another GAM336932 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336932 is therefore inhibition of OGDH, a GAM336932 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM336932 PRNP GGCTGGAGAGTAAAT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A

CAGGTCT Strausler- (PRNP, Accession NM_000311.1) is another GAM336932 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336932 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336932 is therefore inhibition of PRNP, a GAM336932 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336932 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336933 AVP TCTTGTGAAATCTGT AVP (Accession NM_000490.2) is a GAM336933 target gene. AVP A A

GGACCCT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336933 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336933 is therefore inhibition of AVP. Accordingly, utilities of GAM336933 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM336934 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336934 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336934 is therefore inhibition of APPBP2, a GAM336934 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336934 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM336934 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336934 is therefore inhibition of BACE2, a GAM336934 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336934 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336934 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336934 is therefore inhibition of FHL2, a GAM336934 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336934 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336934 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336934 is therefore inhibition of IGF1, a GAM336934 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336934 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336934 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336934 is therefore inhibition of MME, a GAM336934 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336934 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336934 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336934 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336934 is therefore inhibition of PRND, a GAM336934 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336934 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336937 IL1B TAAGGAGCACACAAC CTAGATT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is a GAM336937 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336937 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336937 is therefore inhibition of IL1B, a GAM336937 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336937 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336938 IL1B TAAGGAGCACACAAC CTAGATT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is a GAM336938 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336938 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336938 is therefore inhibition of IL1B, a GAM336938 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336938 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM336939 CASP3 TTTCATTCATTTCTT TCATGGA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is a GAM336939 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336939 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336939 is therefore inhibition of CASP3, a GAM336939 target gene which is one apoptosis- related cysteine

protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336939 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM336939 FPRL1 TTTCATTCATTTCTT FPRL1 (Accession NM_001462.1) is another GAM336939 target gene. A A

TCATGGA FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336939 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336939 is therefore inhibition of FPRL1. Accordingly, utilities of GAM336939 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM336939 GLUL TTTCATTCATTTCTT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

TCATGGA NM_002065.3) is another GAM336939 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336939 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336939 is therefore inhibition of GLUL, a GAM336939 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336939 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM336941 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336941 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336941 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336941 is therefore inhibition of APP.

Accordingly, utilities of GAM336941 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336942 HD AAAGACTTGGCTGTC HD (Accession NM_002111.3) is a GAM336942 target gene. HD A A

AGCCCTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336942 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336942 is therefore inhibition of HD. Accordingly, utilities of GAM336942 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336945 FHL2 AGTGAGCTATGATCA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGCCGGT a GAM336945 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336945 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336945 is therefore inhibition of FHL2, a GAM336945 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336945 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336945 IGF1 AGTGAGCTATGATCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGCCGGT NM_000618.2) is another GAM336945 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336945 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336945 is therefore inhibition of IGF1, a GAM336945 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336945 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336945 PRND AGTGAGCTATGATCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGCCGGT another GAM336945 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336945 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336945 is therefore inhibition of PRND, a GAM336945 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336945 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336946 APP GGAGCTGTAGTTTTT APP (Accession NM_000484.1) is a GAM336946 target gene. APP A A CCCACAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336946 is therefore inhibition of APP. Accordingly, utilities of GAM336946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336946 BACE GGAGCTGTAGTTTTT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A CCCACAT is another GAM336946 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336946 is therefore inhibition of BACE, a GAM336946 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and

therefore is associated with Alzheimer. Accordingly, utilities of GAM336946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336946 IGF1 GGAGCTGTAGTTTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CCCACAT NM_000618.2) is another GAM336946 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336946 is therefore inhibition of IGF1, a GAM336946 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336946 PRNP GGAGCTGTAGTTTTT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A
CCCACAT Strausler- (PRNP, Accession NM_000311.1) is another GAM336946 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336946 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336946 is therefore inhibition of PRNP, a GAM336946 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336946 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM336947 MAPT CAGTGGATGATGTTT Microtubule- associated Protein Tau (MAPT, Accession A A
TCTGTGG NM_016835.1) is a GAM336947 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple

transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336947 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336947 is therefore inhibition of MAPT, a GAM336947 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336947 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM336950 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336950 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336950 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336950 is therefore inhibition of APP. Accordingly, utilities of GAM336950 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336951 APP AGATGACACAGAGCT APP (Accession NM_000484.1) is a GAM336951 target gene. APP A A

CAGGAAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336951 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336951 is therefore inhibition of APP. Accordingly, utilities of GAM336951 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336956 APPBP2 GTCTTCCTCCGTCCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CACCTCC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336956 target gene. APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336956 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM336956 is therefore inhibition of APPBP2, a GAM336956 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336956 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336956 BAX GTCTTCCTCCGTCCC BCL2- associated X Protein (BAX, Accession NM_138763.1) is another GAM336956 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336956 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

CACCTCC

Another function of GAM336956 is therefore inhibition of BAX, a GAM336956 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM336956 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM336956 HD GTCTTCCTCCGTCCC HD (Accession NM_002111.3) is another GAM336956 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336956 RNA are set forth in Tables 6 and 7, hereby incorporated herein. HD A A

CACCTCC

Another function of GAM336956 is therefore inhibition of HD. Accordingly, utilities of GAM336956 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336956 MPO GTCTTCCTCCGTCCC Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM336956 target gene. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336956 RNA are set forth in Tables 6 and A A

CACCTCC

7, hereby incorporated herein.

Another function of GAM336956 is therefore inhibition of MPO, a GAM336956 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336956 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM336956 NGB A A GTCTTCCTCCGTCCC CACCTCC Neuroglobin (NGB, Accession NM_021257.2) is another GAM336956 target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336956 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336956 is therefore inhibition of NGB, a GAM336956 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336956 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM336957 APLP1 A A TTAAACTTCCCTGCT GCCCCAG Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession NM_005166.2) is a GAM336957 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336957 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336957 is therefore inhibition of APLP1, a GAM336957 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336957 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336958 ADAM10 A A AGGTGGAGTTTTGCT A Disintegrin and Metalloproteinase Domain 10 (ADAM10,

TTCCCAT Accession NM_001110.1) is a GAM336958 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336958 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336958 is therefore inhibition of ADAM10, a GAM336958 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336958 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM336958 BACE AGGTGGAGTTTTGCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TTCCCAT is another GAM336958 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336958 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336958 is therefore inhibition of BACE, a GAM336958 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336958 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336958 DHCR24 AGGTGGAGTTTTGCT 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TTCCCAT NM_014762.1) is another GAM336958 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336958 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336958 is therefore inhibition of DHCR24, a GAM336958 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM336958 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336959 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336959 target gene. APP
A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336959 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336959 is therefore inhibition of APP. Accordingly, utilities of GAM336959 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336961 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM336961 target gene. HD
A A

ACTTGTA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336961 is therefore inhibition of HD. Accordingly, utilities of GAM336961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336961 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A

ACTTGTA NM_000868.1) is another GAM336961 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336961 is therefore inhibition of HTR2C, a GAM336961 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336961 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ACTTGTA NM_000618.2) is another GAM336961 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336961 is therefore inhibition of IGF1, a GAM336961 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336961 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM336961 target gene. A A
ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336961 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336961 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM336961 target A A
ACTTGTA gene. TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336961 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336961 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336961 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with TNFRSF6.

GAM336962 BACE2 ATAACTGTGAAGAGG CAATTGT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is a GAM336962 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336962 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336962 is therefore inhibition of BACE2, a GAM336962 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336962 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336963 APLP1 AGCTCCAGGAGCTGG CAGGAGG Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession NM_005166.2) is a GAM336963 target gene. APLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336963 is therefore inhibition of APLP1, a GAM336963 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM336963 BAX AGCTCCAGGAGCTGG CAGGAGG BCL2- associated X Protein (BAX, Accession NM_004324.2) is another GAM336963 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336963 is therefore inhibition of

BAX, a GAM336963 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM336963 CTSK AGCTCCAGGAGCTGG CTSK (Accession NM_000396.2) is another GAM336963 target gene. A A

CAGGAGG CTSK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336963 is therefore inhibition of CTSK. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM336963 GFAP AGCTCCAGGAGCTGG GFAP (Accession NM_002055.2) is another GAM336963 target gene. A A

CAGGAGG GFAP BINDING SITE1 and GFAP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GFAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE1 and GFAP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336963 is therefore inhibition of GFAP. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM336963 MME AGCTCCAGGAGCTGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

CAGGAGG enkephalinase, (MME, Accession NM_007287.1) is another GAM336963 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336963 is therefore inhibition of MME, a GAM336963 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of

Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336963 NCSTN AGCTCCAGGAGCTGG NCSTN (Accession NM_015331.1) is another GAM336963 target gene. A A

CAGGAGG NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336963 is therefore inhibition of NCSTN, a GAM336963 target gene which has a central role in presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336963 S100B AGCTCCAGGAGCTGG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

CAGGAGG NM_006272.1) is another GAM336963 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336963 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336963 is therefore inhibition of S100B, a GAM336963 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336963 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM336964 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336964 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336964 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336964 is therefore inhibition of APP. Accordingly, utilities of GAM336964 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336965 GAL TGACAGAGGTACATA Galanin (GAL, Accession NM_015973.2) is a GAM336965 target A A
GGAGGCT gene. GAL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GAL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336965 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336965 is therefore inhibition of GAL, a GAM336965 target gene which stimulates LH secretion and enhances LHRH- induced LH release from dispersed anterior pituitary cells in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336965 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GAL.The function of GAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3293.

GAM336965 MME TGACAGAGGTACATA Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGAGGCT enkephalinase, (MME, Accession NM_000902.2) is another GAM336965 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336965 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336965 is therefore inhibition of MME, a GAM336965 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336965 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336966 GAL TGACAGAGGTACATA Galanin (GAL, Accession NM_015973.2) is a GAM336966 target A A
GGAGGCT gene. GAL BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by GAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GAL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336966 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336966 is therefore inhibition of GAL, a GAM336966 target gene which stimulates LH secretion and enhances LHRH- induced LH release from dispersed anterior pituitary cells in vitro. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336966 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GAL.The function of GAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3293.

GAM336966 MME TGACAGAGGTACATA Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGAGGCT enkephalinase, (MME, Accession NM_000902.2) is another GAM336966 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336966 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336966 is therefore inhibition of MME, a GAM336966 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336966 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336967 CAV1 TTCCCTTAGGTCTGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
AATGGTA NM_001753.3) is a GAM336967 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336967 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336967 is therefore inhibition of CAV1, a GAM336967 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336967

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM336968 APBA1 AGAGATAAAGAGGTT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

TAGGCAG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM336968 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336968 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336968 is therefore inhibition of APBA1, a GAM336968 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336968 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336968 CNTF AGAGATAAAGAGGTT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

TAGGCAG another GAM336968 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336968 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336968 is therefore inhibition of CNTF, a GAM336968 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336968 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM336969 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336969 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM336969 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336969 is therefore inhibition of APP. Accordingly, utilities of GAM336969 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336970 IGF1 TGTGACTCGTACTTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TAATCCT NM_000618.2) is a GAM336970 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336970 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336970 is therefore inhibition of IGF1, a GAM336970 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336970 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336970 PRND TGTGACTCGTACTTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TAATCCT another GAM336970 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336970 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336970 is therefore inhibition of PRND, a GAM336970 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336970 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336971 IGF1 TGTGACTCGTACTTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TAATCCT NM_000618.2) is a GAM336971 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336971 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336971 is therefore inhibition of IGF1, a GAM336971 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336971 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336971 PRND TGTGACTCGTACTTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TAATCCT another GAM336971 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336971 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336971 is therefore inhibition of PRND, a GAM336971 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336971 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336972 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336972 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336972 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336972 is therefore inhibition of APP. Accordingly, utilities of GAM336972 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336974 ACE TGACTCAGTGGAAGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TCCAGAG (ACE, Accession NM_152831.1) is a GAM336974 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336974 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336974 is therefore inhibition of ACE, a GAM336974 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM336974 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336974 IGF1 TGACTCAGTGGAAGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TCCAGAG NM_000618.2) is another GAM336974 target gene. IGF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336974 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336974 is therefore inhibition of IGF1, a GAM336974 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336974 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336975 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336975 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336975 is therefore inhibition of APPBP2, a GAM336975 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336975 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM336975 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336975 is therefore inhibition of BACE2, a GAM336975 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336975 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM336975 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336975 is therefore inhibition of FHL2, a GAM336975 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336975 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM336975 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336975 is therefore inhibition of IGF1, a GAM336975 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336975 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM336975 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336975 is therefore inhibition of MME, a GAM336975 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336975 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM336975 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM336975 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336975 is therefore inhibition of PRND, a GAM336975 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336975 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336976 APPBP2 ATGCCTGTAATCCCA GCACTTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336976 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336976 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336976 is therefore inhibition of APPBP2, a GAM336976 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336976 IGF1 ATGCCTGTAATCCCA GCACTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM336976 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336976 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336976 is therefore inhibition of IGF1, a GAM336976 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336976 PRND ATGCCTGTAATCCCA GCACTTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336976 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336976 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336976 is therefore inhibition of PRND, a GAM336976 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336976 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336978 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM336978 target gene. HD A A

ACTTGTA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336978 is therefore inhibition of HD. Accordingly, utilities of GAM336978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336978 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACTTGTA NM_000868.1) is another GAM336978 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336978 is therefore inhibition of HTR2C, a GAM336978 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336978 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGTA NM_000618.2) is another GAM336978 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336978 is therefore inhibition of IGF1, a GAM336978 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336978 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM336978 target gene. A A

ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336978 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336978 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM336978 target A A

ACTTGTA gene. TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336978 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336978 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336978 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336979 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM336979 target gene. HD A A

ACTTGTA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336979 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336979 is therefore inhibition of HD. Accordingly, utilities of GAM336979 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336979 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
ACTTGTA NM_000868.1) is another GAM336979 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336979 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336979 is therefore inhibition of HTR2C, a GAM336979 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336979 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336979 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ACTTGTA NM_000618.2) is another GAM336979 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336979 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336979 is therefore inhibition of IGF1, a GAM336979 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336979 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336979 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM336979 target gene. A A

ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336979 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336979 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336979 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336979 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM336979 target A A

ACTTGTA gene. TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336979 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336979 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336979 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336980 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM336980 target gene. HD A A

ACTTGTA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336980 is therefore inhibition of HD. Accordingly, utilities of GAM336980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336980 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACTTGTA NM_000868.1) is another GAM336980 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336980 is therefore inhibition of HTR2C, a GAM336980 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336980 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
ACTTGTA NM_000618.2) is another GAM336980 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336980 is therefore inhibition of IGF1, a GAM336980 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336980 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_000447.1) is another GAM336980 target gene. A A
ACTTGTA PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336980 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336980 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152872.1) is another GAM336980 target A A
ACTTGTA gene. TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE1 and TNFRSF6 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336980 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336980 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336980 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336981 HD TCTGCTGTGATGGAC HD (Accession NM_002111.3) is a GAM336981 target gene. HD A A

ACTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336981 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336981 is therefore inhibition of HD. Accordingly, utilities of GAM336981 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM336981 HTR2C TCTGCTGTGATGGAC 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

ACTTGT NM_000868.1) is another GAM336981 target gene. HTR2C BINDING SITE1 and HTR2C BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2C, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE1 and HTR2C BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336981 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336981 is therefore inhibition of HTR2C, a GAM336981 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336981 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM336981 IGF1 TCTGCTGTGATGGAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGT NM_000618.2) is another GAM336981 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336981 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336981 is therefore inhibition of IGF1, a GAM336981 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336981 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336981 PSEN2 TCTGCTGTGATGGAC PSEN2 (Accession NM_012486.1) is another GAM336981 target gene. A A

ACTTGT PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336981 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336981 is therefore inhibition of PSEN2. Accordingly, utilities of GAM336981 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM336981 TNFRSF6 TCTGCTGTGATGGAC TNFRSF6 (Accession NM_152877.1) is another GAM336981 target A A

ACTTGT gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336981 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336981 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM336981 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM336983 HTR2A ATGTGTCTGGGACTC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A

TATGCCA NM_000621.1) is a GAM336983 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336983 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336983 is therefore inhibition of HTR2A, a GAM336983 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336983 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM336984 BACE TGTAGTTTGATGCTA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

GAACACT is a GAM336984 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336984 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336984 is therefore inhibition of BACE, a GAM336984 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM336984 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM336989 APPBP2 CTGAGGCAGGAGGGC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TCAGGAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336989 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336989 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336989 is therefore inhibition of APPBP2, a GAM336989 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336989 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336989 IGF1 CTGAGGCAGGAGGGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TCAGGAG NM_000618.2) is another GAM336989 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336989 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336989 is therefore inhibition of IGF1, a GAM336989 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336989 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336989 SLC17A7 CTGAGGCAGGAGGGC SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

TCAGGAG NM_020309.1) is another GAM336989 target gene. SLC17A7 BINDING SITE1 and SLC17A7 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SLC17A7, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE1 and SLC17A7 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336989 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336989 is therefore inhibition of SLC17A7, a GAM336989 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM336989 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM336989 TGFB1 CTGAGGCAGGAGGGC TGFB1 (Accession NM_000660.1) is another GAM336989 target gene. A A

TCAGGAG TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TGFB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE1 and TGFB1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336989 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336989 is therefore inhibition of

TGFB1. Accordingly, utilities of GAM336989 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM336990 ADAM17 TGAGATGGTGTCATA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TTGCTGG factor, (ADAM17, Accession NM_021832.1) is a GAM336990 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336990 is therefore inhibition of ADAM17, a GAM336990 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM336990 APBB2 TGAGATGGTGTCATA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TTGCTGG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM336990 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336990 is therefore inhibition of APBB2, a GAM336990 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336990 CAV2 TGAGATGGTGTCATA Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM336990 A A

TTGCTGG target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM336990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336990 is therefore inhibition of CAV2, a GAM336990 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336990 IGF1 TGAGATGGTGTCATA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TTGCTGG NM_000618.2) is another GAM336990 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336990 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336990 is therefore inhibition of IGF1, a GAM336990 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336990 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336991 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM336991 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336991 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336991 is therefore inhibition of APP. Accordingly, utilities of GAM336991 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM336992 CAV2 CCGTAAAATGTTCAA Caveolin 2 (CAV2, Accession NM_001233.2) is a GAM336992 target A A
ATGTTTT gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336992 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336992 is therefore inhibition of CAV2, a GAM336992 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336992 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM336992 PRND AAAGCTTTGTTCATT GTATCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM336992 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336992 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM336992 is therefore inhibition of PRND, a GAM336992 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336992 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336995 APPBP2 ATTGCACTCCAGCTT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336995 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336995 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336995 is therefore inhibition of APPBP2, a GAM336995 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336995 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336995 FHL2 ATTGCACTCCAGCTT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM336995 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336995 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336995 is therefore inhibition of FHL2, a GAM336995 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336995 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336995 IGF1 ATTGCACTCCAGCTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336995 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336995 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336995 is therefore inhibition of IGF1, a GAM336995 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336995 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336995 PRND ATTGCACTCCAGCTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336995 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM336995 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336995 is therefore inhibition of PRND, a GAM336995 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336995 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336996 APPBP2 ATTGCACTCCAGCTT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM336996 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336996 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM336996 is therefore inhibition of APPBP2, a GAM336996 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336996 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336996 FHL2 ATTGCACTCCAGCTT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM336996 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336996 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM336996 is therefore inhibition of FHL2, a GAM336996 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336996 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM336996 IGF1 ATTGCACTCCAGCTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM336996 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336996 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336996 is therefore inhibition of IGF1, a GAM336996 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM336996 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM336996 PRND ATTGCACTCCAGCTT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM336996 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM336996 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM336996 is therefore inhibition of PRND, a GAM336996 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM336996 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM336997 APP TAGGCCCATTAATAG APP (Accession NM_000484.1) is a GAM336997 target gene. APP A A

TGTACAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM336997 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM336997 is therefore inhibition of APP. Accordingly, utilities of GAM336997 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337000 APPBP2 GTATGTATTTATAGA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGTTCTT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337000 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337000 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337000 is therefore inhibition of APPBP2, a GAM337000 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337000 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337000 CAV2 GTATGTATTTATAGA Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM337000 A A
TGTTCTT target gene. CAV2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337000 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337000 is therefore inhibition of CAV2, a GAM337000 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337000 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337000 HD GTATGTATTTATAGA HD (Accession NM_002111.3) is another GAM337000 target gene. HD A A
TGTTCTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337000 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337000 is therefore inhibition of HD. Accordingly, utilities of GAM337000 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337000 MME GTATGTATTTATAGA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGTTCTT enkephalinase, (MME, Accession NM_000902.2) is another GAM337000 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337000 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337000 is therefore inhibition of MME, a GAM337000 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337000 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337001 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337001 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337001 is therefore inhibition of APPBP2, a GAM337001 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337001 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337001 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337001 is therefore inhibition of BACE2, a GAM337001 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337001 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337001 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337001 is therefore inhibition of FHL2, a GAM337001 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337001 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337001 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337001 is therefore inhibition of IGF1, a GAM337001 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337001 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337001 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337001 is therefore inhibition of MME, a GAM337001 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337001 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337001 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337001 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337001 is therefore inhibition of PRND, a GAM337001 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337001 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337003 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337003 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337003 is therefore inhibition of APPBP2, a GAM337003 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337003 BACE2 CATTGCACTCCAGCC A A TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337003 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337003 is therefore inhibition of BACE2, a GAM337003 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337003 FHL2 CATTGCACTCCAGCC A A TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337003 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337003 is therefore inhibition of FHL2, a GAM337003 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337003 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337003 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337003 is therefore inhibition of HD. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337003 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337003 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337003 is therefore inhibition of IGF1, a GAM337003 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337003 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337003 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337003 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337003 is therefore inhibition of PRND, a GAM337003 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337003 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337004 IGF1 GAGGCGGGAAGCCCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CTAGGAG NM_000618.2) is a GAM337004 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337004 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337004 is therefore inhibition of IGF1, a GAM337004 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337004 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337004 RAGE GAGGCGGGAAGCCCA Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A
CTAGGAG GAM337004 target gene. RAGE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337004 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337004 is therefore inhibition of RAGE, a GAM337004 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM337004 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM337007 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337007 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of

GAM337007 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337007 is therefore inhibition of APPBP2, a GAM337007 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337007 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A
A
GGGCAAC NM_012105.3) is another GAM337007 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337007 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337007 is therefore inhibition of BACE2, a GAM337007 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337007 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A
GGGCAAC another GAM337007 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337007 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337007 is therefore inhibition of FHL2, a GAM337007 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM189.

GAM337007 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337007 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337007 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337007 is therefore inhibition of IGF1, a GAM337007 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337007 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337007 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337007 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337007 is therefore inhibition of MME, a GAM337007 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337007 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337007 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337007 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337007 is therefore inhibition of PRND, a GAM337007 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337007 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337008 IGF1 CATTTCAACTTTGTT GTTCTTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM337008 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337008 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337008 is therefore inhibition of IGF1, a GAM337008 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337008 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337009 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337009 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337009 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337009 is therefore inhibition of APP. Accordingly, utilities of GAM337009 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337010 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337010 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337010 A A

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337010 is therefore inhibition of APP. Accordingly, utilities of GAM337010 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337011 BACE TGCTAGGTTTTTTCC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TTTCCCC is a GAM337011 target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by BACE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337011 is therefore inhibition of BACE, a GAM337011 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337011 GYPA TGCTAGGTTTTTTCC Glycophorin A (includes MN blood group) (GYPA, Accession A A

TTTCCCC NM_002099.2) is another GAM337011 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337011 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337011 is therefore inhibition of GYPA, a GAM337011 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337011 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337013 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337013 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM337013 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337013 is therefore inhibition of APP. Accordingly, utilities of GAM337013 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337015 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337015 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337015 is therefore inhibition of APPBP2, a GAM337015 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337015 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337015 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337015 is therefore inhibition of BACE2, a GAM337015 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337015 FHL2 CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337015 target gene. FHL2 BINDING SITE1 and FHL2 BINDING A A

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337015 is therefore inhibition of FHL2, a GAM337015 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337015 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337015 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337015 is therefore inhibition of HD. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337015 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337015 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337015 is therefore inhibition of IGF1, a GAM337015 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM337015 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM337015 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337015 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337015 is therefore inhibition of PRND, a GAM337015 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337015 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337016 ACHE TCTGAGTGGGAACTC Acetylcholinesterase (YT blood group) (ACHE, Accession A A TCATGAC NM_015831.1) is a GAM337016 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337016 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337016 is therefore inhibition of ACHE, a GAM337016 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337016 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM337017 TFCP2 AGGCAGAAAACAATT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is a A A CCAAGCA GAM337017 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337017 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337017 is therefore inhibition of TFCP2, a GAM337017 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337017 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337018 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337018 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337018 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337018 is therefore inhibition of APP. Accordingly, utilities of GAM337018 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337019 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337019 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337019 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337019 is therefore inhibition of APP. Accordingly, utilities of GAM337019 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337022 ACE TCAGTCGTTTCTCTC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TCCCAGC (ACE, Accession NM_152831.1) is a GAM337022 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337022 is therefore inhibition of ACE, a GAM337022 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337022 FLNB TCAGTCGTTTCTCTC A A TCCCAGC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is another GAM337022 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337022 is therefore inhibition of FLNB, a GAM337022 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM337022 GFAP TCAGTCGTTTCTCTC A A TCCCAGC GFAP (Accession NM_002055.2) is another GAM337022 target gene. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337022 is therefore inhibition of GFAP. Accordingly, utilities of GAM337022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337022 TGFB1 TCAGTCGTTTCTCTC A A TCCCAGC TGFB1 (Accession NM_000660.1) is another GAM337022 target gene. TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337022 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337022 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337022 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337023 APBB1 CCCTTTAGTAACTTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CAGGGTC 1 (Fe65) (APBB1, Accession NM_145689.1) is a GAM337023 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337023 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337023 is therefore inhibition of APBB1, a GAM337023 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337023 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337024 APBB1 CCCTTTAGTAACTTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CAGGGTC 1 (Fe65) (APBB1, Accession NM_145689.1) is a GAM337024 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337024 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337024 is therefore inhibition of APBB1, a GAM337024 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337024 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337025 FHL2 TCATCCTTTTCTGCA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

ACCTGTT a GAM337025 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337025 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337025 is therefore inhibition of FHL2, a GAM337025 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337025 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337025 FPRL1 TCATCCTTTTCTGCA FPRL1 (Accession NM_001462.1) is another GAM337025 target gene. A A

ACCTGTT FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337025 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337025 is therefore inhibition of FPRL1. Accordingly, utilities of GAM337025 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM337025 LRP1 TCATCCTTTTCTGCA Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

ACCTGTT macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337025 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337025 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337025 is therefore inhibition of LRP1, a GAM337025 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337025 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337027 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337027 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and

secondary structure complementarity to the nucleotide sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337027 is therefore inhibition of APPBP2, a GAM337027 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337027 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337027 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337027 is therefore inhibition of BACE2, a GAM337027 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337027 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337027 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337027 is therefore inhibition of FHL2, a GAM337027 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337027 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337027 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337027 is therefore inhibition of IGF1, a GAM337027 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337027 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337027 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337027 is therefore inhibition of MME, a GAM337027 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337027 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337027 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide

sequence of GAM337027 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337027 is therefore inhibition of PRND, a GAM337027 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337027 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337028 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337028 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337028 is therefore inhibition of APPBP2, a GAM337028 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337028 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337028 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337028 is therefore inhibition of BACE2, a GAM337028 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337028 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337028 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337028 is therefore inhibition of FHL2, a GAM337028 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337028 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337028 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337028 is therefore inhibition of IGF1, a GAM337028 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337028 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337028 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337028 is therefore inhibition of MME, a GAM337028 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337028 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337028 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337028 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337028 is therefore inhibition of PRND, a GAM337028 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337028 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337029 CAV1 TGGGAAAAAAGGCAG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

TTTAGAA NM_001753.3) is a GAM337029 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337029 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337029 is therefore inhibition of CAV1, a GAM337029 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337029 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337030 CAV1 TGGGAAAAAAGGCAG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

TTTAGAA NM_001753.3) is a GAM337030 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337030 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337030 is therefore inhibition of CAV1, a GAM337030 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337030 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337031 APBB1 AATGGCAGTCCCTGG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

AGCAGGA 1 (Fe65) (APBB1, Accession NM_145689.1) is a GAM337031 target gene. APBB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337031 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337031 is therefore inhibition of APBB1, a GAM337031 target gene which may modulate the internalization of beta- amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337031 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB1.The function of APBB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337031 SLC17A7 AATGGCAGTCCCTGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

AGCAGGA NM_020309.1) is another GAM337031 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337031 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337031 is therefore inhibition of SLC17A7, a GAM337031 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337031 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337032 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337032 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337032 is therefore inhibition of APPBP2, a GAM337032 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337032 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337032 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337032 is therefore inhibition of BACE2, a GAM337032 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337032 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337032 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337032 is therefore inhibition of FHL2, a GAM337032 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337032 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337032 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337032 is therefore inhibition of IGF1, a GAM337032 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337032 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337032 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337032 is therefore inhibition of MME, a GAM337032 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337032 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337032 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337032 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337032 is therefore inhibition of PRND, a GAM337032 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337032 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337033 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337033 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337033 is therefore inhibition of APPBP2, a GAM337033 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337033 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337033 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337033 is therefore inhibition of BACE2, a GAM337033 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337033 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337033 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337033 is therefore inhibition of FHL2, a GAM337033 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337033 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337033 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337033 is therefore inhibition of IGF1, a GAM337033 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337033 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337033 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337033 is therefore inhibition of MME, a GAM337033 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337033 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337033 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337033 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337033 is therefore inhibition of PRND, a GAM337033 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337033 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337035 AVP GTGTATGTGTGTATG AVP (Accession NM_000490.2) is a GAM337035 target gene. AVP A A
TCTGTGT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337035 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337035 is therefore inhibition of AVP. Accordingly, utilities of GAM337035 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM337036 ADAM10 AGGAAACATCCTCCC A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A
CCTTGTT Accession NM_001110.1) is a GAM337036 target gene. ADAM10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337036 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337036 is therefore inhibition of ADAM10, a GAM337036 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337036 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337037 GLUL TAAGCAGTCTTTCTT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
CTTCTTC NM_002065.3) is a GAM337037 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337037 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337037 is therefore inhibition of GLUL, a GAM337037 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337037 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337037 HD TAAGCAGTCTTTCTT HD (Accession NM_002111.3) is another GAM337037 target gene. HD A A

CTTCTTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337037 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337037 is therefore inhibition of HD. Accordingly, utilities of GAM337037 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337037 HTR2C TAAGCAGTCTTTCTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

CTTCTTC NM_000868.1) is another GAM337037 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337037 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337037 is therefore inhibition of HTR2C, a GAM337037 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337037 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337038 GLUL TAAGCAGTCTTTCTT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

CTTCTTC NM_002065.3) is a GAM337038 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337038 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337038 is therefore inhibition of GLUL, a GAM337038 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337038 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337038 HD TAAGCAGTCTTTCTT HD (Accession NM_002111.3) is another GAM337038 target gene. HD
A A
CTTCTTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337038 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337038 is therefore inhibition of HD. Accordingly, utilities of GAM337038 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337038 HTR2C TAAGCAGTCTTTCTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A
CTTCTTC NM_000868.1) is another GAM337038 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337038 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337038 is therefore inhibition of HTR2C, a GAM337038 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337038 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337039 GLUL TAAGCAGTCTTTCTT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession
A A
CTTCTTC NM_002065.3) is a GAM337039 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337039 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337039 is therefore inhibition of GLUL, a GAM337039 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337039 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to GAM519.

GAM337039 HD TAAGCAGTCTTTCTT HD (Accession NM_002111.3) is another GAM337039 target gene. HD
A A
CTTCTTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337039 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337039 is therefore inhibition of HD. Accordingly, utilities of GAM337039 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337039 HTR2C TAAGCAGTCTTTCTT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A
CTTCTTC NM_000868.1) is another GAM337039 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337039 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337039 is therefore inhibition of HTR2C, a GAM337039 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337039 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337041 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A
GGGTGAC a GAM337041 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337041 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337041 is therefore inhibition of FHL2, a GAM337041 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337041 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337041 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTGAC NM_000618.2) is another GAM337041 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337041 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337041 is therefore inhibition of IGF1, a GAM337041 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337041 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337041 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTGAC another GAM337041 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337041 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337041 is therefore inhibition of PRND, a GAM337041 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337041 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337042 BACE GGAGTATGAGAGAGA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A
ATGGGAC is a GAM337042 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337042 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337042 is therefore inhibition of BACE, a GAM337042 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337042 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337042 BACE2 GGAGTATGAGAGAGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

ATGGGAC NM_138991.1) is another GAM337042 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337042 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337042 is therefore inhibition of BACE2, a GAM337042 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337042 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337042 CNTF GGAGTATGAGAGAGA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

ATGGGAC another GAM337042 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337042 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337042 is therefore inhibition of CNTF, a GAM337042 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337042 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337042 HD GGAGTATGAGAGAGA HD (Accession NM_002111.3) is another GAM337042 target gene. HD A A

ATGGGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337042 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337042 is therefore inhibition of HD. Accordingly, utilities of GAM337042 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337043 ACE TTTTCTGGGCTCCCT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TTTCTGC (ACE, Accession NM_152831.1) is a GAM337043 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337043 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337043 is therefore inhibition of ACE, a GAM337043 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337043 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337043 LRP1 TTTTCTGGGCTCCCT Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

TTTCTGC macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337043 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337043 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337043 is therefore inhibition of LRP1, a GAM337043 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337043 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM1975.

GAM337043 OGDH TTTTCTGGGCTCCCT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
TTTCTGC NM_002541.1) is another GAM337043 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337043 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337043 is therefore inhibition of OGDH, a GAM337043 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337043 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM337043 OLR1 TTTTCTGGGCTCCCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A
TTTCTGC (OLR1, Accession NM_002543.1) is another GAM337043 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337043 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337043 is therefore inhibition of OLR1, a GAM337043 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337043 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337045 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337045 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337045 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337045 is therefore inhibition of APP. Accordingly, utilities of GAM337045 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with APP.

GAM337046 MME AGTGGCTTTGAAACT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GTAATGA enkephalinase, (MME, Accession NM_007288.1) is a GAM337046 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337046 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337046 is therefore inhibition of MME, a GAM337046 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337046 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337047 PLAU TAAGGAGTGGTTCCA Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

ATTTGGG is a GAM337047 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337047 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337047 is therefore inhibition of PLAU, a GAM337047 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337047 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337051 IGF1 GGCTGCAGTGCAACT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTTTCTA NM_000618.2) is a GAM337051 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337051 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337051 is therefore inhibition of IGF1, a

GAM337051 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337051 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337052 IGF1 GGCTGCAGTGCAACT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A CTTTCTA NM_000618.2) is a GAM337052 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337052 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337052 is therefore inhibition of IGF1, a GAM337052 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337052 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337053 SNCA TTGATCACAGCTACT SNCA (Accession NM_000345.2) is a GAM337053 target gene. SNCA A A TTTGTCC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337053 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337053 is therefore inhibition of SNCA. Accordingly, utilities of GAM337053 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM337055 IGF1 AAGCTGCCATTGAAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A ATCTGGG NM_000618.2) is a GAM337055 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337055 is therefore inhibition of IGF1, a GAM337055 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337055 MAPK10 AAGCTGCCATTGAAG ATCTGGG A A Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_002753.2) is another GAM337055 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337055 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337055 is therefore inhibition of MAPK10, a GAM337055 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337055 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337056 IGF1 AAGCTGCCATTGAAG ATCTGGG A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM337056 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337056 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337056 is therefore inhibition of IGF1, a GAM337056 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337056 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337056 MAPK10 AAGCTGCCATTGAAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

ATCTGGG NM_002753.2) is another GAM337056 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337056 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337056 is therefore inhibition of MAPK10, a GAM337056 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337056 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337057 IGF1 AAGCTGCCATTGAAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ATCTGGG NM_000618.2) is a GAM337057 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337057 is therefore inhibition of IGF1, a GAM337057 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337057 MAPK10 AAGCTGCCATTGAAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

ATCTGGG NM_002753.2) is another GAM337057 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337057 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337057 is therefore inhibition of MAPK10, a GAM337057 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337057 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337058 IGF1 AAGCTGCCATTGAAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A ATCTGGG NM_000618.2) is a GAM337058 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337058 is therefore inhibition of IGF1, a GAM337058 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337058 MAPK10 AAGCTGCCATTGAAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A ATCTGGG NM_002753.2) is another GAM337058 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337058 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337058 is therefore inhibition of MAPK10, a GAM337058 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337058 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to GAM55.

GAM337059 ADAM17 CCAAAGTGCTGGGAT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A
TACAGGC factor, (ADAM17, Accession NM_021832.1) is a GAM337059 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337059 is therefore inhibition of ADAM17, a GAM337059 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337059 GFAP CCAAAGTGCTGGGAT GFAP (Accession NM_002055.2) is another GAM337059 target gene. A A
TACAGGC GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337059 is therefore inhibition of GFAP. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337059 HTR2A CCAAAGTGCTGGGAT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
TACAGGC NM_000621.1) is another GAM337059 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337059 is therefore inhibition of HTR2A, a GAM337059 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337059 IAPP CCAAAGTGCTGGGAT Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A

TACAGGC another GAM337059 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337059 is therefore inhibition of IAPP, a GAM337059 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337059 MTNR1A CCAAAGTGCTGGGAT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

TACAGGC another GAM337059 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337059 is therefore inhibition of MTNR1A, a GAM337059 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337059 TGFB1 CCAAAGTGCTGGGAT TGFB1 (Accession NM_000660.1) is another GAM337059 target gene. A A

TACAGGC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337059 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337059 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337059 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337060 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337060 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337060 is therefore inhibition of APPBP2, a GAM337060 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337060 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337060 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337060 is therefore inhibition of BACE2, a GAM337060 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337060 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337060 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337060 is therefore inhibition of FHL2, a GAM337060 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337060 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337060 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337060 is therefore inhibition of IGF1, a GAM337060 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337060 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337060 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337060 is therefore inhibition of

MME, a GAM337060 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337060 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337060 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337060 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337060 is therefore inhibition of PRND, a GAM337060 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337060 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337061 CTNND2 TACAGTTCTGGTTTC Catenin (cadherin- associated protein), Delta 2 (neural A A
TTCTTTA plakophilin- rel (CTNND2, Accession NM_001332.1) is a GAM337061 target gene. CTNND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTNND2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337061 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337061 is therefore inhibition of CTNND2, a GAM337061 target gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337061 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTNND2.The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM337061 PSEN1 TACAGTTCTGGTTTC PSEN1 (Accession NM_000021.2) is another GAM337061 target gene. A A
TTCTTTA PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337061 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337061 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337061 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337062 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337062 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337062 is therefore inhibition of APPBP2, a GAM337062 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337062 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337062 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337062 is therefore inhibition of BACE2, a GAM337062 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337062 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337062 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337062 is therefore inhibition of FHL2, a GAM337062 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337062 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337062 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337062 is therefore inhibition of IGF1, a GAM337062 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337062 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337062 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337062 is therefore inhibition of MME, a GAM337062 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337062 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM337062 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337062 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337062 is therefore inhibition of PRND, a GAM337062 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337062 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337063 GYPA GGTTCTCAAATGAGG Glycophorin A (includes MN blood group) (GYPA, Accession A A GACATTT NM_002099.2) is a GAM337063 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337063 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337063 is therefore inhibition of GYPA, a GAM337063 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337063 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337063 NGB GGTTCTCAAATGAGG Neuroglobin (NGB, Accession NM_021257.2) is another GAM337063 A A GACATTT target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337063 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337063 is therefore inhibition of NGB, a GAM337063 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337063 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337063 PLAU GGTTCTCAAATGAGG Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GACATTT is another GAM337063 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337063 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337063 is therefore inhibition of PLAU, a GAM337063 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337063 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337063 PSEN1 GGTTCTCAAATGAGG PSEN1 (Accession NM_000021.2) is another GAM337063 target gene. A A

GACATTT PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337063 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337063 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337063 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337063 CHAT ACATTTCCAATGTTT Choline Acetyltransferase (CHAT, Accession NM_020986.1) is B A

GGGGACA another GAM337063 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337063 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337063 is therefore inhibition of CHAT, a GAM337063 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337063 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337064 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337064 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337064 is therefore inhibition of APPBP2, a GAM337064 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337064 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337064 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337064 is therefore inhibition of

BACE2, a GAM337064 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337064 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337064 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337064 is therefore inhibition of FHL2, a GAM337064 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337064 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337064 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337064 is therefore inhibition of IGF1, a GAM337064 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337064 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337064 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337064 is therefore inhibition of MME, a GAM337064 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337064 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337064 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337064 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337064 is therefore inhibition of PRND, a GAM337064 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337064 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337066 TNFSF5 AAGTGGCTTTTGTCT TNFSF5 (Accession NM_000074.1) is a GAM337066 target gene. A A

GGCAGAT TNFSF5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TNFSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337066 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337066 is therefore inhibition of TNFSF5. Accordingly, utilities of GAM337066 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFSF5.

GAM337068 APBB2 AGTCAGGGAGACTGT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CAGTAAA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337068 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337068 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337068 is therefore inhibition of APBB2, a GAM337068 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337068 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337068 NGB AGTCAGGGAGACTGT Neuroglobin (NGB, Accession NM_021257.2) is another GAM337068 A A

CAGTAAA target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337068 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337068 is therefore inhibition of NGB, a GAM337068 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337068 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337069 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337069 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337069 is therefore inhibition of APPBP2, a GAM337069 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337069 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337069 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337069 is therefore inhibition of BACE2, a GAM337069 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337069 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337069 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337069 is therefore inhibition of FHL2, a GAM337069 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337069 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM337069 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337069 is therefore inhibition of IGF1, a GAM337069 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337069 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337069 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337069 is therefore inhibition of MME, a GAM337069 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337069 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM337069 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337069 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337069 is therefore inhibition of PRND, a GAM337069 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337069 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337070 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337070 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337070 is therefore inhibition of APPBP2, a GAM337070 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337070 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337070 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337070 is therefore inhibition of BACE2, a GAM337070 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337070 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337070 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337070 is therefore inhibition of FHL2, a GAM337070 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337070 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337070 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337070 is therefore inhibition of IGF1, a GAM337070 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337070 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337070 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337070 is therefore inhibition of

MME, a GAM337070 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337070 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337070 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337070 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A

GGGCAAC

Another function of GAM337070 is therefore inhibition of PRND, a GAM337070 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337070 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337071 DHCR24 AGGCTGAGTGCAGTG 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM337071 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337071 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A

GTGTGAT

A function of GAM337071 is therefore inhibition of DHCR24, a GAM337071 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337071 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337071 FPRL1 AGGCTGAGTGCAGTG FPRL1 (Accession NM_001462.1) is another GAM337071 target gene. FPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

A A

GTGTGAT

BINDING SITE III of Fig.8. Nucleotide sequences of FPRL1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337071 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337071 is therefore inhibition of FPRL1. Accordingly, utilities of GAM337071 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FPRL1.

GAM337071 HTR2A AGGCTGAGTGCAGTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
GTGTGAT NM_000621.1) is another GAM337071 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337071 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337071 is therefore inhibition of HTR2A, a GAM337071 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337071 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337071 IAPP AGGCTGAGTGCAGTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
GTGTGAT another GAM337071 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337071 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337071 is therefore inhibition of IAPP, a GAM337071 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337071 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337074 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337074 target

gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337074 is therefore inhibition of APPBP2, a GAM337074 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337074 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM337074 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337074 is therefore inhibition of BACE2, a GAM337074 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337074 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM337074 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337074 is therefore inhibition of FHL2, a GAM337074 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337074 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337074 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337074 is therefore inhibition of HD. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337074 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337074 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337074 is therefore inhibition of IGF1, a GAM337074 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337074 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337074 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337074 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337074 is therefore inhibition of PRND, a GAM337074 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337074 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337075 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337075 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337075 is therefore inhibition of APPBP2, a GAM337075 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337075 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337075 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337075 is therefore inhibition of BACE2, a GAM337075 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337075 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337075 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337075 is therefore inhibition of FHL2, a GAM337075 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337075 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337075 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337075 is therefore inhibition of HD. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337075 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337075 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337075 is therefore inhibition of IGF1, a GAM337075 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337075 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337075 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337075 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337075 is therefore inhibition of PRND, a GAM337075 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337075 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337076 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337076 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337076 is therefore inhibition of APPBP2, a GAM337076 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337076 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337076 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337076 is therefore inhibition of BACE2, a GAM337076 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337076 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337076 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337076 is therefore inhibition of FHL2, a GAM337076 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337076 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337076 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337076 is therefore inhibition of HD. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337076 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337076 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in

untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337076 is therefore inhibition of IGF1, a GAM337076 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337076 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337076 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337076 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337076 is therefore inhibition of PRND, a GAM337076 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337076 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337077 GYPA GGTTCTCAAATGAGG Glycophorin A (includes MN blood group) (GYPA, Accession A A

GACATTT NM_002099.2) is a GAM337077 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337077 is therefore inhibition of GYPA, a GAM337077 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337077 include diagnosis, prevention and treatment of Alzheimer,

and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337077 NGB A A GGTTCTCAAATGAGG GACATTT Neuroglobin (NGB, Accession NM_021257.2) is another GAM337077 target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337077 is therefore inhibition of NGB, a GAM337077 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337077 PLAU A A GGTTCTCAAATGAGG GACATTT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) is another GAM337077 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337077 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337077 is therefore inhibition of PLAU, a GAM337077 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337077 PSEN1 A A GGTTCTCAAATGAGG GACATTT PSEN1 (Accession NM_000021.2) is another GAM337077 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337077 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337077 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337077 CHAT ACATTTCCAATGTTT GGGGACA Choline Acetyltransferase (CHAT, Accession NM_020986.1) is another GAM337077 target gene. CHAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CHAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CHAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337077 RNA are set forth in Tables 6 and 7, hereby incorporated herein. B A

Another function of GAM337077 is therefore inhibition of CHAT, a GAM337077 target gene which synthesizes the neurotransmitter acetylcholine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337077 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CHAT.The function of CHAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337078 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337078 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337078 is therefore inhibition of APPBP2, a GAM337078 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337078 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337078 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of A A

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337078 is therefore inhibition of BACE2, a GAM337078 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337078 FHL2 A ACTGCACTCCAGCCT A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337078 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

GGGCAAC

Another function of GAM337078 is therefore inhibition of FHL2, a GAM337078 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337078 IGF1 A ACTGCACTCCAGCCT A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337078 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

GGGCAAC

Another function of GAM337078 is therefore inhibition of IGF1, a GAM337078 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337078 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337078 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337078 is therefore inhibition of MME, a GAM337078 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337078 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337078 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337078 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337078 is therefore inhibition of PRND, a GAM337078 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337078 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337079 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337079 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337079 is therefore inhibition of APPBP2, a GAM337079 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337079 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337079 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337079 is therefore inhibition of BACE2, a GAM337079 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337079 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337079 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337079 is therefore inhibition of FHL2, a GAM337079 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337079 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337079 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337079 is therefore inhibition of IGF1, a GAM337079 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337079 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337079 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337079 is therefore inhibition of MME, a GAM337079 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337079 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337079 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337079 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337079 is therefore inhibition of PRND, a GAM337079 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337079 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337080 ADAMTS5 ATGATGAGTCTTAGT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GATCTGG Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM337080 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337080 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337080 is therefore inhibition of ADAMTS5, a GAM337080 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337080 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337081 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337081 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337081 is therefore inhibition of APPBP2, a GAM337081 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337081 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337081 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337081 is therefore inhibition of BACE2, a GAM337081 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337081 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337081 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337081 is therefore inhibition of FHL2, a GAM337081 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337081 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337081 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337081 is therefore inhibition of IGF1, a GAM337081 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337081 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337081 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337081 is therefore inhibition of MME, a GAM337081 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337081 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337081 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337081 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337081 is therefore inhibition of PRND, a GAM337081 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337081 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337082 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337082 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337082 is therefore inhibition of APPBP2, a GAM337082 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337082 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337082 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337082 is therefore inhibition of BACE2, a GAM337082 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337082 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337082 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337082 is therefore inhibition of FHL2, a GAM337082 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337082 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337082 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337082 is therefore inhibition of IGF1, a GAM337082 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337082 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337082 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337082 is therefore inhibition of MME, a GAM337082 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337082 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337082 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337082 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337082 is therefore inhibition of PRND, a GAM337082 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337082 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337083 FHL2 ACTGTACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGGCAAC a GAM337083 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337083 is therefore inhibition of FHL2, a GAM337083 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337083 IGF1 ACTGTACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGGCAAC NM_000618.2) is another GAM337083 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337083 is therefore inhibition of IGF1, a GAM337083 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337083 PRND ACTGTACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

AGGCAAC another GAM337083 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337083 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337083 is therefore inhibition of PRND, a GAM337083 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337083 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337084 FHL2 ACTGTACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGGCAAC a GAM337084 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337084 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337084 is therefore inhibition of FHL2, a GAM337084 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337084 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337084 IGF1 ACTGTACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGGCAAC NM_000618.2) is another GAM337084 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337084 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337084 is therefore inhibition of IGF1, a GAM337084 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337084 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337084 PRND ACTGTACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

AGGCAAC another GAM337084 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337084 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337084 is therefore inhibition of PRND, a GAM337084 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337084 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337087 ACE ATTGCTTGAGCCCAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GAGTTCA (ACE, Accession NM_152831.1) is a GAM337087 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337087 is therefore inhibition of ACE, a GAM337087 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with

Alzheimer. Accordingly, utilities of GAM337087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337087 GFAP ATTGCTTGAGCCCAG GFAP (Accession NM_002055.2) is another GAM337087 target gene. A A

GAGTTCA GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337087 is therefore inhibition of GFAP. Accordingly, utilities of GAM337087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337087 IGF1 ATTGCTTGAGCCCAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAGTTCA NM_000618.2) is another GAM337087 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337087 is therefore inhibition of IGF1, a GAM337087 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337087 PRND ATTGCTTGAGCCCAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GAGTTCA another GAM337087 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337087 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337087 is therefore inhibition of PRND, a GAM337087 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337087 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337088 PSEN1 TTCCCCATGTGATGC PSEN1 (Accession NM_000021.2) is a GAM337088 target gene. PSEN1 A A

TATTGCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337088 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337088 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337088 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337089 PSEN1 TTCCCCATGTGATGC PSEN1 (Accession NM_000021.2) is a GAM337089 target gene. PSEN1 A A

TATTGCT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337089 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337089 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337089 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337091 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337091 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337091 is therefore inhibition of APPBP2,

a GAM337091 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337091 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337091 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337091 is therefore inhibition of BACE2, a GAM337091 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337091 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337091 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337091 is therefore inhibition of FHL2, a GAM337091 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337091 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337091 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337091 is therefore inhibition of IGF1, a GAM337091 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337091 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337091 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337091 is therefore inhibition of MME, a GAM337091 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337091 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337091 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337091 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337091 is therefore inhibition of PRND, a GAM337091 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337091 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337092 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337092 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337092 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337092 is therefore inhibition of APP. Accordingly, utilities of GAM337092 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337093 ADAMTS5 TGGCAGGATTCCTGG A Disintegrin- like and Metalloprotease (reprolysin type) with A A

GATTTCA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM337093 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337093 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337093 is therefore inhibition of ADAMTS5, a GAM337093 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337093 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337093 APPBP2 TGGCAGGATTCCTGG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GATTTCA Protein 2 (APPBP2, Accession NM_006380.2) is another GAM337093 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337093 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337093 is therefore inhibition of APPBP2, a GAM337093 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337093 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337094 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337094 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337094 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337094 is therefore inhibition of APP. Accordingly, utilities of GAM337094 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337095 APBB2 AAGGCTGTGTAGGCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAATTCT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337095 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337095 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337095 is therefore inhibition of APBB2, a GAM337095 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337095 B2M AAGGCTGTGTAGGCA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another A A

GAATTCT GAM337095 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337095 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM337095 is therefore inhibition of B2M, a GAM337095 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337095 PSEN1 AAGGCTGTGTAGGCA PSEN1 (Accession NM_007319.1) is another GAM337095 target gene. A A

GAATTCT PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337095 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337095 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337095 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337096 CTSB CACTGCACTCTAGCC CTSB (Accession NM_147782.1) is a GAM337096 target gene. CTSB A A

TCGGTGA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337096 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337096 is therefore inhibition of CTSB. Accordingly, utilities of GAM337096 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337096 FHL2 CACTGCACTCTAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TCGGTGA another GAM337096 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337096 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337096 is therefore inhibition of

FHL2, a GAM337096 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337096 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337096 IGF1 CACTGCACTCTAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCGGTGA NM_000618.2) is another GAM337096 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337096 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337096 is therefore inhibition of IGF1, a GAM337096 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337096 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337096 PRND CACTGCACTCTAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TCGGTGA another GAM337096 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337096 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337096 is therefore inhibition of PRND, a GAM337096 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337096 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337097 CTSB TGGAAAGCATGTACA CTSB (Accession NM_147783.1) is a GAM337097 target gene. CTSB A A
TTTGGAG BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337097 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337097 is therefore inhibition of CTSB. Accordingly, utilities of GAM337097 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337097 IGF1 TGGAAAGCATGTACA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TTTGGAG NM_000618.2) is another GAM337097 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337097 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337097 is therefore inhibition of IGF1, a GAM337097 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337097 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337098 BACE TCTTTTTGTTGTAGC Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

TGTATGG is a GAM337098 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337098 is therefore inhibition of BACE, a GAM337098 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337098 BCHE TCTTTTTGTTGTAGC BCHE (Accession NM_000055.1) is another GAM337098 target gene. A A

TGTATGG BCHE BINDING SITE1 and BCHE BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BCHE, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE1 and BCHE BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337098 is therefore inhibition of BCHE. Accordingly, utilities of GAM337098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM337098 IL1A TCTTTTTGTTGTAGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TGTATGG GAM337098 target gene. IL1A BINDING SITE1 and IL1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE1 and IL1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337098 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337098 is therefore inhibition of IL1A, a GAM337098 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337098 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337099 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337099 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337099 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337099 is therefore inhibition of APP. Accordingly, utilities of GAM337099 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337100 B2M TAAAGTGTGTATGGG Beta- 2- microglobulin (B2M, Accession NM_004048.1) is a A A
CAGGTGT GAM337100 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337100 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337100 is therefore inhibition of B2M, a GAM337100 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337100 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337101 APBB2 TCTTGGGATAGTGTC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TCATGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337101 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337101 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337101 is therefore inhibition of APBB2, a GAM337101 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337101 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337101 MAPT TCTTGGGATAGTGTC Microtubule- associated Protein Tau (MAPT, Accession A A

TCATGGC NM_173727.1) is another GAM337101 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337101 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337101 is therefore inhibition of MAPT, a GAM337101 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337101 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337105 CTSK TGCAAGTTGTCTTCT CTSK (Accession NM_000396.2) is a GAM337105 target gene. CTSK A A

AGGGTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337105 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337105 is therefore inhibition of CTSK. Accordingly, utilities of GAM337105 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM337105 DLST TGCAAGTTGTCTTCT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

AGGGTGT oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337105 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337105 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337105 is therefore inhibition of DLST, a GAM337105 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337105 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337106 DLST CACAGCATTGGTCAT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGGTCA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM337106 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337106 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337106 is therefore inhibition of DLST, a GAM337106 target gene which catalyzes the oxidative decarboxylation

of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337106 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337108 DLST CACAGCATTGGTCAT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GAGGTCA oxo- glutarat (DLST, Accession NM_001933.2) is a GAM337108 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337108 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337108 is therefore inhibition of DLST, a GAM337108 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337108 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337109 IGF1 ATGGCTCATGTTTGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

AGTCTCA NM_000618.2) is a GAM337109 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337109 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337109 is therefore inhibition of IGF1, a GAM337109 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337109 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337110 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337110 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337110 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337110 is therefore inhibition of APP. Accordingly, utilities of GAM337110 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337111 APPBP2 ACTGTACTTCAGCCT GGGTAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337111 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337111 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337111 is therefore inhibition of APPBP2, a GAM337111 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337111 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337111 FHL2 ACTGTACTTCAGCCT GGGTAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337111 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337111 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337111 is therefore inhibition of FHL2, a GAM337111 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337111 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337111 IGF1 ACTGTACTTCAGCCT GGGTAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337111 target gene. IGF1 BINDING SITE is A A

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337111 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337111 is therefore inhibition of IGF1, a GAM337111 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337111 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337111 PRND ACTGTACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTAAC another GAM337111 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337111 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337111 is therefore inhibition of PRND, a GAM337111 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337111 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337112 APPBP2 ACTGTACTTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGTAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337112 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337112 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337112 is therefore inhibition of APPBP2, a GAM337112 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337112 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337112 FHL2 ACTGTACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTAAC another GAM337112 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337112 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337112 is therefore inhibition of FHL2, a GAM337112 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337112 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337112 IGF1 ACTGTACTTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTAAC NM_000618.2) is another GAM337112 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337112 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337112 is therefore inhibition of IGF1, a GAM337112 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337112 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337112 PRND ACTGTACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTAAC another GAM337112 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337112 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337112 is therefore inhibition of PRND, a GAM337112 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337112 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337113 APPBP2 ACTGTACTTCAGCCT GGGTAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337113 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337113 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337113 is therefore inhibition of APPBP2, a GAM337113 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337113 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337113 FHL2 ACTGTACTTCAGCCT GGGTAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337113 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337113 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337113 is therefore inhibition of FHL2, a GAM337113 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337113 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM337113 IGF1 ACTGTACTTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGTAAC NM_000618.2) is another GAM337113 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337113 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337113 is therefore inhibition of IGF1, a GAM337113 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337113 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337113 PRND ACTGTACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGTAAC another GAM337113 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337113 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337113 is therefore inhibition of PRND, a GAM337113 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337113 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337115 GLUL AGCAGCTCAAGTCTT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
CTCCAGA NM_002065.3) is a GAM337115 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337115 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337115 is therefore inhibition of GLUL, a GAM337115 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337115 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337115 HD AGCAGCTCAAGTCTT HD (Accession NM_002111.3) is another GAM337115 target gene. HD A A CTCCAGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337115 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337115 is therefore inhibition of HD. Accordingly, utilities of GAM337115 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337118 APPBP2 GAGTATTACCTATAT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A CACCGTG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337118 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337118 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337118 is therefore inhibition of APPBP2, a GAM337118 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337118 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337119 ACE AGTGATTTTCCTGCC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TCAGCCT (ACE, Accession NM_152831.1) is a GAM337119 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337119 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337119 is therefore inhibition of ACE, a GAM337119 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337119 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337119 HTR2A AGTGATTTTCCTGCC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
TCAGCCT NM_000621.1) is another GAM337119 target gene. HTR2A BINDING SITE1 and HTR2A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HTR2A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE1 and HTR2A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337119 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337119 is therefore inhibition of HTR2A, a GAM337119 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337119 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337119 IAPP AGTGATTTTCCTGCC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
TCAGCCT another GAM337119 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337119 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337119 is therefore inhibition of IAPP, a GAM337119 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337119 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337119 MTNR1A AGTGATTTTCCTGCC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A
TCAGCCT another GAM337119 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337119 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337119 is therefore inhibition of MTNR1A, a GAM337119 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337119 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337119 RAGE AGTGATTTTCCTGCC Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another A A
TCAGCCT GAM337119 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337119 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337119 is therefore inhibition of RAGE, a GAM337119 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM337119 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM337126 MAPT GCTGAGAAAACCAGG Microtubule- associated Protein Tau (MAPT, Accession A A
TTAATGG NM_016835.1) is a GAM337126 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337126 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337126 is therefore inhibition of MAPT, a

GAM337126 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337126 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337127 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337127 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337127 is therefore inhibition of APPBP2, a GAM337127 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337127 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337127 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337127 is therefore inhibition of BACE2, a GAM337127 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337127 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337127 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337127 is therefore inhibition of FHL2, a GAM337127 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337127 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337127 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337127 is therefore inhibition of HD. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337127 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM337127 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337127 is therefore inhibition of IGF1, a GAM337127 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337127 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337127 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337127 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337127 is therefore inhibition of PRND, a GAM337127 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337127 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337128 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337128 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337128 is therefore inhibition of APPBP2, a GAM337128 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337128 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337128 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337128 is therefore inhibition of BACE2, a GAM337128 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337128 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337128 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337128 is therefore inhibition of FHL2, a GAM337128 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337128 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337128 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337128 is therefore inhibition of HD. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337128 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337128 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337128 is therefore inhibition of IGF1, a GAM337128 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337128 PRND CATTGCACTCCAGCC TGGGCAA A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337128 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337128 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337128 is therefore inhibition of PRND, a GAM337128 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337128 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337129 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337129 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337129 is therefore inhibition of APPBP2, a GAM337129 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337129 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337129 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337129 is therefore inhibition of BACE2, a GAM337129 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337129 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337129 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337129 is therefore inhibition of FHL2, a GAM337129 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337129 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337129 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337129 is therefore inhibition of IGF1, a GAM337129 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337129 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337129 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337129 is therefore inhibition of MME, a GAM337129 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337129 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337129 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337129 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337129 is therefore inhibition of PRND, a GAM337129 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337129 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337130 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCGAT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337130 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337130 is therefore inhibition of APPBP2, a GAM337130 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337130 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCGAT another GAM337130 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337130 is therefore inhibition of FHL2, a GAM337130 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337130 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCGAT NM_000618.2) is another GAM337130 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337130 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337130 is therefore inhibition of IGF1, a GAM337130 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337130 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCGAT another GAM337130 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337130 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337130 is therefore inhibition of PRND, a GAM337130 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337130 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337131 LRP1 TTCTCCCTGCCCACA Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
CATCCAG macroglobulin recep (LRP1, Accession NM_002332.1) is a GAM337131 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337131 is therefore inhibition of LRP1, a GAM337131 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337131 OLR1 TTCTCCCTGCCCACA Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A
CATCCAG (OLR1, Accession NM_002543.1) is another GAM337131 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337131 is therefore inhibition of OLR1, a GAM337131 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337131 TFCP2 TTCTCCCTGCCCACA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM337131 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337131 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A
CATCCAG

Another function of GAM337131 is therefore inhibition of TFCP2, a GAM337131 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337131 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337133 AVP TGAGGACAGGAGGTT AVP (Accession NM_000490.2) is a GAM337133 target gene. AVP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A A
GTGAGTT

A function of GAM337133 is therefore inhibition of AVP. Accordingly, utilities of GAM337133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM337133 IL1B TGAGGACAGGAGGTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A
A
GTGAGTT GAM337133 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337133 is therefore inhibition of IL1B, a GAM337133 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM337133 MAPK10 TGAGGACAGGAGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A
A
GTGAGTT NM_138980.1) is another GAM337133 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337133 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337133 is therefore inhibition of MAPK10, a GAM337133 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337133 MME TGAGGACAGGAGGTT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GTGAGTT enkephalinase, (MME, Accession NM_007287.1) is another GAM337133 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337133 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

Another function of GAM337133 is therefore inhibition of MME, a GAM337133 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337133 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337135 FHL2 CACTGCACTCCAACC TGGACAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM337135 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337135 is therefore inhibition of FHL2, a GAM337135 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337135 IGF1 CACTGCACTCCAACC TGGACAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337135 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337135 is therefore inhibition of IGF1, a GAM337135 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337135 PRND CACTGCACTCCAACC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A

TGGACAA another GAM337135 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337135 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337135 is therefore inhibition of PRND, a GAM337135 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337135 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337136 PSEN1 GAGGGAAGCATGGGA PSEN1 (Accession NM_000021.2) is a GAM337136 target gene. PSEN1 A A

CCATGAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337136 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337136 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337136 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337138 ABCD1 TGAGGCAGGAGTTGG ABCD1 (Accession NM_000033.2) is a GAM337138 target gene. ABCD1 A A

CAAGAGG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337138 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337138 SLC17A7 TGAGGCAGGAGTTGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

CAAGAGG NM_020309.1) is another GAM337138 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM337138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337138 is therefore inhibition of SLC17A7, a GAM337138 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337138 TGFB1 TGAGGCAGGAGTTGG TGFB1 (Accession NM_000660.1) is another GAM337138 target gene. A A

CAAGAGG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337138 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337138 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337138 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337140 AVP TGAGGACAGGAGGTT AVP (Accession NM_000490.2) is a GAM337140 target gene. AVP A A

GTGAGTT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337140 is therefore inhibition of AVP. Accordingly, utilities of GAM337140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM337140 IL1B TGAGGACAGGAGGTT Interleukin 1, Beta (IL1B, Accession NM_000576.2) is another A A

GTGAGTT GAM337140 target gene. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337140 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337140 is therefore inhibition of

IL1B, a GAM337140 target gene which stimulates thymocyte proliferation. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1B.The function of IL1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM604.

GAM337140 MAPK10 TGAGGACAGGAGGTT GTGAGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138980.1) is another GAM337140 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337140 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337140 is therefore inhibition of MAPK10, a GAM337140 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337140 MME TGAGGACAGGAGGTT GTGAGTT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is another GAM337140 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337140 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337140 is therefore inhibition of MME, a GAM337140 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337140 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337143 FHL2 CACTGCACTCCAACC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGACAA a GAM337143 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337143 is therefore inhibition of FHL2, a GAM337143 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337143 IGF1 CACTGCACTCCAACC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGACAA NM_000618.2) is another GAM337143 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337143 is therefore inhibition of IGF1, a GAM337143 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337143 PRND CACTGCACTCCAACC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGACAA another GAM337143 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337143 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337143 is therefore inhibition of PRND, a GAM337143 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM337143 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337144 CRAT CGGTGCTGTTCAACA GGTCCTG A A Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is a GAM337144 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337144 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337144 is therefore inhibition of CRAT, a GAM337144 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337144 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337145 ACE AGGCACTGTGCAGGA TGATGGG A A Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM337145 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337145 is therefore inhibition of ACE, a GAM337145 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337145 APCS AGGCACTGTGCAGGA TGATGGG A A Amyloid P Component, Serum (APCS, Accession NM_001639.2) is another GAM337145 target gene. APCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of APCS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337145 is therefore inhibition of APCS, a GAM337145 target gene which can interact with dna and histones and may scavenge nuclear material released from damaged circulating cells. may also function as a calcium- dependent lectin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APCS.The function of APCS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM772.

GAM337145 NOTCH1 AGGCACTGTGCAGGA Notch (Drosophila) Homolog 1 (translocation- associated) A A

TGATGGG (NOTCH1, Accession NM_017617.2) is another GAM337145 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337145 is therefore inhibition of NOTCH1, a GAM337145 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM337145 OLR1 AGGCACTGTGCAGGA Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

TGATGGG (OLR1, Accession NM_002543.1) is another GAM337145 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337145 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337145 is therefore inhibition of OLR1, a GAM337145 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337145 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337146 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337146 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337146 is therefore inhibition of APPBP2, a GAM337146 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337146 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337146 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337146 is therefore inhibition of BACE2, a GAM337146 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337146 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337146 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337146 is therefore inhibition of FHL2, a GAM337146 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337146 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337146 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337146 is therefore inhibition of IGF1, a GAM337146 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337146 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337146 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337146 is therefore inhibition of MME, a GAM337146 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337146 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337146 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337146 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337146 is therefore inhibition of PRND, a GAM337146 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337146 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337147 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337147 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337147 is therefore inhibition of APPBP2, a GAM337147 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337147 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337147 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide A A

sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337147 is therefore inhibition of BACE2, a GAM337147 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337147 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337147 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337147 is therefore inhibition of FHL2, a GAM337147 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337147 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337147 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337147 is therefore inhibition of IGF1, a GAM337147 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337147 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337147 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337147 is therefore inhibition of MME, a GAM337147 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337147 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337147 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337147 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337147 is therefore inhibition of PRND, a GAM337147 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337147 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337148 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337148 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated

herein.

A function of GAM337148 is therefore inhibition of APPBP2, a GAM337148 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337148 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337148 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337148 is therefore inhibition of BACE2, a GAM337148 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337148 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337148 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337148 is therefore inhibition of FHL2, a GAM337148 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM337148 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM337148 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337148 is therefore inhibition of IGF1, a GAM337148 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337148 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337148 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337148 is therefore inhibition of MME, a GAM337148 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337148 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM337148 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337148 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337148 is therefore inhibition of PRND, a GAM337148 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337148 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337149 OGDH AGGGCAGTGGATCTC Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
TGCAAAG NM_002541.1) is a GAM337149 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337149 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337149 is therefore inhibition of OGDH, a GAM337149 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337149 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM337150 FHL2 CACTGCACTCCAACC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGACAA a GAM337150 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337150 is therefore inhibition of FHL2, a GAM337150 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337150 IGF1 CACTGCACTCCAACC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGACAA NM_000618.2) is another GAM337150 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337150 is therefore inhibition of IGF1, a GAM337150 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337150 PRND CACTGCACTCCAACC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGACAA another GAM337150 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337150 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337150 is therefore inhibition of PRND, a GAM337150 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337150 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337151 FHL2 ACTGCACTCTAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

AGGTGAT a GAM337151 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337151 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337151 is therefore inhibition of FHL2, a GAM337151 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337151 IGF1 ACTGCACTCTAGCCT AGGTGAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337151 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337151 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337151 is therefore inhibition of IGF1, a GAM337151 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337151 PRND ACTGCACTCTAGCCT AGGTGAT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337151 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337151 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337151 is therefore inhibition of PRND, a GAM337151 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337151 TFCP2 ACTGCACTCTAGCCT AGGTGAT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM337151 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337151 RNA are set A A

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337151 is therefore inhibition of TFCP2, a GAM337151 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337151 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337152 ADAM17 AGATGATGTTGGAGT A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

CTGTGCT factor, (ADAM17, Accession NM_021832.1) is a GAM337152 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337152 is therefore inhibition of ADAM17, a GAM337152 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337152 IGF1 AGATGATGTTGGAGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CTGTGCT NM_000618.2) is another GAM337152 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337152 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337152 is therefore inhibition of IGF1, a GAM337152 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337152 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337153 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337153 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337153 is therefore inhibition of APBA1, a GAM337153 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337153 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGGAGC another GAM337153 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337153 is therefore inhibition of FHL2, a GAM337153 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337153 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GGGGAGC NM_000618.2) is another GAM337153 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337153 is therefore inhibition of IGF1, a GAM337153 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337153 PLAU ACTGCACTCCATCCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GGGGAGC is another GAM337153 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337153 is therefore inhibition of PLAU, a GAM337153 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337153 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGGAGC another GAM337153 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337153 is therefore inhibition of PRND, a GAM337153 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337153 TNF ACTGCACTCCATCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

GGGGAGC Accession NM_000594.2) is another GAM337153 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337153 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337153 is therefore inhibition of TNF, a GAM337153 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337153 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337154 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337154 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337154 is therefore inhibition of APPBP2, a GAM337154 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337154 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337154 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337154 is therefore inhibition of

BACE2, a GAM337154 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337154 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337154 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337154 is therefore inhibition of FHL2, a GAM337154 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337154 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337154 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337154 is therefore inhibition of IGF1, a GAM337154 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337154 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337154 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337154 is therefore inhibition of MME, a GAM337154 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337154 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337154 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337154 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337154 is therefore inhibition of PRND, a GAM337154 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337154 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337155 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337155 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337155 is therefore inhibition of APPBP2, a GAM337155 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337155 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337155 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337155 is therefore inhibition of BACE2, a GAM337155 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337155 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337155 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337155 is therefore inhibition of FHL2, a GAM337155 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337155 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337155 target gene. IGF1 BINDING SITE is A A

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337155 is therefore inhibition of IGF1, a GAM337155 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337155 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337155 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337155 is therefore inhibition of MME, a GAM337155 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337155 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337155 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337155 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337155 is therefore inhibition of PRND, a GAM337155 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM337155 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337156 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337156 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337156 is therefore inhibition of APPBP2, a GAM337156 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337156 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337156 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337156 is therefore inhibition of BACE2, a GAM337156 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337156 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337156 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337156 is therefore inhibition of FHL2, a GAM337156 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337156 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337156 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337156 is therefore inhibition of IGF1, a GAM337156 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337156 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337156 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337156 is therefore inhibition of MME, a GAM337156 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337156 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337156 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337156 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337156 is therefore inhibition of PRND, a GAM337156 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337156 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337157 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGTGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337157 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337157 is therefore inhibition of APPBP2, a GAM337157 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337157 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGTGA another GAM337157 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337157 is therefore inhibition of FHL2, a GAM337157 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337157 IGF1 CATTGCACTCCAGCC A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
TGGGTGA NM_000618.2) is another GAM337157 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337157 is therefore inhibition of IGF1, a GAM337157 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337157 PRND CATTGCACTCCAGCC A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
TGGGTGA another GAM337157 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337157 is therefore inhibition of PRND, a GAM337157 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337157 target A A TNFRSF5 CATTGCACTCCAGCC TGGGTGA

TNFRSF5 (Accession NM_152854.1) is another GAM337157 target gene. TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE1 and TNFRSF5 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337157 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337157 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM337157 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM337158 DLST AATGTGCATGGATCG A A CTCAGAA

Dihydrolipoamide S- succinyltransferase (E2 component of 2- oxo- glutarat (DLST, Accession NM_001933.2) is a GAM337158 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337158 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337158 is therefore inhibition of DLST, a GAM337158 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337158 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337159 APP TGTGCACAACATGCA A A GGTTTGT

APP (Accession NM_000484.1) is a GAM337159 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337159 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337159 is therefore inhibition of APP. Accordingly, utilities of GAM337159 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337160 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337160 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337160 is therefore inhibition of APPBP2, a GAM337160 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337160 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337160 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337160 is therefore inhibition of BACE2, a GAM337160 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337160 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337160 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337160 is therefore inhibition of FHL2, a GAM337160 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337160 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337160 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337160 is therefore inhibition of IGF1, a GAM337160 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337160 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337160 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337160 is therefore inhibition of MME, a GAM337160 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337160 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337160 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337160 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337160 is therefore inhibition of PRND, a GAM337160 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337160 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337161 AVP AGGGGGTTTAGCTCC AVP (Accession NM_000490.2) is a GAM337161 target gene. AVP A A

ACAGGGT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337161 is therefore inhibition of AVP. Accordingly, utilities of GAM337161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM337161 BACE2 AGGGGGTTTAGCTCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

ACAGGGT NM_138992.1) is another GAM337161 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337161 is therefore inhibition of BACE2, a GAM337161 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337161 HD AGGGGGTTTAGCTCC HD (Accession NM_002111.3) is another GAM337161 target gene. HD A A

ACAGGGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337161 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337161 is therefore inhibition of HD. Accordingly, utilities of GAM337161 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337162 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337162 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337162 is therefore inhibition of APPBP2, a GAM337162 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337162 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337162 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337162 is therefore inhibition of BACE2, a GAM337162 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337162 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337162 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337162 is therefore inhibition of FHL2, a GAM337162 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337162 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337162 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337162 is therefore inhibition of IGF1, a GAM337162 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337162 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337162 target gene. MME BINDING SITE is a target binding site found in the

5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337162 is therefore inhibition of MME, a GAM337162 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337162 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM337162 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337162 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337162 is therefore inhibition of PRND, a GAM337162 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337162 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337166 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337166 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337166 is therefore inhibition of APBA1, a GAM337166 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337166 FHL2 ACTGCACTCCATCCT A A GGGGAGC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337166 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337166 is therefore inhibition of FHL2, a GAM337166 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337166 IGF1 ACTGCACTCCATCCT A A GGGGAGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337166 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337166 is therefore inhibition of IGF1, a GAM337166 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337166 PLAU ACTGCACTCCATCCT A A GGGGAGC Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) is another GAM337166 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337166 is therefore inhibition of PLAU, a GAM337166 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337166 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGGAGC another GAM337166 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337166 is therefore inhibition of PRND, a GAM337166 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337166 TNF ACTGCACTCCATCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A GGGGAGC Accession NM_000594.2) is another GAM337166 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337166 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337166 is therefore inhibition of TNF, a GAM337166 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337166 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337167 CNTF TTTGCAGCTTCCAAA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

TTTCTGA GAM337167 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337167 is therefore inhibition of CNTF, a GAM337167 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337167 SLC17A7 TTTGCAGCTTCCAAA SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

TTTCTGA NM_020309.1) is another GAM337167 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337167 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337167 is therefore inhibition of SLC17A7, a GAM337167 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337167 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337168 APPBP2 TGAGATGAACCCGGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

ACCTCAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337168 target gene. APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337168 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337168 is therefore inhibition of APPBP2,

a GAM337168 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337168 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337169 DLST GAGAAGTAGGAATAT Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

CAGGAGT oxo- glutarat (DLST, Accession NM_001933.2) is a GAM337169 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337169 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337169 is therefore inhibition of DLST, a GAM337169 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337169 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337170 MME CAGAGCAGTGGAGAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TAGGTCT enkephalinase, (MME, Accession NM_007288.1) is a GAM337170 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337170 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337170 is therefore inhibition of MME, a GAM337170 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337170 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337171 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337171 target gene.

APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337171 is therefore inhibition of APBA1, a GAM337171 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337171 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGGAGC another GAM337171 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337171 is therefore inhibition of FHL2, a GAM337171 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337171 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGGAGC NM_000618.2) is another GAM337171 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337171 is therefore inhibition of IGF1, a GAM337171 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer.

Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337171 PLAU ACTGCACTCCATCCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GGGGAGC is another GAM337171 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337171 is therefore inhibition of PLAU, a GAM337171 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337171 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGGAGC another GAM337171 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337171 is therefore inhibition of PRND, a GAM337171 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337171 TNF ACTGCACTCCATCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

GGGGAGC Accession NM_000594.2) is another GAM337171 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337171 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337171 is therefore inhibition of TNF, a GAM337171 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337171 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337172 APPBP2 ACAAAAAATTAGCCA GACTGGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337172 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337172 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337172 is therefore inhibition of APPBP2, a GAM337172 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337172 IGF1 ACAAAAAATTAGCCA GACTGGT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337172 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337172 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337172 is therefore inhibition of IGF1, a GAM337172 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337172 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337173 PRND TTGAGAATGCTGTAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

TTGGAGG GAM337173 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337173 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337173 is therefore inhibition of PRND, a GAM337173 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337173 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337174 CNTF GCAGGTGTGCAAATC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

ACAACTT GAM337174 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337174 is therefore inhibition of CNTF, a GAM337174 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337174 IGF1 GCAGGTGTGCAAATC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACAACTT NM_000618.2) is another GAM337174 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337174 is therefore inhibition of IGF1, a GAM337174 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337174 PLAU GCAGGTGTGCAAATC Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

ACAACTT is another GAM337174 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337174 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337174 is therefore inhibition of PLAU, a GAM337174 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337174 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337177 ACE GTGAAGAAGTTGCTT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

CATCCTT (ACE, Accession NM_152831.1) is a GAM337177 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337177 is therefore inhibition of ACE, a GAM337177 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337177 APPBP2 GTGAAGAAGTTGCTT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CATCCTT Protein 2 (APPBP2, Accession NM_006380.2) is another GAM337177

target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337177 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337177 is therefore inhibition of APPBP2, a GAM337177 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337177 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337179 IGF1 CTGTGGGTGAGAGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGAGA NM_000618.2) is a GAM337179 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337179 is therefore inhibition of IGF1, a GAM337179 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337179 OGDH CTGTGGGTGAGAGAG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A
TGGGAGA NM_002541.1) is another GAM337179 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337179 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337179 is therefore inhibition of OGDH, a GAM337179 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337179 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM337179 OLR1 CTGTGGGTGAGAGAG TGGGAGA Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 (OLR1, Accession NM_002543.1) is another GAM337179 target gene. OLR1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337179 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337179 is therefore inhibition of OLR1, a GAM337179 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337179 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337180 TNFRSF6 AGTGCTTTGATTATG AGAAAGT TNFRSF6 (Accession NM_152875.1) is a GAM337180 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337180 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337180 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM337180 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM337181 TNFRSF6 AGTGCTTTGATTATG AGAAAGT TNFRSF6 (Accession NM_152875.1) is a GAM337181 target gene. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337181 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337181 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM337181 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with TNFRSF6.

GAM337183 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337183 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337183 is therefore inhibition of APPBP2, a GAM337183 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337183 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337183 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337183 is therefore inhibition of BACE2, a GAM337183 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337183 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337183 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337183 is therefore inhibition of FHL2, a GAM337183 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337183 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337183 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337183 is therefore inhibition of HD. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337183 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337183 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337183 is therefore inhibition of IGF1, a GAM337183 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337183 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337183 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337183 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337183 is therefore inhibition of PRND, a GAM337183 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337183 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337184 APPBP2 GACTGGCTAATTTAT AAAGGAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337184 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337184 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337184 is therefore inhibition of APPBP2, a GAM337184 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337184 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337185 APPBP2 ATTGTTCTCCAGCCT GGGCGAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337185 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337185 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337185 is therefore inhibition of APPBP2, a GAM337185 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337185 FHL2 ATTGTTCTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCGAC another GAM337185 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337185 is therefore inhibition of FHL2, a GAM337185 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337185 IGF1 ATTGTTCTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCGAC NM_000618.2) is another GAM337185 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337185 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337185 is therefore inhibition of IGF1, a GAM337185 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337185 PRND ATTGTTCTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCGAC another GAM337185 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337185 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337185 is therefore inhibition of PRND, a GAM337185 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337185 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337186 APPBP2 ATTGTTCTCCAGCCT GGGCGAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337186 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337186 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337186 is therefore inhibition of APPBP2, a GAM337186 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337186 FHL2 ATTGTTCTCCAGCCT GGGCGAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337186 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337186 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337186 is therefore inhibition of FHL2, a GAM337186 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337186 IGF1 ATTGTTCTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCGAC NM_000618.2) is another GAM337186 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337186 is therefore inhibition of IGF1, a GAM337186 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337186 PRND ATTGTTCTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCGAC another GAM337186 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337186 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337186 is therefore inhibition of PRND, a GAM337186 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337186 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337187 IGF1 GGACTGAGACATGAT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TAACTTG NM_000618.2) is a GAM337187 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337187 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337187 is therefore inhibition of IGF1, a GAM337187 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity

and therefore is associated with Alzheimer. Accordingly, utilities of GAM337187 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337188 FHL2 TGCACCAATGCACTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CAGCCTG a GAM337188 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337188 is therefore inhibition of FHL2, a GAM337188 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337188 IGF1 TGCACCAATGCACTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CAGCCTG NM_000618.2) is another GAM337188 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337188 is therefore inhibition of IGF1, a GAM337188 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337188 MAPT TGCACCAATGCACTC Microtubule- associated Protein Tau (MAPT, Accession A A

CAGCCTG NM_173727.1) is another GAM337188 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337188 is therefore inhibition of MAPT, a GAM337188 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337188 PRND TGCACCAATGCACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A CAGCCTG another GAM337188 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337188 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337188 is therefore inhibition of PRND, a GAM337188 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337188 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337189 FHL2 TGCACCAATGCACTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A CAGCCTG a GAM337189 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337189 is therefore inhibition of FHL2, a GAM337189 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337189 IGF1 TGCACCAATGCACTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

CAGCCTG NM_000618.2) is another GAM337189 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337189 is therefore inhibition of IGF1, a GAM337189 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337189 MAPT TGCACCAATGCACTC Microtubule- associated Protein Tau (MAPT, Accession A A

CAGCCTG NM_173727.1) is another GAM337189 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337189 is therefore inhibition of MAPT, a GAM337189 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337189 PRND TGCACCAATGCACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CAGCCTG another GAM337189 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2,

and secondary structure complementarity to the nucleotide sequence of GAM337189 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337189 is therefore inhibition of PRND, a GAM337189 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337189 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337190 MAPK10 ACTGGCACAGACATC A A TGTCAAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession NM_138981.1) is a GAM337190 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337190 is therefore inhibition of MAPK10, a GAM337190 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337190 MTNR1A ACTGGCACAGACATC A A TGTCAAG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM337190 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337190 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337190 is therefore inhibition of MTNR1A, a GAM337190 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337190 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337191 SLC6A4 TCACAGTTGAGAGAA GGTTCTG Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is a GAM337191 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337191 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337191 is therefore inhibition of SLC6A4, a GAM337191 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337191 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM337192 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337192 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337192 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337192 is therefore inhibition of APP. Accordingly, utilities of GAM337192 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337193 S100B TATTTGTTTTTAATG CTGGGTG S100 Calcium- binding Protein, Beta (neural) (S100B, Accession NM_006272.1) is a GAM337193 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337193 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337193 is therefore inhibition of S100B, a GAM337193 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337193 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM337194 ABCD1 CTGGCTCCCAGGAGG ABCD1 (Accession NM_000033.2) is a GAM337194 target gene.
ABCD1 A A

CCTCTCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337194 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337194 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337194 CAV2 CTGGCTCCCAGGAGG Caveolin 2 (CAV2, Accession NM_001233.2) is another
GAM337194 A A

CCTCTCT target gene. CAV2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337194 is therefore inhibition of CAV2, a GAM337194 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337194 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337194 HD CTGGCTCCCAGGAGG HD (Accession NM_002111.3) is another GAM337194 target gene.
HD A A

CCTCTCT BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337194 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337194 is therefore inhibition of HD. Accordingly, utilities of GAM337194 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337195 ABCD1 CTGGCTCCCAGGAGG ABCD1 (Accession NM_000033.2) is a GAM337195 target gene. ABCD1 A A

CCTCTCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337195 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337195 CAV2 CTGGCTCCCAGGAGG Caveolin 2 (CAV2, Accession NM_001233.2) is another GAM337195 A A

CCTCTCT target gene. CAV2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337195 is therefore inhibition of CAV2, a GAM337195 target gene which may function as an accessory protein in conjunction with caveolin- 1and act as a scaffolding protein within caveolar membranes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV2.The function of CAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337195 HD CTGGCTCCCAGGAGG HD (Accession NM_002111.3) is another GAM337195 target gene. HD A A

CCTCTCT BINDING SITE1 and HD BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE1 and HD BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337195 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337195 is therefore inhibition of HD. Accordingly, utilities of GAM337195 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337196 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337196 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337196 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337196 is therefore inhibition of APP. Accordingly, utilities of GAM337196 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337197 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337197 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337197 is therefore inhibition of APPBP2, a GAM337197 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337197 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337197 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337197 is therefore inhibition of BACE2, a GAM337197 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM337197 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337197 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337197 is therefore inhibition of FHL2, a GAM337197 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337197 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337197 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337197 is therefore inhibition of HD. Accordingly, utilities of GAM337197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337197 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337197 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337197 is therefore inhibition of IGF1, a GAM337197 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337197 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337197 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337197 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337197 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337197 is therefore inhibition of PRND, a GAM337197 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337197 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337199 BACE TGGTTAGTTTTATGG Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

GCCTGGA is a GAM337199 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337199 is therefore inhibition of BACE, a GAM337199 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337199 CLU TGGTTAGTTTTATGG Clusterin (complement lysis inhibitor, SP- 40,40, sulfated A A

GCCTGGA glycoprotein (CLU, Accession NM_001831.1) is another GAM337199 target gene. CLU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CLU BINDING SITE, and secondary structure complementarity to the nucleotide sequence

of GAM337199 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337199 is therefore inhibition of CLU, a GAM337199 target gene which has a role in the terminal complement reaction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CLU.The function of CLU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM337199 LRP1 TGGTTAGTTTTATGG GCCTGGA Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337199 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337199 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337199 is therefore inhibition of LRP1, a GAM337199 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337199 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337200 CRAT TGCGCCCCTGTACTC TGGGCAA Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is a GAM337200 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337200 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337200 is therefore inhibition of CRAT, a GAM337200 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337200 PRND TGCGCCCCTGTACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337200 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337200 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337200 is therefore inhibition of PRND, a GAM337200 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337200 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337202 IL1A TTGAGGTCATCTAAT Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is a A A
GGTGTTG GAM337202 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337202 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337202 is therefore inhibition of IL1A, a GAM337202 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337202 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337203 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337203 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337203 is therefore inhibition of APPBP2,

a GAM337203 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337203 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337203 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337203 is therefore inhibition of BACE2, a GAM337203 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337203 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337203 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337203 is therefore inhibition of FHL2, a GAM337203 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337203 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337203 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337203 is therefore inhibition of IGF1, a GAM337203 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337203 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337203 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337203 is therefore inhibition of MME, a GAM337203 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337203 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337203 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337203 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337203 is therefore inhibition of PRND, a GAM337203 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337203 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337204 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337204 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337204 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337204 is therefore inhibition of APP. Accordingly, utilities of GAM337204 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337206 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337206 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337206 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337206 is therefore inhibition of APP. Accordingly, utilities of GAM337206 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337207 IAPP TTTTGCAAATTACTA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a A A

AATTTCT GAM337207 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337207 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337207 is therefore inhibition of IAPP, a GAM337207 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337207 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM347.

GAM337208 IAPP TTTTGCAAATTACTA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a A A

AATTTCT GAM337208 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337208 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337208 is therefore inhibition of IAPP, a GAM337208 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337208 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337209 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337209 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337209 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337209 is therefore inhibition of APP. Accordingly, utilities of GAM337209 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337210 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337210 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337210 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337210 is therefore inhibition of APP. Accordingly, utilities of GAM337210 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337211 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337211 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337211 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337211 is therefore inhibition of APP. Accordingly, utilities of GAM337211 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337212 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337212 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337212 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337212 is therefore inhibition of APP. Accordingly, utilities of GAM337212 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337213 APPBP2 ACTGTACTTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337213 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337213 is therefore inhibition of APPBP2, a GAM337213 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337213 FHL2 ACTGTACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337213 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337213 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337213 is therefore inhibition of FHL2, a GAM337213 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337213 IGF1 ACTGTACTTCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337213 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337213 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337213 is therefore inhibition of IGF1, a GAM337213 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337213 PRND ACTGTACTTCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337213 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337213 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337213 is therefore inhibition of PRND, a GAM337213 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337213 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337214 APPBP2 ACTGTACTTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337214 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337214 is therefore inhibition of APPBP2, a GAM337214 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337214 FHL2 ACTGTACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337214 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337214 is therefore inhibition of FHL2, a GAM337214 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337214 IGF1 ACTGTACTTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337214 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337214 is therefore inhibition of IGF1, a GAM337214 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337214 PRND ACTGTACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337214 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337214 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337214 is therefore inhibition of PRND, a GAM337214 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337214 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337215 APPBP2 ACTGTACTTCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337215 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337215 is therefore inhibition of APPBP2, a GAM337215 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337215 FHL2 ACTGTACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337215 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337215 is therefore inhibition of FHL2, a GAM337215 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337215 IGF1 ACTGTACTTCAGCCT AA GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337215 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337215 is therefore inhibition of IGF1, a GAM337215 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337215 PRND ACTGTACTTCAGCCT AA GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337215 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337215 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337215 is therefore inhibition of PRND, a GAM337215 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337215 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337216 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337216 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337216 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337216 is therefore inhibition of APP. Accordingly, utilities of GAM337216 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337217 DLST AGGCAGTAAGGGAGA Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

GTTTTGC oxo- glutarat (DLST, Accession NM_001933.2) is a GAM337217 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337217 is therefore inhibition of DLST, a GAM337217 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337217 HD AGGCAGTAAGGGAGA HD (Accession NM_002111.3) is another GAM337217 target gene. HD A A

GTTTTGC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337217 is therefore inhibition of HD. Accordingly, utilities of GAM337217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337217 TRPM2 AGGCAGTAAGGGAGA TRPM2 (Accession NM_003307.1) is another GAM337217 target gene. A A

GTTTTGC TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337217 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337217 is therefore inhibition of TRPM2, a GAM337217 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337217 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337218 APBB2 TGGCTCTGTCTATTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGATGTG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337218 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337218 is therefore inhibition of APBB2, a GAM337218 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337218 CASP3 TGGCTCTGTCTATTG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

GGATGTG Accession NM_032991.1) is another GAM337218 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337218 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337218 is therefore inhibition of CASP3, a GAM337218 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic

cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337218 MPO TGGCTCTGTCTATTG GGATGTG Myeloperoxidase (MPO, Accession NM_000250.1) is another GAM337218 target gene. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337218 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337218 is therefore inhibition of MPO, a GAM337218 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337218 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM337220 APBB2 GCTGGGTTGAGCTGG GCTGAGA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337220 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337220 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337220 is therefore inhibition of APBB2, a GAM337220 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337220 CRAT GCTGGGTTGAGCTGG GCTGAGA Carnitine Acetyltransferase (CRAT, Accession NM_144782.1) is another GAM337220 target gene. CRAT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337220 is therefore inhibition of CRAT, a GAM337220 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337220 IGF1 GCTGGGTTGAGCTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCTGAGA NM_000618.2) is another GAM337220 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337220 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337220 is therefore inhibition of IGF1, a GAM337220 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337220 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337221 BACE GCAGAGAGGAAGGCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A

ATGAAAC is a GAM337221 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337221 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337221 is therefore inhibition of BACE, a GAM337221 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337221 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The

function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337224 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337224 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337224 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337224 is therefore inhibition of APP. Accordingly, utilities of GAM337224 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337225 HD GGTGACAGAGACTCT HD (Accession NM_002111.3) is a GAM337225 target gene. HD A A
GCCTCGA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337225 is therefore inhibition of HD. Accordingly, utilities of GAM337225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337225 TFCP2 GGTGACAGAGACTCT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
GCCTCGA another GAM337225 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337225 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337225 is therefore inhibition of TFCP2, a GAM337225 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337225 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337226 APPBP2 TACCCTGTGATCATC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGTGTGC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337226 target

gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337226 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337226 is therefore inhibition of APPBP2, a GAM337226 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337226 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337227 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337227 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337227 is therefore inhibition of APPBP2, a GAM337227 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337227 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337227 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337227 is therefore inhibition of

BACE2, a GAM337227 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337227 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337227 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337227 is therefore inhibition of FHL2, a GAM337227 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337227 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337227 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337227 is therefore inhibition of IGF1, a GAM337227 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337227 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337227 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337227 is therefore inhibition of MME, a GAM337227 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337227 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337227 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337227 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337227 is therefore inhibition of PRND, a GAM337227 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337227 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337228 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337228 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337228 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337228 is therefore inhibition of APP. Accordingly, utilities of GAM337228 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337229 ACE AGCACCACAACAGGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

ACTGGGC (ACE, Accession NM_152831.1) is a GAM337229 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337229 is therefore inhibition of ACE, a GAM337229 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337229 PLCD1 AGCACCACAACAGGG Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is
A A

ACTGGGC another GAM337229 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337229 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337229 is therefore inhibition of PLCD1, a GAM337229 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM337229 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337230 UBB TTCACCAACCACTCC Ubiquitin B (UBB, Accession NM_018955.2) is a GAM337230 target
A A

ACCAGCT gene. UBB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by UBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of UBB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337230 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337230 is therefore inhibition of UBB, a GAM337230 target gene which marks cellular proteins for degradation

and therefore is associated with Alzheimer. Accordingly, utilities of GAM337230 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with UBB.The function of UBB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3298.

GAM337232 PSEN1 TATTGGGTTTAAAGT PSEN1 (Accession NM_007318.1) is a GAM337232 target gene. PSEN1 A A

CACCGTT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337232 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337232 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337232 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337233 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337233 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337233 is therefore inhibition of APPBP2, a GAM337233 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337233 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337233 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337233 is therefore inhibition of BACE2, a GAM337233 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337233 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337233 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337233 is therefore inhibition of FHL2, a GAM337233 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337233 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337233 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337233 is therefore inhibition of IGF1, a GAM337233 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM337233 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337233 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337233 is therefore inhibition of MME, a GAM337233 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337233 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337233 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337233 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337233 is therefore inhibition of PRND, a GAM337233 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337233 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337234 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337234 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337234 is therefore inhibition of APPBP2, a GAM337234 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337234 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337234 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337234 is therefore inhibition of BACE2, a GAM337234 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337234 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337234 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337234 is therefore inhibition of FHL2, a GAM337234 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337234 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM337234 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337234 is therefore inhibition of IGF1, a GAM337234 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337234 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337234 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337234 is therefore inhibition of MME, a GAM337234 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337234 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM337234 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337234 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337234 is therefore inhibition of PRND, a GAM337234 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337234 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337235 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337235 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337235 is therefore inhibition of APPBP2, a GAM337235 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337235 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337235 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337235 is therefore inhibition of BACE2, a GAM337235 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337235 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337235 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337235 is therefore inhibition of FHL2, a GAM337235 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337235 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337235 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337235 is therefore inhibition of IGF1, a GAM337235 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337235 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337235 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337235 is therefore inhibition of

MME, a GAM337235 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337235 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337235 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337235 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337235 is therefore inhibition of PRND, a GAM337235 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337235 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337237 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337237 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337237 is therefore inhibition of APPBP2, a GAM337237 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337237 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337237 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337237 is therefore inhibition of BACE2, a GAM337237 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337237 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337237 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337237 is therefore inhibition of FHL2, a GAM337237 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337237 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337237 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337237 is therefore inhibition of IGF1, a GAM337237 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337237 MME ACTGCACTCCAGCCT GGGCAAC A A

Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337237 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337237 is therefore inhibition of MME, a GAM337237 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337237 PRND ACTGCACTCCAGCCT GGGCAAC A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337237 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337237 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337237 is therefore inhibition of PRND, a GAM337237 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337237 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337238 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337238 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by

APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337238 is therefore inhibition of APPBP2, a GAM337238 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337238 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337238 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337238 is therefore inhibition of BACE2, a GAM337238 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337238 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337238 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337238 is therefore inhibition of FHL2, a GAM337238 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337238 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337238 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337238 is therefore inhibition of IGF1, a GAM337238 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337238 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337238 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337238 is therefore inhibition of MME, a GAM337238 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337238 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337238 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337238 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337238 is therefore inhibition of PRND, a GAM337238 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337238 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337242 NGB AGATATGGTGAACAG Neuroglobin (NGB, Accession NM_021257.2) is a GAM337242 target A A
ACAGATG gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337242 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337242 is therefore inhibition of NGB, a GAM337242 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337242 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337243 APPBP2 TGCTACATTTCTTCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TTCTTGG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337243 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337243 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337243 is therefore inhibition of APPBP2, a GAM337243 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337243 IGF1 TGCTACATTTCTTCA TTCTTGG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337243 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337243 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337243 is therefore inhibition of IGF1, a GAM337243 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337243 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337245 HTR2A TAGAAAGCTAACAAG CTAGAGA 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is a GAM337245 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337245 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337245 is therefore inhibition of HTR2A, a GAM337245 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337245 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337245 MME TAGAAAGCTAACAAG CTAGAGA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337245 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337245 RNA are set forth in Tables 6 and A A

7, hereby incorporated herein.

Another function of GAM337245 is therefore inhibition of MME, a GAM337245 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337245 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337246 HTR2A TAGAAAGCTAACAAG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
CTAGAGA NM_000621.1) is a GAM337246 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337246 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337246 is therefore inhibition of HTR2A, a GAM337246 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337246 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337246 MME TAGAAAGCTAACAAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A
CTAGAGA enkephalinase, (MME, Accession NM_000902.2) is another GAM337246 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337246 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337246 is therefore inhibition of MME, a GAM337246 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337246 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337247 MAPK10 AAGAGCTGAGTAATT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

GGGGGCA NM_002753.2) is a GAM337247 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337247 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337247 is therefore inhibition of MAPK10, a GAM337247 target gene which is a members of the mitogen- activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337247 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337247 MAPT AAGAGCTGAGTAATT Microtubule- associated Protein Tau (MAPT, Accession A A
GGGGGCA NM_005910.2) is another GAM337247 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337247 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337247 is therefore inhibition of MAPT, a GAM337247 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337247 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337247 SNCA AAGAGCTGAGTAATT SNCA (Accession NM_000345.2) is another GAM337247 target gene. A A
GGGGGCA SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337247 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337247 is therefore inhibition of SNCA. Accordingly, utilities of GAM337247 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM337248 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337248 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337248 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337248 is therefore inhibition of APP. Accordingly, utilities of GAM337248 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337250 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337250 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337250 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337250 is therefore inhibition of APP. Accordingly, utilities of GAM337250 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337251 GFAP TATCGCTTGAGCCCA GFAP (Accession NM_002055.2) is a GAM337251 target gene. GFAP A A

GGAGTTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337251 is therefore inhibition of GFAP. Accordingly, utilities of GAM337251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337251 IGF1 TATCGCTTGAGCCCA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGAGTTT NM_000618.2) is another GAM337251 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337251 is therefore inhibition of IGF1, a GAM337251 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337251 PRND TATCGCTTGAGCCCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGAGTTT another GAM337251 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337251 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337251 is therefore inhibition of PRND, a GAM337251 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337251 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337254 BACE TTTCCTGTTTTGGTT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138973.1) A A TGGAGAG is a GAM337254 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337254 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337254 is therefore inhibition of BACE, a GAM337254 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337254 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337254 GYPA TTTCCTGTTTTGGTT Glycophorin A (includes MN blood group) (GYPA, Accession A A

TGGAGAG NM_002099.2) is another GAM337254 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337254 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337254 is therefore inhibition of GYPA, a GAM337254 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337254 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337255 GFAP TGGCTCAGTTTGCTC GFAP (Accession NM_002055.2) is a GAM337255 target gene. GFAP A A

AGCAGTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337255 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337255 is therefore inhibition of GFAP. Accordingly, utilities of GAM337255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337255 IL1A TGGCTCAGTTTGCTC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

AGCAGTG GAM337255 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337255 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337255 is therefore inhibition of IL1A, a GAM337255 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337255 PSEN2 TGGCTCAGTTTGCTC PSEN2 (Accession NM_012486.1) is another GAM337255 target gene. A A

AGCAGTG PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337255 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337255 is therefore inhibition of PSEN2. Accordingly, utilities of GAM337255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM337255 S100B TGGCTCAGTTTGCTC S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A
AGCAGTG NM_006272.1) is another GAM337255 target gene. S100B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337255 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337255 is therefore inhibition of S100B, a GAM337255 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM337255 SNCAIP TGGCTCAGTTTGCTC Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, A A
AGCAGTG Accession NM_005460.1) is another GAM337255 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337255 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337255 is therefore inhibition of SNCAIP, a GAM337255 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337255 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337256 GFAP TGGCTCAGTTTGCTC GFAP (Accession NM_002055.2) is a GAM337256 target gene. GFAP A A

AGCAGTG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337256 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337256 is therefore inhibition of GFAP. Accordingly, utilities of GAM337256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337256 IL1A TGGCTCAGTTTGCTC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

AGCAGTG GAM337256 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337256 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337256 is therefore inhibition of IL1A, a GAM337256 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337256 PSEN2 TGGCTCAGTTTGCTC PSEN2 (Accession NM_012486.1) is another GAM337256 target gene. A A

AGCAGTG PSEN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337256 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337256 is therefore inhibition of PSEN2. Accordingly, utilities of GAM337256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM337256 S100B TGGCTCAGTTTGCTC S100 Calcium- binding Protein, Beta (neural) (S100B, Accession A A

AGCAGTG NM_006272.1) is another GAM337256 target gene. S100B BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of S100B BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337256 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337256 is therefore inhibition of S100B, a GAM337256 target gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with S100B.The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.

GAM337256 SNCAIP TGGCTCAGTTTGCTC AGCAGTG Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is another GAM337256 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337256 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337256 is therefore inhibition of SNCAIP, a GAM337256 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337256 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337257 FHL2 TGGCTGTTTGGGGTT GCCGTGT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is a GAM337257 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337257 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337257 is therefore inhibition of FHL2, a GAM337257 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337257 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337257 MAPK10 TGGCTGTTTGGGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

GCCGTGT NM_138980.1) is another GAM337257 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337257 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337257 is therefore inhibition of MAPK10, a GAM337257 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337257 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337258 FHL2 TGGCTGTTTGGGGTT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GCCGTGT a GAM337258 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337258 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337258 is therefore inhibition of FHL2, a GAM337258 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337258 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337258 MAPK10 TGGCTGTTTGGGGTT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

GCCGTGT NM_138980.1) is another GAM337258 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337258 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337258 is therefore inhibition of MAPK10, a GAM337258 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337258 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337263 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337263 target gene. APP
A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337263 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337263 is therefore inhibition of APP. Accordingly, utilities of GAM337263 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337264 APBA2 TAGTTGTTTGGGATT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A
A

GGTAGTG 2 (X11- I (APBA2, Accession NM_005503.2) is a GAM337264 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337264 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337264 is therefore inhibition of APBA2, a GAM337264 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337264 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337264 HTR2C TAGTTGTTTGGGATT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A

GGTAGTG NM_000868.1) is another GAM337264 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337264 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337264 is therefore inhibition of HTR2C, a GAM337264 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337264 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337265 APBA2 TAGTTGTTTGGGATT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGTAGTG 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM337265 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337265 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337265 is therefore inhibition of APBA2, a GAM337265 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337265 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337265 HTR2C TAGTTGTTTGGGATT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

GGTAGTG NM_000868.1) is another GAM337265 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337265 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337265 is therefore inhibition of HTR2C, a GAM337265 target gene which activates phospholipase C and

regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337265 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337266 APBA2 TAGTTGTTTGGGATT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGTAGTG 2 (X11- l (APBA2, Accession NM_005503.2) is a GAM337266 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337266 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337266 is therefore inhibition of APBA2, a GAM337266 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337266 HTR2C TAGTTGTTTGGGATT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A

GGTAGTG NM_000868.1) is another GAM337266 target gene. HTR2C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337266 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337266 is therefore inhibition of HTR2C, a GAM337266 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337266 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337267 ESR2 TGCAGCAGACCTTTT Estrogen Receptor 2 (ER beta) (ESR2, Accession NM_001437.1) is A A

GCCTTCT a GAM337267 target gene. ESR2 BINDING SITE is a target binding site

found in the 5` untranslated region of mRNA encoded by ESR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ESR2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337267 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337267 is therefore inhibition of ESR2, a GAM337267 target gene which transcriptional activator involved in regulation of reproduction. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337267 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ESR2.The function of ESR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM4188.

GAM337269 CAV1 AGTAAGCAAACTCAG TTTAATC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM337269 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337269 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337269 is therefore inhibition of CAV1, a GAM337269 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337269 FOS AGTAAGCAAACTCAG TTTAATC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is another GAM337269 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337269 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337269 is therefore inhibition of FOS, a GAM337269 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337269 MAPK10 AGTAAGCAAACTCAG Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

TTTAATC NM_138982.1) is another GAM337269 target gene. MAPK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337269 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337269 is therefore inhibition of MAPK10, a GAM337269 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337269 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337270 APBB2 TGATGACTGAAGTGG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CCTGGAC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337270 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337270 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337270 is therefore inhibition of APBB2, a GAM337270 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337270 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337271 APBB2 TGATGACTGAAGTGG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

CCTGGAC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337271 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337271 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337271 is therefore inhibition of APBB2, a GAM337271 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337271 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337273 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337273 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337273 is therefore inhibition of APPBP2, a GAM337273 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337273 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337273 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337273 is therefore inhibition of BACE2, a GAM337273 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337273 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337273 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337273 is therefore inhibition of FHL2, a GAM337273 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337273 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337273 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337273 is therefore inhibition of IGF1, a GAM337273 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337273 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337273 target gene. MME BINDING SITE is a target binding site found in the

5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337273 is therefore inhibition of MME, a GAM337273 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337273 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM337273 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337273 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337273 is therefore inhibition of PRND, a GAM337273 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337273 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337274 ADAM10 ACTGGAGTTTGTTCA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, A A AGAAATA Accession NM_001110.1) is a GAM337274 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337274 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337274 is therefore inhibition of ADAM10, a GAM337274 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337274 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337275 ADAM10 ACTGGAGTTTGTTCA AGAAATA A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110.1) is a GAM337275 target gene. ADAM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337275 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337275 is therefore inhibition of ADAM10, a GAM337275 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337275 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM10.The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337277 ADAM17 TTAGATATGTCCCCT TCTATAA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM337277 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337277 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337277 is therefore inhibition of ADAM17, a GAM337277 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337277 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337278 HD AGTCCAGTGTTCTCT GCTCTGT HD (Accession NM_002111.3) is a GAM337278 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337278 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337278 is therefore inhibition of HD. Accordingly, utilities of GAM337278 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337278 TFCP2 AGTCCAGTGTTCTCT GCTCTGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is another GAM337278 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337278 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337278 is therefore inhibition of TFCP2, a GAM337278 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337278 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337279 ACE GAGGTCACTGTTGGA TGTCAGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM337279 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337279 is therefore inhibition of ACE, a GAM337279 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337279 APLP2 GAGGTCACTGTTGGA TGTCAGA Amyloid Beta (A4) Precursor- like Protein 2 (APLP2, Accession NM_001642.1) is another GAM337279 target gene. APLP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APLP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of APLP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337279 is therefore inhibition of APLP2, a GAM337279 target gene which may play a role in the regulation of hemostasis. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP2.The function of APLP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM674.

GAM337279 APOC1 GAGGTCACTGTTGGA A A TGTCAGA Apolipoprotein C- I (APOC1, Accession NM_001645.2) is another GAM337279 target gene. APOC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APOC1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337279 is therefore inhibition of APOC1, a GAM337279 target gene which appears to modulate the interaction of apoe with beta- migrating vldl and inhibit binding of beta- vldl to the ldl receptor- related protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APOC1.The function of APOC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1144.

GAM337279 B2M GAGGTCACTGTTGGA A A TGTCAGA Beta- 2- microglobulin (B2M, Accession NM_004048.1) is another GAM337279 target gene. B2M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of B2M BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337279 is therefore inhibition of B2M, a GAM337279 target gene which is the beta- chain of major histocompatibility complex class I molecules. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with B2M.The function of B2M and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337279 FOS A TGTCAGA A GAGGTCACTGTTGGA V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, Accession NM_005252.2) is another GAM337279 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337279 is therefore inhibition of FOS, a GAM337279 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337279 HD A TGTCAGA A GAGGTCACTGTTGGA HD (Accession NM_002111.3) is another GAM337279 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337279 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337279 is therefore inhibition of HD. Accordingly, utilities of GAM337279 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337281 APPBP2 A GGGCAAC A ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337281 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337281 is therefore inhibition of APPBP2, a GAM337281 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337281 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337281 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337281 is therefore inhibition of BACE2, a GAM337281 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337281 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337281 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337281 is therefore inhibition of FHL2, a GAM337281 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337281 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337281 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337281 is therefore inhibition of IGF1, a GAM337281 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337281 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337281 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337281 is therefore inhibition of MME, a GAM337281 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337281 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337281 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337281 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337281 is therefore inhibition of PRND, a GAM337281 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337281 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337282 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337282 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337282 is therefore inhibition of APPBP2, a GAM337282 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337282 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337282 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337282 is therefore inhibition of BACE2, a GAM337282 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337282 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337282 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337282 is therefore inhibition of FHL2, a GAM337282 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337282 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337282 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337282 is therefore inhibition of IGF1, a GAM337282 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337282 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337282 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337282 is therefore inhibition of MME, a GAM337282 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337282 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337282 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337282 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337282 is therefore inhibition of PRND, a GAM337282 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337282 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337283 ABCD1 GGCACTGAGAAGCAA ABCD1 (Accession NM_000033.2) is a GAM337283 target gene. ABCD1 A A

ACAGGAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337283 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337283 GLUL GGCACTGAGAAGCAA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

ACAGGAT NM_002065.3) is another GAM337283 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337283 is therefore inhibition of GLUL, a GAM337283 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337283 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337283 MAPT GGCACTGAGAAGCAA Microtubule- associated Protein Tau (MAPT, Accession A A

ACAGGAT NM_173727.1) is another GAM337283 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337283 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337283 is therefore inhibition of MAPT, a GAM337283 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337283 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337285 APPBP2 GGAGGAGGTGTGAAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

AAATGAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337285 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337285 is therefore inhibition of APPBP2, a GAM337285 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337285 GLUL GGAGGAGGTGTGAAG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

AAATGAA NM_002065.3) is another GAM337285 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337285 is therefore inhibition of GLUL, a GAM337285 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337285 MME GGAGGAGGTGTGAAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

AAATGAA enkephalinase, (MME, Accession NM_007288.1) is another GAM337285 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337285 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337285 is therefore inhibition of MME, a GAM337285 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337285 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337286 APPBP2 GGAGGAGGTGTGAAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

AAATGAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337286 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337286 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337286 is therefore inhibition of APPBP2, a GAM337286 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337286 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337286 GLUL GGAGGAGGTGTGAAG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

AAATGAA NM_002065.3) is another GAM337286 target gene. GLUL BINDING SITE1 and GLUL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GLUL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE1 and GLUL BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337286 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337286 is therefore inhibition of GLUL, a GAM337286 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337286 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337286 MME GGAGGAGGTGTGAAG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

AAATGAA enkephalinase, (MME, Accession NM_007288.1) is another GAM337286 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337286 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337286 is therefore inhibition of MME, a GAM337286 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337286 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337288 ADAM17 CACTGGGATTACAGA A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

TGTGAGC factor, (ADAM17, Accession NM_021832.1) is a GAM337288 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337288 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337288 is therefore inhibition of ADAM17, a GAM337288 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337288 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337288 MTNR1A CACTGGGATTACAGA A A TGTGAGC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM337288 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337288 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337288 is therefore inhibition of MTNR1A, a GAM337288 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337288 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337288 TGFB1 CACTGGGATTACAGA A A TGTGAGC TGFB1 (Accession NM_000660.1) is another GAM337288 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337288 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337288 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337288 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337289 ADAM17 CACTGGGATTACAGA A A TGTGAGC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, (ADAM17, Accession NM_021832.1) is a GAM337289 target gene. ADAM17 BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337289 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337289 is therefore inhibition of ADAM17, a GAM337289 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337289 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337289 MTNR1A CACTGGGATTACAGA A A TGTGAGC Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM337289 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337289 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337289 is therefore inhibition of MTNR1A, a GAM337289 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337289 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337289 TGFB1 CACTGGGATTACAGA A A TGTGAGC TGFB1 (Accession NM_000660.1) is another GAM337289 target gene. TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337289 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337289 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337289 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337290 ADAM17 TCACAGAGACTTGGG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis
A A
CCTCAAA factor, (ADAM17, Accession NM_003183.3) is a GAM337290 target gene.
ADAM17 BINDING SITE is a target binding site found in the 3`
untranslated region of multiple transcripts of mRNA encoded by
ADAM17, corresponding to a target binding site such as BINDING SITE
I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide
sequences of ADAM17 BINDING SITE, and secondary structure
complementarity to the nucleotide sequence of GAM337290 RNA are set
forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337290 is therefore inhibition of ADAM17,
a GAM337290 target gene which is a member of ADAM family of zinc
metalloproteases. and therefore is associated with Alzheimer.
Accordingly, utilities of GAM337290 include diagnosis, prevention
and treatment of Alzheimer, and of other diseases and clinical
conditions associated with ADAM17.The function of ADAM17 and its
association with various diseases and clinical conditions, has been
established by previous studies, as described hereinabove with
reference to GAM317.
GAM337291 HD ATAAGCACAGGGAGG HD (Accession NM_002111.3) is a GAM337291 target gene. HD
A A
TTCTGTC BINDING SITE is a target binding site found in the 3` untranslated
region of mRNA encoded by HD, corresponding to a target binding site
such as BINDING SITE I, BINDING SITE II or BINDING SITE III of
Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary
structure complementarity to the nucleotide sequence of GAM337291
RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337291 is therefore inhibition of HD.
Accordingly, utilities of GAM337291 include diagnosis, prevention
and treatment of Alzheimer, and of other diseases and clinical
conditions associated with HD.
GAM337291 HTR2C ATAAGCACAGGGAGG 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession
A A
TTCTGTC NM_000868.1) is another GAM337291 target gene. HTR2C BINDING SITE is
a target binding site found in the 3` untranslated region of mRNA
encoded by HTR2C, corresponding to a target binding site such as
BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.
Nucleotide sequences of HTR2C BINDING SITE, and secondary structure
complementarity to the nucleotide sequence of GAM337291 RNA are set
forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337291 is therefore inhibition of
HTR2C, a GAM337291 target gene which activates phospholipase C and
regulates intracellular calcium flux. and therefore is associated
with Alzheimer. Accordingly, utilities of GAM337291 include
diagnosis, prevention and treatment of Alzheimer, and of other
diseases and clinical conditions associated with HTR2C.The function
of HTR2C and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337291 LRP1 ATAAGCACAGGGAGG TTCTGTC A A Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337291 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337291 is therefore inhibition of LRP1, a GAM337291 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337291 TRPM2 ATAAGCACAGGGAGG TTCTGTC A A TRPM2 (Accession NM_003307.1) is another GAM337291 target gene. TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337291 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337291 is therefore inhibition of TRPM2, a GAM337291 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337291 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337292 APP TGTGCACAACATGCA GGTTTGT A A APP (Accession NM_000484.1) is a GAM337292 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337292 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337292 is therefore inhibition of APP. Accordingly, utilities of GAM337292 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337293 GFAP TTCAGTTCTTGACCT GFAP (Accession NM_002055.2) is a GAM337293 target gene. GFAP A A

GCCCCAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337293 is therefore inhibition of GFAP. Accordingly, utilities of GAM337293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337293 NGB TTCAGTTCTTGACCT Neuroglobin (NGB, Accession NM_021257.2) is another GAM337293 A A

GCCCCAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337293 is therefore inhibition of NGB, a GAM337293 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337293 TFCP2 TTCAGTTCTTGACCT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

GCCCCAG another GAM337293 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337293 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337293 is therefore inhibition of TFCP2, a GAM337293 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337293 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337294 GFAP TTCAGTTCTTGACCT GFAP (Accession NM_002055.2) is a GAM337294 target gene.
GFAP A A
GCCCCAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337294 is therefore inhibition of GFAP. Accordingly, utilities of GAM337294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337294 NGB TTCAGTTCTTGACCT Neuroglobin (NGB, Accession NM_021257.2) is another GAM337294
A A
GCCCCAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337294 is therefore inhibition of NGB, a GAM337294 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337294 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337294 TFCP2 TTCAGTTCTTGACCT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A
A
GCCCCAG another GAM337294 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337294 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337294 is therefore inhibition of TFCP2, a GAM337294 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337294 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337296 BAX GTGAGAATGGAGGAA A A GAACAGT BCL2- associated X Protein (BAX, Accession NM_138763.1) is a GAM337296 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337296 is therefore inhibition of BAX, a GAM337296 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM337296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM337296 CASP3 GTGAGAATGGAGGAA A A GAACAGT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_004346.2) is another GAM337296 target gene. CASP3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337296 is therefore inhibition of CASP3, a GAM337296 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337296 MME GTGAGAATGGAGGAA A A GAACAGT Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337296 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337296 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337296 is therefore inhibition of MME, a GAM337296 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337296 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337297 BAX GTGAGAATGGAGGAA BCL2- associated X Protein (BAX, Accession NM_138763.1) is a A A
GAACAGT GAM337297 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337297 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337297 is therefore inhibition of BAX, a GAM337297 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM337297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM337297 CASP3 GTGAGAATGGAGGAA Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A
GAACAGT Accession NM_004346.2) is another GAM337297 target gene. CASP3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337297 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337297 is therefore inhibition of CASP3, a GAM337297 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337297 MME GTGAGAATGGAGGAA Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GAACAGT enkephalinase, (MME, Accession NM_000902.2) is another GAM337297 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337297 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337297 is therefore inhibition of MME, a GAM337297 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337297 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337298 CTSB AGGCTGAGTGACTGG CTSB (Accession NM_147782.1) is a GAM337298 target gene. CTSB A A

GAGTTAG BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337298 is therefore inhibition of CTSB. Accordingly, utilities of GAM337298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337298 MME AGGCTGAGTGACTGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GAGTTAG enkephalinase, (MME, Accession NM_007288.1) is another GAM337298 target gene. MME BINDING SITE1 and MME BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MME, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE1 and MME BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337298 is therefore inhibition of MME, a GAM337298 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM337298 NCSTN AGGCTGAGTGACTGG NCSTN (Accession NM_015331.1) is another GAM337298 target gene. A A

GAGTTAG NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337298 is therefore inhibition of NCSTN, a GAM337298 target gene which has a central role in presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337298 SLC17A7 AGGCTGAGTGACTGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

GAGTTAG NM_020309.1) is another GAM337298 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337298 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337298 is therefore inhibition of SLC17A7, a GAM337298 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337298 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337299 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GAGTGAC a GAM337299 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337299 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337299 is therefore inhibition of FHL2, a GAM337299 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337299 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337299 HD ACTGCACTCCATCCT HD (Accession NM_002111.3) is another GAM337299 target gene. HD A A

GAGTGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337299 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337299 is therefore inhibition of HD. Accordingly, utilities of GAM337299 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337299 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAGTGAC NM_000618.2) is another GAM337299 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337299 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337299 is therefore inhibition of IGF1, a GAM337299 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337299 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337299 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GAGTGAC another GAM337299 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337299 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337299 is therefore inhibition of PRND, a GAM337299 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337299 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337300 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GAGTGAC a GAM337300 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337300 is therefore inhibition of FHL2, a GAM337300 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337300 HD ACTGCACTCCATCCT HD (Accession NM_002111.3) is another GAM337300 target gene. HD A A

GAGTGAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337300 is therefore inhibition of HD. Accordingly, utilities of GAM337300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337300 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GAGTGAC NM_000618.2) is another GAM337300 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337300 is therefore inhibition of IGF1, a GAM337300 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337300 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GAGTGAC another GAM337300 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337300 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337300 is therefore inhibition of PRND, a GAM337300 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337300 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337301 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337301 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337301 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337301 is therefore inhibition of APP. Accordingly, utilities of GAM337301 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337302 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337302 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary

structure complementarity to the nucleotide sequence of GAM337302 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337302 is therefore inhibition of APP. Accordingly, utilities of GAM337302 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337303 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337303 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337303 is therefore inhibition of APPBP2, a GAM337303 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337303 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337303 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337303 is therefore inhibition of BACE2, a GAM337303 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337303 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337303 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337303 is therefore inhibition of FHL2, a GAM337303 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337303 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337303 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337303 is therefore inhibition of IGF1, a GAM337303 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337303 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337303 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337303 is therefore inhibition of

MME, a GAM337303 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337303 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337303 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337303 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337303 is therefore inhibition of PRND, a GAM337303 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337303 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337304 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337304 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337304 is therefore inhibition of APPBP2, a GAM337304 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337304 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337304 target gene. BACE2 BINDING SITE is A A

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337304 is therefore inhibition of BACE2, a GAM337304 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337304 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337304 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337304 is therefore inhibition of FHL2, a GAM337304 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337304 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337304 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337304 is therefore inhibition of IGF1, a GAM337304 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337304 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337304 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337304 is therefore inhibition of MME, a GAM337304 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337304 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337304 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337304 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337304 is therefore inhibition of PRND, a GAM337304 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337304 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337305 SNCAIP CAGAAAGTAGAAAGC AGATTCG Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is a GAM337305 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. A A

Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337305 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337305 is therefore inhibition of SNCAIP, a GAM337305 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337305 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337306 SNCAIP CAGAAAGTAGAAAGC AGATTCG Synuclein, Alpha Interacting Protein (synphilin) (SNCAIP, Accession NM_005460.1) is a GAM337306 target gene. SNCAIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCAIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCAIP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337306 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337306 is therefore inhibition of SNCAIP, a GAM337306 target gene which promotes formation of cytosolic inclusions in neurons. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337306 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCAIP.The function of SNCAIP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1300.

GAM337310 APP TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337310 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337310 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337310 is therefore inhibition of APP. Accordingly, utilities of GAM337310 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337311 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337311 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or A A

BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337311 is therefore inhibition of APPBP2, a GAM337311 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337311 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337311 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337311 is therefore inhibition of BACE2, a GAM337311 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337311 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337311 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337311 is therefore inhibition of FHL2, a GAM337311 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337311 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337311 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337311 is therefore inhibition of HD. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337311 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337311 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337311 is therefore inhibition of IGF1, a GAM337311 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337311 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337311 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337311 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337311 is therefore inhibition of

PRND, a GAM337311 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337311 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337312 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337312 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337312 is therefore inhibition of APPBP2, a GAM337312 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337312 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337312 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337312 is therefore inhibition of BACE2, a GAM337312 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337312 FHL2 CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337312 target gene. FHL2 BINDING SITE1 and FHL2 BINDING A A

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337312 is therefore inhibition of FHL2, a GAM337312 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337312 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337312 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337312 is therefore inhibition of HD. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337312 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337312 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337312 is therefore inhibition of IGF1, a GAM337312 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM337312 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337312 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337312 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337312 is therefore inhibition of PRND, a GAM337312 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337312 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337313 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337313 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337313 is therefore inhibition of APPBP2, a GAM337313 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337313 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337313 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337313 is therefore inhibition of BACE2, a GAM337313 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337313 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337313 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337313 is therefore inhibition of FHL2, a GAM337313 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337313 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337313 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337313 is therefore inhibition of HD. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337313 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337313 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337313 is therefore inhibition of IGF1, a GAM337313 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337313 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337313 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337313 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337313 is therefore inhibition of PRND, a GAM337313 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337313 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337314 APPBP2 ATTGCACTTCAGCCT GGGTGAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337314 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337314 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337314 is therefore inhibition of APPBP2, a GAM337314 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337314 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337314 FHL2 ATTGCACTTCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGTGAC another GAM337314 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337314 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337314 is therefore inhibition of FHL2, a GAM337314 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337314 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337314 IGF1 ATTGCACTTCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGTGAC NM_000618.2) is another GAM337314 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337314 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337314 is therefore inhibition of IGF1, a GAM337314 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337314 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337314 PRND ATTGCACTTCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGTGAC another GAM337314 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337314 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337314 is therefore inhibition of PRND, a GAM337314 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337314 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337314 TNFRSF5 ATTGCACTTCAGCCT TNFRSF5 (Accession NM_152854.1) is another GAM337314 target A A

GGGTGAC gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337314 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337314 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM337314 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM337315 ACE AGGTGGCACTGTGTG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GGGTGGG (ACE, Accession NM_152831.1) is a GAM337315 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337315 is therefore inhibition of ACE, a GAM337315 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337315 APBB2 AGGTGGCACTGTGTG Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGGTGGG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM337315 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337315 is therefore inhibition of APBB2, a GAM337315 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337315 FOS AGGTGGCACTGTGTG V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
GGGTGGG Accession NM_005252.2) is another GAM337315 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337315 is therefore inhibition of FOS, a GAM337315 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337315 HD AGGTGGCACTGTGTG HD (Accession NM_002111.3) is another GAM337315 target gene. HD A A
GGGTGGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337315 is therefore inhibition of HD. Accordingly, utilities of GAM337315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337315 NCSTN AGGTGGCACTGTGTG NCSTN (Accession NM_015331.1) is another GAM337315 target gene. A A
GGGTGGG NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337315 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337315 is therefore inhibition of NCSTN, a GAM337315 target gene which has a central role in presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337315 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337317 APBB2 GAGGTGAAGGAACAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

ATGCTGA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337317 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337317 is therefore inhibition of APBB2, a GAM337317 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337317 SNCA GAGGTGAAGGAACAA SNCA (Accession NM_000345.2) is another GAM337317 target gene. A A

ATGCTGA SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337317 is therefore inhibition of SNCA. Accordingly, utilities of GAM337317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and

clinical conditions associated with SNCA.

GAM337317 TFCP2 GAGGTGAAGGAACAA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

ATGCTGA another GAM337317 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337317 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337317 is therefore inhibition of TFCP2, a GAM337317 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337317 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337318 APBB2 GAGGTGAAGGAACAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

ATGCTGA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337318 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337318 is therefore inhibition of APBB2, a GAM337318 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337318 SNCA GAGGTGAAGGAACAA SNCA (Accession NM_000345.2) is another GAM337318 target gene. A A

ATGCTGA SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337318 is therefore inhibition of SNCA. Accordingly, utilities of GAM337318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM337318 TFCP2 GAGGTGAAGGAACAA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is
A A
ATGCTGA another GAM337318 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337318 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337318 is therefore inhibition of TFCP2, a GAM337318 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337318 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337319 APBB2 GAGGTGAAGGAACAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member
A A
ATGCTGA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337319 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337319 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337319 is therefore inhibition of APBB2, a GAM337319 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337319 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337319 SNCA GAGGTGAAGGAACAA SNCA (Accession NM_000345.2) is another GAM337319 target gene. A A
ATGCTGA SNCA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCA BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337319 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337319 is therefore inhibition of SNCA. Accordingly, utilities of GAM337319 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCA.

GAM337319 TFCP2 GAGGTGAAGGAACAA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
ATGCTGA another GAM337319 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337319 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337319 is therefore inhibition of TFCP2, a GAM337319 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337319 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337320 CAV1 TCCCCAAGCCTTGTA Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A
CCAGCGT NM_001753.3) is a GAM337320 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337320 is therefore inhibition of CAV1, a GAM337320 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337320 GFAP TCCCCAAGCCTTGTA GFAP (Accession NM_002055.2) is another GAM337320 target gene. A A
CCAGCGT GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337320 is therefore inhibition of GFAP. Accordingly, utilities of GAM337320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337320 TFCP2 TCCCCAAGCCTTGTA Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A
CCAGCGT another GAM337320 target gene. TFCP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337320 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337320 is therefore inhibition of TFCP2, a GAM337320 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337320 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337321 FHL2 ACCTGCATTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGCTGAC a GAM337321 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337321 is therefore inhibition of FHL2, a GAM337321 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337321 IGF1 ACCTGCATTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGCTGAC NM_000618.2) is another GAM337321 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337321 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337321 is therefore inhibition of IGF1, a GAM337321 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337321 MAPT ACCTGCATTCCAGCC TGCTGAC Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is another GAM337321 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337321 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337321 is therefore inhibition of MAPT, a GAM337321 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337321 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337324 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337324 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337324 is therefore inhibition of APPBP2,

a GAM337324 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337324 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337324 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337324 is therefore inhibition of BACE2, a GAM337324 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337324 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337324 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337324 is therefore inhibition of FHL2, a GAM337324 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337324 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337324 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337324 is therefore inhibition of IGF1, a GAM337324 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337324 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337324 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337324 is therefore inhibition of MME, a GAM337324 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337324 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337324 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337324 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337324 is therefore inhibition of PRND, a GAM337324 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337324 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337326 ABCD1 CTTTGGCCACGGGGA ABCD1 (Accession NM_000033.2) is a GAM337326 target gene.
ABCD1 A A
TATGAAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337326 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337326 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337326 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337326 DHCR24 CTTTGGCCACGGGGA 24- dehydrocholesterol Reductase (DHCR24, Accession
A A
TATGAAT NM_014762.1) is another GAM337326 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337326 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337326 is therefore inhibition of DHCR24, a GAM337326 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337326 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337327 ABCD1 CTTTGGCCACGGGGA ABCD1 (Accession NM_000033.2) is a GAM337327 target gene.
ABCD1 A A
TATGAAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337327 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337327 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337327 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with ABCD1.

GAM337327 DHCR24 CTTTGGCCACGGGGA A A TATGAAT 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM337327 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337327 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337327 is therefore inhibition of DHCR24, a GAM337327 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337327 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337328 ABCD1 CTTTGGCCACGGGGA A A TATGAAT ABCD1 (Accession NM_000033.2) is a GAM337328 target gene. ABCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337328 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337328 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337328 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337328 DHCR24 CTTTGGCCACGGGGA A A TATGAAT 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is another GAM337328 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337328 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337328 is therefore inhibition of DHCR24, a GAM337328 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337328 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM44.

GAM337329 CNTF TGGAATTGAGTTCCC Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

TGGGTTT GAM337329 target gene. CNTF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337329 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337329 is therefore inhibition of CNTF, a GAM337329 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337329 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337330 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337330 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337330 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337330 is therefore inhibition of APP. Accordingly, utilities of GAM337330 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337331 APPBP2 TTGCACTCCAGCCTG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGTAACA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337331 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337331 is therefore inhibition of APPBP2, a GAM337331 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337331 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337331 FHL2 TTGCACTCCAGCCTG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGTAACA another GAM337331 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337331 is therefore inhibition of FHL2, a GAM337331 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337331 IGF1 TTGCACTCCAGCCTG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGTAACA NM_000618.2) is another GAM337331 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337331 is therefore inhibition of IGF1, a GAM337331 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337331 PRND TTGCACTCCAGCCTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGTAACA another GAM337331 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337331 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337331 is therefore inhibition of PRND, a GAM337331 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337331 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337333 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337333 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337333 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337333 is therefore inhibition of APP. Accordingly, utilities of GAM337333 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337334 BACE GAGAGTGCTTTGGGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

GTAGGCC is a GAM337334 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337334 is therefore inhibition of BACE, a GAM337334 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337334 SLC17A7 GAGAGTGCTTTGGGT SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

GTAGGCC NM_020309.1) is another GAM337334 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337334 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337334 is therefore inhibition of SLC17A7, a GAM337334 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337334 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337336 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337336 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337336 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337336 is therefore inhibition of APP. Accordingly, utilities of GAM337336 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337337 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337337 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337337 is therefore inhibition of APPBP2, a GAM337337 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337337 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337337 target gene. BACE2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337337 is therefore inhibition of BACE2, a GAM337337 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337337 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337337 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337337 is therefore inhibition of FHL2, a GAM337337 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337337 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337337 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337337 is therefore inhibition of IGF1, a GAM337337 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337337 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337337 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337337 is therefore inhibition of MME, a GAM337337 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337337 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337337 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337337 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337337 is therefore inhibition of PRND, a GAM337337 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337337 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337341 APBB2 AGTGGGATGGAGTCA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GCAGAAG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337341 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337341 is therefore inhibition of APBB2, a GAM337341 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337341 GLUL AGTGGGATGGAGTCA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
GCAGAAG NM_002065.3) is another GAM337341 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337341 is therefore inhibition of GLUL, a GAM337341 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337341 IL1A AGTGGGATGGAGTCA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
GCAGAAG GAM337341 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337341 is therefore inhibition of IL1A, a GAM337341 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337341 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337341 NGB AGTGGGATGGAGTCA Neuroglobin (NGB, Accession NM_021257.2) is another GAM337341 A A

GCAGAAG target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337341 is therefore inhibition of NGB, a GAM337341 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337341 PRND AGTGGGATGGAGTCA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GCAGAAG another GAM337341 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337341 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337341 is therefore inhibition of PRND, a GAM337341 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337341 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337343 CNTF AGATGGAGTTGCAGG Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is a A A

TGGTCCT GAM337343 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337343 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337343 is therefore inhibition of CNTF, a GAM337343 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337343 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337344 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337344 target gene. APP
A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337344 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337344 is therefore inhibition of APP. Accordingly, utilities of GAM337344 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337345 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A
A

GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337345 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337345 is therefore inhibition of APBA1, a GAM337345 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337345 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A

GGGGAGC another GAM337345 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337345 is therefore inhibition of FHL2, a GAM337345 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337345 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGGAGC NM_000618.2) is another GAM337345 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337345 is therefore inhibition of IGF1, a GAM337345 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337345 PLAU ACTGCACTCCATCCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GGGGAGC is another GAM337345 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337345 is therefore inhibition of PLAU, a GAM337345 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM282.

GAM337345 PRND ACTGCACTCCATCCT GGGGAGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337345 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337345 is therefore inhibition of PRND, a GAM337345 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337345 TNF ACTGCACTCCATCCT GGGGAGC Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM337345 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337345 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337345 is therefore inhibition of TNF, a GAM337345 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337345 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337346 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337346 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337346 is therefore inhibition of APPBP2, a GAM337346 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337346 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337346 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337346 is therefore inhibition of BACE2, a GAM337346 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337346 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337346 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337346 is therefore inhibition of FHL2, a GAM337346 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337346 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM337346 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337346 is therefore inhibition of IGF1, a GAM337346 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337346 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337346 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337346 is therefore inhibition of MME, a GAM337346 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337346 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM337346 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337346 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337346 is therefore inhibition of PRND, a GAM337346 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337346 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337350 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337350 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337350 is therefore inhibition of APPBP2, a GAM337350 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337350 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337350 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337350 is therefore inhibition of BACE2, a GAM337350 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337350 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337350 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337350 is therefore inhibition of FHL2, a GAM337350 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337350 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337350 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337350 is therefore inhibition of IGF1, a GAM337350 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337350 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337350 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337350 is therefore inhibition of

MME, a GAM337350 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337350 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337350 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337350 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337350 is therefore inhibition of PRND, a GAM337350 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337350 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337351 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337351 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337351 is therefore inhibition of APPBP2, a GAM337351 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337351 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337351 target gene. BACE2 BINDING SITE is A A

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337351 is therefore inhibition of BACE2, a GAM337351 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337351 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337351 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337351 is therefore inhibition of FHL2, a GAM337351 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337351 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337351 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337351 is therefore inhibition of IGF1, a GAM337351 target gene which are structurally and functionally related to insulin but have a much higher growth-

promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337351 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337351 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337351 is therefore inhibition of MME, a GAM337351 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337351 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337351 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337351 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337351 is therefore inhibition of PRND, a GAM337351 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337351 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337352 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337352 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by A A

APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337352 is therefore inhibition of APPBP2, a GAM337352 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337352 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337352 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337352 is therefore inhibition of BACE2, a GAM337352 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337352 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337352 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337352 is therefore inhibition of FHL2, a GAM337352 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer.

Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337352 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337352 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337352 is therefore inhibition of IGF1, a GAM337352 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337352 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337352 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337352 is therefore inhibition of MME, a GAM337352 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337352 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337352 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337352 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337352 is therefore inhibition of PRND, a GAM337352 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337352 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337353 PRND TACATGTGCCCAGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

GCTGCTG GAM337353 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337353 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337353 is therefore inhibition of PRND, a GAM337353 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337353 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337354 PRND TACATGTGCCCAGTG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

GCTGCTG GAM337354 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337354 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337354 is therefore inhibition of PRND, a GAM337354 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337354 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337355 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337355 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337355 is therefore inhibition of APBA1, a GAM337355 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337355 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGGAGC another GAM337355 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337355 is therefore inhibition of FHL2, a GAM337355 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337355 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGGAGC NM_000618.2) is another GAM337355 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337355 is therefore inhibition of

IGF1, a GAM337355 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337355 PLAU ACTGCACTCCATCCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GGGGAGC is another GAM337355 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337355 is therefore inhibition of PLAU, a GAM337355 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337355 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGGAGC another GAM337355 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337355 is therefore inhibition of PRND, a GAM337355 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337355 TNF ACTGCACTCCATCCT Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

GGGGAGC Accession NM_000594.2) is another GAM337355 target gene. TNF BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337355 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337355 is therefore inhibition of TNF, a GAM337355 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337355 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337356 HTR2C AGCAGCGCAGGTAGA A A TGGGGCT 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is a GAM337356 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337356 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337356 is therefore inhibition of HTR2C, a GAM337356 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337356 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337356 RAGE AGCAGCGCAGGTAGA A A TGGGGCT Renal Tumor Antigen (RAGE, Accession NM_014226.1) is another GAM337356 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337356 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337356 is therefore inhibition of RAGE, a GAM337356 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM337356 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM337357 APBA1 ACTGCACTCCATCCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

GGGGAGC 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337357 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337357 is therefore inhibition of APBA1, a GAM337357 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337357 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGGAGC another GAM337357 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337357 is therefore inhibition of FHL2, a GAM337357 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337357 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGGAGC NM_000618.2) is another GAM337357 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337357 is therefore inhibition of IGF1, a GAM337357 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337357 PLAU ACTGCACTCCATCCT Plasminogen Activator, Urokinase (PLAU, Accession NM_002658.1) A A

GGGGAGC is another GAM337357 target gene. PLAU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLAU BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337357 is therefore inhibition of PLAU, a GAM337357 target gene which is an urokinase plasminogen activator and serine protease . and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLAU.The function of PLAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337357 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGGAGC another GAM337357 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337357 is therefore inhibition of PRND, a GAM337357 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM337357 TNF ACTGCACTCCATCCT GGGGAGC Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession NM_000594.2) is another GAM337357 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337357 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337357 is therefore inhibition of TNF, a GAM337357 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337357 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337358 CAV1 AGGCTTTTGGAGAAG CATATGC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM337358 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337358 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337358 is therefore inhibition of CAV1, a GAM337358 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337358 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337358 HTR2A AGGCTTTTGGAGAAG CATATGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM337358 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337358 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337358 is therefore inhibition of

HTR2A, a GAM337358 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337358 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337359 CAV1 AGGCTTTTGGAGAAG CATATGC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM337359 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337359 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337359 is therefore inhibition of CAV1, a GAM337359 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337359 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337359 HTR2A AGGCTTTTGGAGAAG CATATGC 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM337359 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337359 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337359 is therefore inhibition of HTR2A, a GAM337359 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337359 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337361 CAV1 GTGGCACCATTGGAG TCTAAGG Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is a GAM337361 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA A A

encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337361 is therefore inhibition of CAV1, a GAM337361 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337361 IGF1 GTGGCACCATTGGAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCTAAGG NM_000618.2) is another GAM337361 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337361 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337361 is therefore inhibition of IGF1, a GAM337361 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337361 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337363 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337363 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337363 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337363 is therefore inhibition of APP. Accordingly, utilities of GAM337363 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337364 APBA1 AGAAGGCTCGCTCTC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A

TCAGGGG 1 (X11) (APBA1, Accession NM_001163.2) is a GAM337364 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337364 is therefore inhibition of APBA1, a GAM337364 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337364 MAPT AGAAGGCTCGCTCTC Microtubule- associated Protein Tau (MAPT, Accession A A

TCAGGGG NM_173727.1) is another GAM337364 target gene. MAPT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337364 is therefore inhibition of MAPT, a GAM337364 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337364 NCSTN AGAAGGCTCGCTCTC NCSTN (Accession NM_015331.1) is another GAM337364 target gene. A A

TCAGGGG NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337364 is therefore inhibition of NCSTN, a GAM337364 target gene which has a central role in

presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337364 PLCD1 AGAAGGCTCGCTCTC Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is A A

TCAGGGG another GAM337364 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337364 is therefore inhibition of PLCD1, a GAM337364 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM337364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337364 PRND AGAAGGCTCGCTCTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TCAGGGG another GAM337364 target gene. PRND BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337364 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337364 is therefore inhibition of PRND, a GAM337364 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337364 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337366 CTSK ACTGCACTCCATCCT CTSK (Accession NM_000396.2) is a GAM337366 target gene. CTSK A A

GGGACAG BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337366 is therefore inhibition of CTSK. Accordingly, utilities of GAM337366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM337366 FHL2 ACTGCACTCCATCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGACAG another GAM337366 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337366 is therefore inhibition of FHL2, a GAM337366 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337366 IGF1 ACTGCACTCCATCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGACAG NM_000618.2) is another GAM337366 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337366 is therefore inhibition of IGF1, a GAM337366 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337366 PRND ACTGCACTCCATCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGACAG another GAM337366 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337366 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337366 is therefore inhibition of PRND, a GAM337366 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337366 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337367 NGB target A A ACCACAGTGTCACAG AGTCCAT Neuroglobin (NGB, Accession NM_021257.2) is a GAM337367 gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337367 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337367 is therefore inhibition of NGB, a GAM337367 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337367 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337368 NGB target A A ACCACAGTGTCACAG AGTCCAT Neuroglobin (NGB, Accession NM_021257.2) is a GAM337368 gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337368 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337368 is therefore inhibition of NGB, a GAM337368 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337368 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337370 ABCD1 TTGTTGCGGGTGGGG ABCD1 (Accession NM_000033.2) is a GAM337370 target gene. ABCD1 A A

AGAGGAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337370 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337370 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337370 ACHE TTGTTGCGGGTGGGG Acetylcholinesterase (YT blood group) (ACHE, Accession A A

AGAGGAT NM_015831.1) is another GAM337370 target gene. ACHE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337370 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337370 is therefore inhibition of ACHE, a GAM337370 target gene which rapidly hydrolyzes choline released into the synapse. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACHE.The function of ACHE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1191.

GAM337370 OGDH TTGTTGCGGGTGGGG Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession A A

AGAGGAT NM_002541.1) is another GAM337370 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337370 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337370 is therefore inhibition of OGDH, a GAM337370 target gene which helps convert a- ketoglutarate

to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM337370 PRNP TTGTTGCGGGTGGGG AGAGGAT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler- (PRNP, Accession NM_000311.1) is another GAM337370 target gene. PRNP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337370 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337370 is therefore inhibition of PRNP, a GAM337370 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337370 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM337371 APPBP2 TTGTAAATAACATTT TTTAGCA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337371 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337371 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337371 is therefore inhibition of APPBP2, a GAM337371 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337371 GYPA TTGTAAATAACATTT Glycophorin A (includes MN blood group) (GYPA, Accession A A

TTTAGCA NM_002099.2) is another GAM337371 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337371 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337371 is therefore inhibition of GYPA, a GAM337371 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337371 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337372 ABCD1 TGGAGGCAGGTGCAG ABCD1 (Accession NM_000033.2) is a GAM337372 target gene. ABCD1 A A

ATGGAGG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337372 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337372 CRAT TGGAGGCAGGTGCAG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is A A

ATGGAGG another GAM337372 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337372 is therefore inhibition of CRAT, a GAM337372 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337372 DLST TGGAGGCAGGTGCAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

ATGGAGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337372 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337372 is therefore inhibition of DLST, a GAM337372 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337372 HD TGGAGGCAGGTGCAG HD (Accession NM_002111.3) is another GAM337372 target gene.
HD A A

ATGGAGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337372 is therefore inhibition of HD. Accordingly, utilities of GAM337372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337372 NGB TGGAGGCAGGTGCAG Neuroglobin (NGB, Accession NM_021257.2) is another
GAM337372 A A

ATGGAGG target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337372 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337372 is therefore inhibition of NGB, a GAM337372 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337372 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337373 ABCD1 TGGAGGCAGGTGCAG ABCD1 (Accession NM_000033.2) is a GAM337373 target gene. ABCD1 A A

ATGGAGG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ABCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337373 is therefore inhibition of ABCD1. Accordingly, utilities of GAM337373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ABCD1.

GAM337373 CRAT TGGAGGCAGGTGCAG Carnitine Acetyltransferase (CRAT, Accession NM_004003.2) is A A

ATGGAGG another GAM337373 target gene. CRAT BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRAT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337373 is therefore inhibition of CRAT, a GAM337373 target gene which catalyzes the reversible transfer of acyl groups from an acyl- CoA thioester to carnitine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRAT.The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337373 DLST TGGAGGCAGGTGCAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

ATGGAGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337373 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337373 is therefore inhibition of DLST, a GAM337373 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337373 HD TGGAGGCAGGTGCAG HD (Accession NM_002111.3) is another GAM337373 target gene. HD A A

ATGGAGG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337373 is therefore inhibition of HD. Accordingly, utilities of GAM337373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337373 NGB TGGAGGCAGGTGCAG Neuroglobin (NGB, Accession NM_021257.2) is another GAM337373 A A

ATGGAGG target gene. NGB BINDING SITE1 and NGB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NGB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE1 and NGB BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337373 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337373 is therefore inhibition of NGB, a GAM337373 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337373 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337374 IAPP CACTGCTGTAATGGA Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is a A A

CGGTGAG GAM337374 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337374 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337374 is therefore inhibition of IAPP, a GAM337374 target gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337374 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The

function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337375 APLP1 TCCATTGCACTCCAG Amyloid Beta (A4) Precursor- like Protein 1 (APLP1, Accession A A

TCTGGGC NM_005166.2) is a GAM337375 target gene. APLP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APLP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337375 is therefore inhibition of APLP1, a GAM337375 target gene which is a membrane- associated glycoprotein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APLP1.The function of APLP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.

GAM337375 FHL2 TCCATTGCACTCCAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TCTGGGC another GAM337375 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337375 is therefore inhibition of FHL2, a GAM337375 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337375 FLNB TCCATTGCACTCCAG Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

TCTGGGC NM_001457.1) is another GAM337375 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337375 is therefore inhibition of FLNB, a GAM337375 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM337375 IGF1 TCCATTGCACTCCAG TCTGGGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337375 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337375 is therefore inhibition of IGF1, a GAM337375 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337375 PRND TCCATTGCACTCCAG TCTGGGC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337375 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337375 is therefore inhibition of PRND, a GAM337375 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337375 PSEN1 TCCATTGCACTCCAG PSEN1 (Accession NM_007318.1) is another GAM337375 target gene. A A

TCTGGGC PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337375 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337375 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337375 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337376 NCKAP1 GTCTTCCAGCCTCCA NCKAP1 (Accession NM_013436.2) is a GAM337376 target gene. A A

TCTTTCT NCKAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCKAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCKAP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337376 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337376 is therefore inhibition of NCKAP1. Accordingly, utilities of GAM337376 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCKAP1.

GAM337377 APPBP2 CTCTGCCTCCCGGGT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CTAGGCT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337377 target gene. APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337377 is therefore inhibition of APPBP2, a GAM337377 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337377 BACE CTCTGCCTCCCGGGT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

CTAGGCT is another GAM337377 target gene. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple

transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337377 is therefore inhibition of BACE, a GAM337377 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337377 CASP3 CTCTGCCTCCCGGGT CTAGGCT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is another GAM337377 target gene. CASP3 BINDING SITE1 and CASP3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE1 and CASP3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337377 is therefore inhibition of CASP3, a GAM337377 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337377 CAV1 CTCTGCCTCCCGGGT CTAGGCT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM337377 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337377 is therefore inhibition of CAV1, a GAM337377 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and

therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337377 MTNR1A CTCTGCCTCCCGGGT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CTAGGCT another GAM337377 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337377 is therefore inhibition of MTNR1A, a GAM337377 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337377 TFCP2 CTCTGCCTCCCGGGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

CTAGGCT another GAM337377 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337377 is therefore inhibition of TFCP2, a GAM337377 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337377 TGFB1 CTCTGCCTCCCGGGT TGFB1 (Accession NM_000660.1) is another GAM337377 target gene. A A

CTAGGCT TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337377 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337377 TRPM2 CTCTGCCTCCCGGGT CTAGGCT TRPM2 (Accession NM_003307.1) is another GAM337377 target gene. A A A A

TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337377 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337377 is therefore inhibition of TRPM2, a GAM337377 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337377 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337378 APPBP2 CTCTGCCTCCCGGGT CTAGGCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337378 target gene. A A A A APPBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337378 is therefore inhibition of APPBP2, a GAM337378 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337378 BACE CTCTGCCTCCCGGGT CTAGGCT Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) is another GAM337378 target gene. A A A A BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple

transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337378 is therefore inhibition of BACE, a GAM337378 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337378 CASP3 CTCTGCCTCCCGGGT CTAGGCT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is another GAM337378 target gene. CASP3 BINDING SITE1 and CASP3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE1 and CASP3 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337378 is therefore inhibition of CASP3, a GAM337378 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337378 CAV1 CTCTGCCTCCCGGGT CTAGGCT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession NM_001753.3) is another GAM337378 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337378 is therefore inhibition of CAV1, a GAM337378 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and

therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337378 MTNR1A CTCTGCCTCCCGGGT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is A A

CTAGGCT another GAM337378 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337378 is therefore inhibition of MTNR1A, a GAM337378 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337378 TFCP2 CTCTGCCTCCCGGGT Transcription Factor CP2 (TFCP2, Accession NM_005653.2) is A A

CTAGGCT another GAM337378 target gene. TFCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TFCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TFCP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337378 is therefore inhibition of TFCP2, a GAM337378 target gene which is a transcription factor CP2 and recognizes sites within the alpha- globin gene and SV40 late promoters. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TFCP2.The function of TFCP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM760.

GAM337378 TGFB1 CTCTGCCTCCCGGGT TGFB1 (Accession NM_000660.1) is another GAM337378 target gene. A A

CTAGGCT TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337378 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337378 TRPM2 CTCTGCCTCCCGGGT TRPM2 (Accession NM_003307.1) is another GAM337378 target gene. A A

CTAGGCT TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337378 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337378 is therefore inhibition of TRPM2, a GAM337378 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337378 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337379 CAV1 AACTGCTTTTGTTGT Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

GCAGGGA NM_001753.3) is a GAM337379 target gene. CAV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337379 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337379 is therefore inhibition of CAV1, a GAM337379 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337379 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337380 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337380 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337380 is therefore inhibition of APPBP2, a GAM337380 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337380 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM337380 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337380 is therefore inhibition of BACE2, a GAM337380 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337380 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM337380 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337380 is therefore inhibition of FHL2, a GAM337380 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337380 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337380 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337380 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337380 is therefore inhibition of HD. Accordingly, utilities of GAM337380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337380 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337380 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337380 is therefore inhibition of IGF1, a GAM337380 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337380 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337380 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337380 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337380 is therefore inhibition of PRND, a GAM337380 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337380 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337383 IGF1 GTGTCACTTTCAGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GCTCTAA NM_000618.2) is a GAM337383 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337383 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337383 is therefore inhibition of IGF1, a GAM337383 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337383 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337384 CAV1 GAGGAGGGCTTTCCC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

TGACTTT NM_001753.3) is a GAM337384 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337384 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337384 is therefore inhibition of CAV1, a GAM337384 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337384 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337385 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337385 target

gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337385 is therefore inhibition of APPBP2, a GAM337385 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337385 BACE2 ACTGCACTCCAGCCT A A GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337385 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337385 is therefore inhibition of BACE2, a GAM337385 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337385 FHL2 ACTGCACTCCAGCCT A A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337385 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337385 is therefore inhibition of

FHL2, a GAM337385 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337385 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337385 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337385 is therefore inhibition of IGF1, a GAM337385 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337385 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337385 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337385 is therefore inhibition of MME, a GAM337385 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337385 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337385 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337385 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337385 is therefore inhibition of PRND, a GAM337385 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337385 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337386 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337386 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337386 is therefore inhibition of APPBP2, a GAM337386 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337386 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337386 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337386 is therefore inhibition of BACE2, a GAM337386 target gene which cleaves intracellularly the b-

secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337386 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337386 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337386 is therefore inhibition of FHL2, a GAM337386 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337386 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337386 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337386 is therefore inhibition of IGF1, a GAM337386 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337386 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337386

target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337386 is therefore inhibition of MME, a GAM337386 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337386 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM337386 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337386 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337386 is therefore inhibition of PRND, a GAM337386 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337386 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337387 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337387 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337387 is therefore inhibition of APPBP2, a GAM337387 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337387 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337387 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337387 is therefore inhibition of BACE2, a GAM337387 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337387 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337387 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337387 is therefore inhibition of FHL2, a GAM337387 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337387 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337387 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337387 is therefore inhibition of IGF1, a GAM337387 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337387 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A
A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337387 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337387 is therefore inhibition of MME, a GAM337387 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337387 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
A
GGGCAAC another GAM337387 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337387 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337387 is therefore inhibition of PRND, a GAM337387 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337387 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337388 APBB2 GAATAATGTCCCACT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGGAGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337388 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337388 is therefore inhibition of APBB2, a GAM337388 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337388 IGF1 GAATAATGTCCCACT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGAGGC NM_000618.2) is another GAM337388 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337388 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337388 is therefore inhibition of IGF1, a GAM337388 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337388 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337389 APBB2 GAATAATGTCCCACT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GGGAGGC 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337389 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337389 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337389 is therefore inhibition of APBB2, a GAM337389 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337389 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337389 IGF1 GAATAATGTCCCACT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGAGGC NM_000618.2) is another GAM337389 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337389 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337389 is therefore inhibition of IGF1, a GAM337389 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337389 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337390 SNCB TGAGGACAGAAAGTT Synuclein, Beta (SNCB, Accession NM_003085.2) is a GAM337390 A A
TGTGCTG target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337390 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337390 is therefore inhibition of SNCB, a GAM337390 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337390 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337391 SNCB TGAGGACAGAAAGTT TGTGCTG Synuclein, Beta (SNCB, Accession NM_003085.2) is a GAM337391 target gene. SNCB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNCB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SNCB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337391 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337391 is therefore inhibition of SNCB, a GAM337391 target gene which may inhibit phospholipase D2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337391 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SNCB.The function of SNCB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337393 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337393 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337393 is therefore inhibition of APPBP2, a GAM337393 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337393 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337393 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337393 is therefore inhibition of BACE2, a GAM337393 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337393 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337393 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337393 is therefore inhibition of FHL2, a GAM337393 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337393 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337393 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337393 is therefore inhibition of HD. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337393 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337393 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337393 is therefore inhibition of IGF1, a GAM337393 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337393 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337393 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337393 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337393 is therefore inhibition of PRND, a GAM337393 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337393 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337394 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337394 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337394 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337394 is therefore inhibition of APPBP2, a GAM337394 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337394 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337394 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337394 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337394 is therefore inhibition of BACE2, a GAM337394 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337394 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337394 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337394 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337394 is therefore inhibition of FHL2, a GAM337394 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337394 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337394 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337394

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337394 is therefore inhibition of HD. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337394 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TGGGCAA NM_000618.2) is another GAM337394 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337394 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337394 is therefore inhibition of IGF1, a GAM337394 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337394 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337394 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337394 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337394 is therefore inhibition of PRND, a GAM337394 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337394 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337395 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337395 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337395 is therefore inhibition of APPBP2, a GAM337395 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337395 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337395 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337395 is therefore inhibition of BACE2, a GAM337395 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337395 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337395 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337395 is therefore inhibition of FHL2, a GAM337395 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337395 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337395 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337395 is therefore inhibition of IGF1, a GAM337395 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337395 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337395 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337395 is therefore inhibition of MME, a GAM337395 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337395 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337395 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337395 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337395 is therefore inhibition of PRND, a GAM337395 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337395 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337396 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337396 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337396 is therefore inhibition of APPBP2, a GAM337396 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337396 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337396 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337396 is therefore inhibition of BACE2, a GAM337396 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is

associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337396 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337396 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337396 is therefore inhibition of FHL2, a GAM337396 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337396 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337396 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337396 is therefore inhibition of IGF1, a GAM337396 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337396 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337396 target gene. MME BINDING SITE is a target binding site found in the

5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337396 is therefore inhibition of MME, a GAM337396 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337396 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337396 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337396 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337396 is therefore inhibition of PRND, a GAM337396 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337396 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337397 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337397 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337397 is therefore inhibition of APPBP2, a GAM337397 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337397 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337397 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337397 is therefore inhibition of BACE2, a GAM337397 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337397 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337397 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337397 is therefore inhibition of FHL2, a GAM337397 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337397 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337397 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337397 is therefore inhibition of IGF1, a GAM337397 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337397 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337397 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337397 is therefore inhibition of MME, a GAM337397 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337397 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337397 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337397 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337397 is therefore inhibition of PRND, a GAM337397 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337397 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337399 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337399 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337399 is therefore inhibition of APPBP2, a GAM337399 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337399 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337399 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337399 is therefore inhibition of BACE2, a GAM337399 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337399 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337399 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337399 is therefore inhibition of FHL2, a GAM337399 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337399 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337399 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337399 is therefore inhibition of IGF1, a GAM337399 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337399 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337399 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337399 is therefore inhibition of MME, a GAM337399 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337399 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337399 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337399 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337399 is therefore inhibition of PRND, a GAM337399 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337399 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337400 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337400 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337400 is therefore inhibition of APPBP2, a GAM337400 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337400 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337400 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337400 is therefore inhibition of BACE2, a GAM337400 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337400 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337400 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337400 is therefore inhibition of FHL2, a GAM337400 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337400 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337400 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337400 is therefore inhibition of IGF1, a GAM337400 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337400 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337400 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337400 is therefore inhibition of MME, a GAM337400 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337400 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337400 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337400 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337400 is therefore inhibition of PRND, a GAM337400 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337400 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337401 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337401 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of

GAM337401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337401 is therefore inhibition of APPBP2, a GAM337401 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337401 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337401 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337401 is therefore inhibition of BACE2, a GAM337401 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337401 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337401 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337401 is therefore inhibition of FHL2, a GAM337401 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM189.

GAM337401 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337401 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337401 is therefore inhibition of IGF1, a GAM337401 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337401 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337401 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337401 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337401 is therefore inhibition of MME, a GAM337401 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337401 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337401 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337401 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337401 is therefore inhibition of PRND, a GAM337401 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337401 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337402 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337402 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337402 is therefore inhibition of APPBP2, a GAM337402 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337402 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337402 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337402 is therefore inhibition of BACE2, a GAM337402 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM337402 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337402 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337402 is therefore inhibition of FHL2, a GAM337402 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337402 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337402 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337402 is therefore inhibition of IGF1, a GAM337402 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337402 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337402 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and

7, hereby incorporated herein.

Another function of GAM337402 is therefore inhibition of MME, a GAM337402 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337402 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337402 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337402 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337402 is therefore inhibition of PRND, a GAM337402 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337402 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337403 PRND GTACACATTTTCATG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A
TTACCAT GAM337403 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337403 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337403 is therefore inhibition of PRND, a GAM337403 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337403 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337405 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337405 target

gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337405 is therefore inhibition of APPBP2, a GAM337405 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337405 BACE2 ACTGCACTCCAGCCT A A GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337405 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337405 is therefore inhibition of BACE2, a GAM337405 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337405 FHL2 ACTGCACTCCAGCCT A A GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337405 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337405 is therefore inhibition of

FHL2, a GAM337405 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337405 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337405 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337405 is therefore inhibition of IGF1, a GAM337405 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337405 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337405 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337405 is therefore inhibition of MME, a GAM337405 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337405 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337405 target gene. PRND BINDING SITE1 through PRND

BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337405 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337405 is therefore inhibition of PRND, a GAM337405 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337405 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337407 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337407 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337407 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337407 is therefore inhibition of APP. Accordingly, utilities of GAM337407 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337408 LRP1 ATCTCATAGGCCCCC Low Density Lipoprotein- related Protein 1 (alpha- 2- A A

AGTGGGG macroglobulin recep (LRP1, Accession NM_002332.1) is a GAM337408 target gene. LRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337408 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337408 is therefore inhibition of LRP1, a GAM337408 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337408 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337409 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337409 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337409 is therefore inhibition of APPBP2, a GAM337409 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337409 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337409 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337409 is therefore inhibition of BACE2, a GAM337409 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337409 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337409 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337409 is therefore inhibition of FHL2, a GAM337409 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337409 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337409 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337409 is therefore inhibition of IGF1, a GAM337409 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337409 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337409 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337409 is therefore inhibition of MME, a GAM337409 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337409 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337409 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337409 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337409 is therefore inhibition of PRND, a GAM337409 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337409 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337410 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337410 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337410 is therefore inhibition of APPBP2, a GAM337410 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337410 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337410 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337410 is therefore inhibition of

BACE2, a GAM337410 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337410 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337410 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337410 is therefore inhibition of FHL2, a GAM337410 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337410 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337410 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337410 is therefore inhibition of IGF1, a GAM337410 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337410 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337410 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337410 is therefore inhibition of MME, a GAM337410 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337410 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337410 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337410 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337410 is therefore inhibition of PRND, a GAM337410 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337410 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337411 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337411 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337411 is therefore inhibition of APPBP2, a GAM337411 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337411 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337411 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337411 is therefore inhibition of BACE2, a GAM337411 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337411 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337411 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337411 is therefore inhibition of FHL2, a GAM337411 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337411 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337411 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337411 is therefore inhibition of IGF1, a GAM337411 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337411 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337411 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337411 is therefore inhibition of MME, a GAM337411 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337411 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337411 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337411 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337411 is therefore inhibition of PRND, a GAM337411 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM337411 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337413 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337413 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337413 is therefore inhibition of APPBP2, a GAM337413 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337413 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337413 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337413 is therefore inhibition of BACE2, a GAM337413 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337413 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337413 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337413 is therefore inhibition of FHL2, a GAM337413 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337413 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337413 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337413 is therefore inhibition of IGF1, a GAM337413 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337413 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337413 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337413 is therefore inhibition of MME, a GAM337413 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities

of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337413 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337413 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337413 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337413 is therefore inhibition of PRND, a GAM337413 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337413 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337414 ADAM17 AAGTGCTGGGATTAC A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

AGGCCTG factor, (ADAM17, Accession NM_021832.1) is a GAM337414 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337414 is therefore inhibition of ADAM17, a GAM337414 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337414 GFAP AAGTGCTGGGATTAC GFAP (Accession NM_002055.2) is another GAM337414 target gene. A A

AGGCCTG GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337414 is therefore inhibition of GFAP. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337414 HTR2A AAGTGCTGGGATTAC A A AGGCCTG 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is another GAM337414 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337414 is therefore inhibition of HTR2A, a GAM337414 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337414 IAPP AAGTGCTGGGATTAC A A AGGCCTG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is another GAM337414 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337414 is therefore inhibition of IAPP, a GAM337414 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337414 MTNR1A AAGTGCTGGGATTAC A A AGGCCTG Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is another GAM337414 target gene. MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2 are target binding sites found in untranslated regions

of mRNA encoded by MTNR1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE1 and MTNR1A BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337414 is therefore inhibition of MTNR1A, a GAM337414 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337414 TGFB1 AAGTGCTGGGATTAC TGFB1 (Accession NM_000660.1) is another GAM337414 target gene. A A

AGGCCTG TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337414 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337414 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337414 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337415 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337415 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337415 is therefore inhibition of APPBP2, a GAM337415 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to GAM44.

GAM337415 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337415 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337415 is therefore inhibition of BACE2, a GAM337415 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337415 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337415 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337415 is therefore inhibition of FHL2, a GAM337415 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337415 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337415 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337415 is therefore inhibition of IGF1, a GAM337415 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337415 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337415 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337415 is therefore inhibition of MME, a GAM337415 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337415 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337415 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337415 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337415 is therefore inhibition of PRND, a GAM337415 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337415 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337416 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337416 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337416 is therefore inhibition of APPBP2, a GAM337416 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337416 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337416 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337416 is therefore inhibition of BACE2, a GAM337416 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337416 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337416 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337416 is therefore inhibition of FHL2, a GAM337416 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337416 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337416 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337416 is therefore inhibition of IGF1, a GAM337416 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337416 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337416 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337416 is therefore inhibition of MME, a GAM337416 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337416 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337416 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337416 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337416 is therefore inhibition of PRND, a GAM337416 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337416 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337417 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337417 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337417 is therefore inhibition of APPBP2, a GAM337417 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337417 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337417 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337417 is therefore inhibition of

BACE2, a GAM337417 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337417 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337417 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337417 is therefore inhibition of FHL2, a GAM337417 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337417 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337417 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337417 is therefore inhibition of IGF1, a GAM337417 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337417 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337417 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337417 is therefore inhibition of MME, a GAM337417 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337417 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337417 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337417 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337417 is therefore inhibition of PRND, a GAM337417 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337417 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337418 ACE GAGTGAGTGTGATCT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

TGGCTCA (ACE, Accession NM_152831.1) is a GAM337418 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337418 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337418 is therefore inhibition of ACE, a GAM337418 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337418 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337418 APBA1 GAGTGAGTGTGATCT Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A
TGGCTCA 1 (X11) (APBA1, Accession NM_001163.2) is another GAM337418 target gene. APBA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337418 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337418 is therefore inhibition of APBA1, a GAM337418 target gene which stabilises APP and inhibits production of proteolytic APP fragments. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337418 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA1.The function of APBA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337418 HTR2A GAGTGAGTGTGATCT 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
TGGCTCA NM_000621.1) is another GAM337418 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337418 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337418 is therefore inhibition of HTR2A, a GAM337418 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337418 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337419 APPBP2 AGTAGAACAGAATAT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TTTAGCT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337419 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337419 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337419 is therefore inhibition of APPBP2, a GAM337419 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337419 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337420 PRND CTGGAGGATAACAAT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A
GATAATG GAM337420 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337420 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337420 is therefore inhibition of PRND, a GAM337420 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337420 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337421 MPO AACACGTAGTAGGTG Myeloperoxidase (MPO, Accession NM_000250.1) is a GAM337421 A A
TTCGATA target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337421 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337421 is therefore inhibition of MPO, a GAM337421 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337421 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM337424 APPBP2 ACTGCACTCTAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337424 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337424 is therefore inhibition of APPBP2, a GAM337424 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337424 FHL2 ACTGCACTCTAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337424 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337424 is therefore inhibition of FHL2, a GAM337424 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337424 IGF1 ACTGCACTCTAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337424 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337424 is therefore inhibition of IGF1, a GAM337424 target gene which are structurally and

functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337424 PRND ACTGCACTCTAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337424 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337424 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337424 is therefore inhibition of PRND, a GAM337424 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337424 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337425 APPBP2 ACTGCACTCTAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337425 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337425 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337425 is therefore inhibition of APPBP2, a GAM337425 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337425 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337425 FHL2 ACTGCACTCTAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337425 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337425 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337425 is therefore inhibition of FHL2, a GAM337425 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337425 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337425 IGF1 ACTGCACTCTAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337425 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337425 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337425 is therefore inhibition of IGF1, a GAM337425 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337425 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337425 PRND ACTGCACTCTAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337425 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337425 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337425 is therefore inhibition of PRND, a GAM337425 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337425 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337426 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337426 target gene. APP
A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337426 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337426 is therefore inhibition of APP. Accordingly, utilities of GAM337426 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337428 FHL2 TGTGCCACTGCACTC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A
CATGGGT a GAM337428 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337428 is therefore inhibition of FHL2, a GAM337428 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337428 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337428 IAPP TGTGCCACTGCACTC Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A
A
CATGGGT another GAM337428 target gene. IAPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337428 is therefore inhibition of IAPP, a GAM337428 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337428

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337428 IGF1 TGTGCCACTGCACTC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CATGGGT NM_000618.2) is another GAM337428 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337428 is therefore inhibition of IGF1, a GAM337428 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337428 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337428 PRND TGTGCCACTGCACTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
CATGGGT another GAM337428 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337428 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337428 is therefore inhibition of PRND, a GAM337428 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337428 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337429 HTR2C TTCCAGTTTTTCCTA 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession A A
CCCCTTA NM_000868.1) is a GAM337429 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337429 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337429 is therefore inhibition of HTR2C, a GAM337429 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337429 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337430 DHCR24 TGATGGAGGAAATGG A A TGGTATC 24- dehydrocholesterol Reductase (DHCR24, Accession NM_014762.1) is a GAM337430 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337430 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337430 is therefore inhibition of DHCR24, a GAM337430 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337430 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337430 MME TGATGGAGGAAATGG A A TGGTATC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007288.1) is another GAM337430 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337430 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337430 is therefore inhibition of MME, a GAM337430 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337430 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to GAM25.

GAM337431 DHCR24 TGATGGAGGAAATGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGTATC NM_014762.1) is a GAM337431 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337431 is therefore inhibition of DHCR24, a GAM337431 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337431 MME TGATGGAGGAAATGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGGTATC enkephalinase, (MME, Accession NM_007288.1) is another GAM337431 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337431 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337431 is therefore inhibition of MME, a GAM337431 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337431 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337432 DHCR24 TGATGGAGGAAATGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGTATC NM_014762.1) is a GAM337432 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337432 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337432 is therefore inhibition of DHCR24,

a GAM337432 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337432 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337432 MME TGATGGAGGAAATGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGGTATC enkephalinase, (MME, Accession NM_007288.1) is another GAM337432 target gene. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337432 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337432 is therefore inhibition of MME, a GAM337432 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337432 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337433 DHCR24 TGATGGAGGAAATGG 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGTATC NM_014762.1) is a GAM337433 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337433 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337433 is therefore inhibition of DHCR24, a GAM337433 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337433 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337433 MME TGATGGAGGAAATGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGGTATC enkephalinase, (MME, Accession NM_007288.1) is another GAM337433 target gene. MME BINDING SITE is a target binding site found in the

3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337433 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337433 is therefore inhibition of MME, a GAM337433 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337433 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337435 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337435 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337435 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337435 is therefore inhibition of APP. Accordingly, utilities of GAM337435 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337437 ACE TGTGTACTTGTCTTA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
GTTTGCT (ACE, Accession NM_152831.1) is a GAM337437 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337437 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337437 is therefore inhibition of ACE, a GAM337437 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337437 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337437 IL1A TGTGTACTTGTCTTA Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
GTTTGCT GAM337437 target gene. IL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1A,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337437 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337437 is therefore inhibition of IL1A, a GAM337437 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337437 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337437 OLR1 TGTGTACTTGTCTTA GTTTGCT Oxidised Low Density Lipoprotein (lectin- like) Receptor 1 A A

(OLR1, Accession NM_002543.1) is another GAM337437 target gene. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OLR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337437 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337437 is therefore inhibition of OLR1, a GAM337437 target gene which is involved in degradation of oxidized LDL by vascular endothelial cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337437 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OLR1.The function of OLR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337438 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337438 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337438 is therefore inhibition of APPBP2, a GAM337438 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include

diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337438 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337438 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337438 is therefore inhibition of BACE2, a GAM337438 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337438 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337438 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337438 is therefore inhibition of FHL2, a GAM337438 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337438 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337438 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337438 is therefore inhibition of IGF1, a GAM337438 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337438 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337438 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337438 is therefore inhibition of MME, a GAM337438 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337438 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337438 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337438 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337438 is therefore inhibition of PRND, a GAM337438 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337438 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions

associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337439 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337439 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337439 is therefore inhibition of APPBP2, a GAM337439 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337439 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337439 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337439 is therefore inhibition of BACE2, a GAM337439 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337439 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337439 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337439 is therefore inhibition of FHL2, a GAM337439 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337439 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337439 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337439 is therefore inhibition of IGF1, a GAM337439 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337439 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337439 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337439 is therefore inhibition of MME, a GAM337439 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337439 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337439 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337439 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337439 is therefore inhibition of PRND, a GAM337439 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337439 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337440 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337440 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337440 is therefore inhibition of APPBP2, a GAM337440 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337440 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337440 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337440 is therefore inhibition of BACE2, a GAM337440 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337440 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337440 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337440 is therefore inhibition of FHL2, a GAM337440 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337440 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337440 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337440 is therefore inhibition of IGF1, a GAM337440 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337440 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337440 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337440 is therefore inhibition of MME, a GAM337440 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337440 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337440 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337440 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337440 is therefore inhibition of PRND, a GAM337440 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337440 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337441 HD TCCCTCTGCCTGCAG HD (Accession NM_002111.3) is a GAM337441 target gene. HD A A

TCCTGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337441 is therefore inhibition of HD. Accordingly, utilities of GAM337441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337441 LRP1 TCCCTCTGCCTGCAG Low Density Lipoprotein- related Protein 1 (alpha- 2- A A
TCCTGCT macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337441 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337441 is therefore inhibition of LRP1, a GAM337441 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337441 MAPT TCCCTCTGCCTGCAG Microtubule- associated Protein Tau (MAPT, Accession A A
TCCTGCT NM_016835.1) is another GAM337441 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337441 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337441 is therefore inhibition of MAPT, a GAM337441 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337441 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337442 HD TCCCTCTGCCTGCAG HD (Accession NM_002111.3) is a GAM337442 target gene. HD A A
TCCTGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337442

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337442 is therefore inhibition of HD. Accordingly, utilities of GAM337442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337442 LRP1 TCCCTCTGCCTGCAG TCCTGCT Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337442 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337442 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337442 is therefore inhibition of LRP1, a GAM337442 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337442 MAPT TCCCTCTGCCTGCAG TCCTGCT Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM337442 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337442 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337442 is therefore inhibition of MAPT, a GAM337442 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337442 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337443 HD TCCCTCTGCCTGCAG TCCTGCT HD (Accession NM_002111.3) is a GAM337443 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of A A

Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337443 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337443 is therefore inhibition of HD. Accordingly, utilities of GAM337443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337443 LRP1 TCCCTCTGCCTGCAG TCCTGCT Low Density Lipoprotein- related Protein 1 (alpha- 2- macroglobulin recep (LRP1, Accession NM_002332.1) is another GAM337443 target gene. LRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of LRP1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337443 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337443 is therefore inhibition of LRP1, a GAM337443 target gene which is a recycling lipoprotein receptor with possible growth- modulating effects. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with LRP1.The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1975.

GAM337443 MAPT TCCCTCTGCCTGCAG TCCTGCT Microtubule- associated Protein Tau (MAPT, Accession NM_016835.1) is another GAM337443 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337443 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337443 is therefore inhibition of MAPT, a GAM337443 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337443 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337445 BLMH CTGGCTGCATTTAGG AACAAGG Bleomycin Hydrolase (BLMH, Accession NM_000386.1) is a GAM337445 target gene. BLMH BINDING SITE is a target binding site A A

found in the 3` untranslated region of mRNA encoded by BLMH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BLMH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337445 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337445 is therefore inhibition of BLMH, a GAM337445 target gene which is a cysteine protease that inactivates bleomycin and therefore is associated with Alzheimer. Accordingly, utilities of GAM337445 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BLMH.The function of BLMH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM828.

GAM337445 DLST CTGGCTGCATTTAGG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A
AACAAGG oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337445 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337445 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337445 is therefore inhibition of DLST, a GAM337445 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337445 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337445 SLC17A7 CTGGCTGCATTTAGG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A
AACAAGG NM_020309.1) is another GAM337445 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337445 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337445 is therefore inhibition of SLC17A7, a GAM337445 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337445 include diagnosis, prevention and treatment of Alzheimer, and of

other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.

GAM337446 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337446 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337446 is therefore inhibition of APPBP2, a GAM337446 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337446 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337446 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337446 is therefore inhibition of BACE2, a GAM337446 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337446 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337446 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as A A

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337446 is therefore inhibition of FHL2, a GAM337446 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337446 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337446 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337446 is therefore inhibition of IGF1, a GAM337446 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337446 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337446 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337446 is therefore inhibition of MME, a GAM337446 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of

Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337446 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337446 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337446 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337446 is therefore inhibition of PRND, a GAM337446 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337446 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337447 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337447 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337447 is therefore inhibition of APPBP2, a GAM337447 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337447 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337447 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337447 is therefore inhibition of BACE2, a GAM337447 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337447 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337447 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337447 is therefore inhibition of FHL2, a GAM337447 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337447 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337447 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337447 is therefore inhibition of IGF1, a GAM337447 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337447 MME ACTGCACTCCAGCCT GGGCAAC A A

Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337447 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337447 is therefore inhibition of MME, a GAM337447 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337447 PRND ACTGCACTCCAGCCT GGGCAAC A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337447 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337447 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337447 is therefore inhibition of PRND, a GAM337447 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337447 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337448 APPBP2 ACTGCACTCCAGCCT GGGCAAC A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337448 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and

secondary structure complementarity to the nucleotide sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337448 is therefore inhibition of APPBP2, a GAM337448 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337448 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337448 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337448 is therefore inhibition of BACE2, a GAM337448 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337448 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337448 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337448 is therefore inhibition of FHL2, a GAM337448 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337448 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337448 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337448 is therefore inhibition of IGF1, a GAM337448 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337448 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337448 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337448 is therefore inhibition of MME, a GAM337448 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337448 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337448 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide

sequence of GAM337448 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337448 is therefore inhibition of PRND, a GAM337448 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337448 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337449 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337449 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337449 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337449 is therefore inhibition of APP. Accordingly, utilities of GAM337449 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337450 CASP3 ATAAAGCTAGACGTT Caspase 3, Apoptosis- related Cysteine Protease (CASP3, A A

CATTGAC Accession NM_032991.1) is a GAM337450 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337450 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337450 is therefore inhibition of CASP3, a GAM337450 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337450 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337452 TNFRSF6 TTTGGCTGTTTGTCT TNFRSF6 (Accession NM_152872.1) is a GAM337452 target gene. A A

TGGGCAA TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of TNFRSF6 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337452 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337452 is therefore inhibition of TNFRSF6. Accordingly, utilities of GAM337452 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF6.

GAM337453 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337453 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337453 is therefore inhibition of APPBP2, a GAM337453 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337453 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337453 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337453 is therefore inhibition of BACE2, a GAM337453 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337453 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337453 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337453 is therefore inhibition of FHL2, a GAM337453 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337453 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337453 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337453 is therefore inhibition of HD. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337453 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM337453 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337453 is therefore inhibition of IGF1, a GAM337453 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337453 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337453 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337453 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337453 is therefore inhibition of PRND, a GAM337453 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337453 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337454 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337454 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337454 is therefore inhibition of APPBP2, a GAM337454 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337454 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337454 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337454 is therefore inhibition of BACE2, a GAM337454 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337454 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337454 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337454 is therefore inhibition of FHL2, a GAM337454 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337454 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337454 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337454 is therefore inhibition of HD. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337454 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337454 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337454 is therefore inhibition of IGF1, a GAM337454 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337454 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM337454 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337454 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337454 is therefore inhibition of PRND, a GAM337454 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337454 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337456 APPBP2 CACTGCACTCCACCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337456 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337456 is therefore inhibition of APPBP2, a GAM337456 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337456 include diagnosis, prevention and treatment of Alzheimer, and of other

diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337456 BACE2 CACTGCACTCCACCC TGGGCAA A A Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM337456 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337456 is therefore inhibition of BACE2, a GAM337456 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337456 FHL2 CACTGCACTCCACCC TGGGCAA A A Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337456 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337456 is therefore inhibition of FHL2, a GAM337456 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337456 IGF1 CACTGCACTCCACCC TGGGCAA A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337456 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337456 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337456 is therefore inhibition of IGF1, a GAM337456 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337456 PRND CACTGCACTCCACCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337456 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337456 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337456 is therefore inhibition of PRND, a GAM337456 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337456 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337457 APPBP2 CACTGCACTCCACCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337457 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337457 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337457 is therefore inhibition of APPBP2, a GAM337457 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337457 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337457 BACE2 CACTGCACTCCACCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138991.1) is another GAM337457 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337457 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337457 is therefore inhibition of BACE2, a GAM337457 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337457 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337457 FHL2 CACTGCACTCCACCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337457 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337457 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337457 is therefore inhibition of FHL2, a GAM337457 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337457 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337457 IGF1 CACTGCACTCCACCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337457 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337457 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337457 is therefore inhibition of IGF1, a GAM337457 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337457 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337457 PRND CACTGCACTCCACCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337457 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337457 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337457 is therefore inhibition of PRND, a GAM337457 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337457 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337458 ADAMTS5 CTGGTGAGGAAGGAG A Disintegrin- like and Metalloprotease (reprolysin type) with A A
CAGAGTT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM337458 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337458 is therefore inhibition of ADAMTS5, a GAM337458 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337458 HD CTGGTGAGGAAGGAG HD (Accession NM_002111.3) is another GAM337458 target gene.
HD A A

CAGAGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337458 is therefore inhibition of HD. Accordingly, utilities of GAM337458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337458 MPO CTGGTGAGGAAGGAG Myeloperoxidase (MPO, Accession NM_000250.1) is another
A A

CAGAGTT GAM337458 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337458 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337458 is therefore inhibition of MPO, a GAM337458 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337458 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM337459 ADAMTS5 CTGGTGAGGAAGGAG A Disintegrin- like and Metalloprotease (reprolysin type) with A
A

CAGAGTT Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM337459 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337459 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337459 is therefore inhibition of ADAMTS5, a GAM337459 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337459 HD CTGGTGAGGAAGGAG HD (Accession NM_002111.3) is another GAM337459 target gene.
HD A A

CAGAGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337459 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337459 is therefore inhibition of HD. Accordingly, utilities of GAM337459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337459 MPO CTGGTGAGGAAGGAG Myeloperoxidase (MPO, Accession NM_000250.1) is another
A A

CAGAGTT GAM337459 target gene. MPO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MPO BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337459 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337459 is therefore inhibition of MPO, a GAM337459 target gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337459 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MPO.The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM337460 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A

GGGTGAC a GAM337460 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337460 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337460 is therefore inhibition of FHL2, a GAM337460 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337460 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337460 IGF1 ACTGCACTCCAGCCT GGGTGAC A A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337460 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337460 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337460 is therefore inhibition of IGF1, a GAM337460 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337460 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337460 PRND ACTGCACTCCAGCCT GGGTGAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337460 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337460 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337460 is therefore inhibition of PRND, a GAM337460 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337460 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337461 APPBP2 AATCCCAGCTACTCG GGAGGCT A A Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337461 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM337461 is therefore inhibition of APPBP2, a GAM337461 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337461 CTSB AATCCCAGCTACTCG CTSB (Accession NM_147782.1) is another GAM337461 target gene. A A

GGAGGCT CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337461 is therefore inhibition of CTSB. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337461 FHL2 AATCCCAGCTACTCG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGAGGCT another GAM337461 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337461 is therefore inhibition of FHL2, a GAM337461 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337461 GFAP AATCCCAGCTACTCG GFAP (Accession NM_002055.2) is another GAM337461 target gene. A A

GGAGGCT GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING

SITE, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337461 is therefore inhibition of GFAP. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337461 IGF1 AATCCCAGCTACTCG GGAGGCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337461 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337461 is therefore inhibition of IGF1, a GAM337461 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337461 PRND AATCCCAGCTACTCG GGAGGCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337461 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337461 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337461 is therefore inhibition of PRND, a GAM337461 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337461 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337462 APPBP2 GCCATTGCACTCCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CCTGGGC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337462 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337462 is therefore inhibition of APPBP2, a GAM337462 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337462 CTSB GCCATTGCACTCCAG CTSB (Accession NM_147780.1) is another GAM337462 target gene. A A

CCTGGGC CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337462 is therefore inhibition of CTSB. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337462 FHL2 GCCATTGCACTCCAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CCTGGGC another GAM337462 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337462 is therefore inhibition of FHL2, a GAM337462 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM189.

GAM337462 IGF1 GCCATTGCACTCCAG Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
CCTGGGC NM_000618.2) is another GAM337462 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337462 is therefore inhibition of IGF1, a GAM337462 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337462 PRND GCCATTGCACTCCAG Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
CCTGGGC another GAM337462 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337462 is therefore inhibition of PRND, a GAM337462 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337462 PSEN2 GCCATTGCACTCCAG PSEN2 (Accession NM_000447.1) is another GAM337462 target gene. A A
CCTGGGC PSEN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337462 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337462 is therefore inhibition of PSEN2. Accordingly, utilities of GAM337462 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN2.

GAM337463 APPBP2 TGGAAGAATAGGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TATTGGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337463 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337463 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337463 is therefore inhibition of APPBP2, a GAM337463 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337463 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337463 CTSK TGGAAGAATAGGCAG CTSK (Accession NM_000396.2) is another GAM337463 target gene. A A

TATTGGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337463 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337463 is therefore inhibition of CTSK. Accordingly, utilities of GAM337463 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM337463 DLST TGGAAGAATAGGCAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TATTGGA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337463 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337463 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337463 is therefore inhibition of

DLST, a GAM337463 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337463 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337464 APPBP2 TGGAAGAATAGGCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TATTGGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337464 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337464 is therefore inhibition of APPBP2, a GAM337464 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337464 CTSK TGGAAGAATAGGCAG CTSK (Accession NM_000396.2) is another GAM337464 target gene. A A

TATTGGA CTSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSK BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337464 is therefore inhibition of CTSK. Accordingly, utilities of GAM337464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSK.

GAM337464 DLST TGGAAGAATAGGCAG Dihydrolipoamide S- succinyltransferase (E2 component of 2- A A

TATTGGA oxo- glutarat (DLST, Accession NM_001933.2) is another GAM337464 target gene. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DLST BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM337464 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337464 is therefore inhibition of DLST, a GAM337464 target gene which catalyzes the oxidative decarboxylation of alpha- keto acids. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337464 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DLST.The function of DLST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.

GAM337465 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337465 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337465 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337465 is therefore inhibition of APP. Accordingly, utilities of GAM337465 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337466 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337466 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337466 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337466 is therefore inhibition of APP. Accordingly, utilities of GAM337466 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337469 PRND AATGTGAATGTTGTA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A

TGCAGTG GAM337469 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337469 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337469 is therefore inhibition of PRND, a GAM337469 target gene which is similar to prion protein PRNP. and

therefore is associated with Alzheimer. Accordingly, utilities of GAM337469 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337470 SERPINA3 CTAGACTGAAGCTTTATGAGGA Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha- 1 antiprotei (SERPINA3, Accession NM_001085.2) is a GAM337470 target gene. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SERPINA3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337470 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337470 is therefore inhibition of SERPINA3, a GAM337470 target gene which is a member of the serpin family of serine protease inhibitors. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337470 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SERPINA3.The function of SERPINA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1032.

GAM337472 GYPA AGAGGCACAGATTAATGGAGTT Glycophorin A (includes MN blood group) (GYPA, Accession NM_002099.2) is a GAM337472 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337472 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337472 is therefore inhibition of GYPA, a GAM337472 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337472 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337472 IGF1 AGAGGCACAGATTAATGGAGTT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337472 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure A A

complementarity to the nucleotide sequence of GAM337472 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337472 is therefore inhibition of IGF1, a GAM337472 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337472 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337473 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337473 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337473 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337473 is therefore inhibition of APP. Accordingly, utilities of GAM337473 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337476 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337476 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337476 is therefore inhibition of APPBP2, a GAM337476 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337476 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337476 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337476 is therefore inhibition of BACE2, a GAM337476 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337476 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337476 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337476 is therefore inhibition of FHL2, a GAM337476 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337476 HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337476 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337476 is therefore inhibition of HD. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337476 IGF1 A A CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession

TGGGCAA NM_000618.2) is another GAM337476 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337476 is therefore inhibition of IGF1, a GAM337476 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337476 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337476 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337476 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337476 is therefore inhibition of PRND, a GAM337476 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337476 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337477 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337477 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337477 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337477 is therefore inhibition of APP. Accordingly, utilities of GAM337477 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with APP.

GAM337478 FLNB TATGTCACTCCTTTG CCCAGAC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession NM_001457.1) is a GAM337478 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337478 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337478 is therefore inhibition of FLNB, a GAM337478 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337478 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM337479 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337479 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337479 is therefore inhibition of APPBP2, a GAM337479 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337479 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337479 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337479 is therefore inhibition of BACE2, a GAM337479 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337479 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337479 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337479 is therefore inhibition of FHL2, a GAM337479 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337479 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337479 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337479 is therefore inhibition of IGF1, a GAM337479 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337479 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337479 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337479 is therefore inhibition of MME, a GAM337479 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337479 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337479 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337479 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337479 is therefore inhibition of PRND, a GAM337479 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337479 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337480 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337480 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337480 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337480 is therefore inhibition of APP. Accordingly, utilities of GAM337480 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with APP.

GAM337481 MAPT TACAAATGTTTCTTC TCCTTTT Microtubule- associated Protein Tau (MAPT, Accession NM_173727.1) is a GAM337481 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337481 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337481 is therefore inhibition of MAPT, a GAM337481 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337481 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337482 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337482 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337482 is therefore inhibition of APPBP2, a GAM337482 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337482 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337482 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337482 is therefore inhibition of BACE2, a GAM337482 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337482 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337482 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337482 is therefore inhibition of FHL2, a GAM337482 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337482 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337482 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337482 is therefore inhibition of HD. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337482 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337482 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING

SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337482 is therefore inhibition of IGF1, a GAM337482 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337482 PRND CATTGCACTCCAGCC TGGGCAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337482 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337482 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337482 is therefore inhibition of PRND, a GAM337482 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337482 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337485 MME GTGGGCTGAGAAAGG CTGCCCA Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_007287.1) is a GAM337485 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337485 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337485 is therefore inhibition of MME, a GAM337485 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337485 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases

and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337485 NCSTN GTGGGCTGAGAAAGG NCSTN (Accession NM_015331.1) is another GAM337485 target gene. A A

CTGCCCA NCSTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337485 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337485 is therefore inhibition of NCSTN, a GAM337485 target gene which has a central role in presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337485 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337485 NOTCH1 GTGGGCTGAGAAAGG Notch (Drosophila) Homolog 1 (translocation- associated) A A

CTGCCCA (NOTCH1, Accession NM_017617.2) is another GAM337485 target gene. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NOTCH1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337485 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337485 is therefore inhibition of NOTCH1, a GAM337485 target gene which is possibly involved in cell differentiation and lymphocyte function. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337485 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NOTCH1.The function of NOTCH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM869.

GAM337486 DHCR24 TAAGGCACTGCTTCT 24- dehydrocholesterol Reductase (DHCR24, Accession A A

AAGTAGG NM_014762.1) is a GAM337486 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337486 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337486 is therefore inhibition of DHCR24, a GAM337486 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337486 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337488 APPBP2 TGAGGCAGAAGGATT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

ACTTGAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337488 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337488 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337488 is therefore inhibition of APPBP2, a GAM337488 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337488 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337488 IGF1 TGAGGCAGAAGGATT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

ACTTGAG NM_000618.2) is another GAM337488 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337488 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337488 is therefore inhibition of IGF1, a GAM337488 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337488 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337489 ACE GGAGGAGGAGGCTGG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TGCTGGT (ACE, Accession NM_000789.2) is a GAM337489 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337489 is therefore inhibition of ACE, a GAM337489 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337489 BACE2 GGAGGAGGAGGCTGG Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGCTGGT NM_012105.3) is another GAM337489 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of BACE2, a GAM337489 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337489 GLUL GGAGGAGGAGGCTGG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
TGCTGGT NM_002065.3) is another GAM337489 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of GLUL, a GAM337489 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337489 HD GGAGGAGGAGGCTGG HD (Accession NM_002111.3) is another GAM337489 target gene. HD A A

TGCTGGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of HD. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337489 MAPT GGAGGAGGAGGCTGG Microtubule- associated Protein Tau (MAPT, Accession A A

TGCTGGT NM_173727.1) is another GAM337489 target gene. MAPT BINDING SITE1 and MAPT BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MAPT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE1 and MAPT BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of MAPT, a GAM337489 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337489 MME GGAGGAGGAGGCTGG Membrane Metallo- endopeptidase (neutral endopeptidase, A A

TGCTGGT enkephalinase, (MME, Accession NM_007287.1) is another GAM337489 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of MME, a GAM337489 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337489 OGDH GGAGGAGGAGGCTGG A A TGCTGGT Oxoglutarate Dehydrogenase (lipoamide) (OGDH, Accession NM_002541.1) is another GAM337489 target gene. OGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of OGDH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of OGDH, a GAM337489 target gene which helps convert a- ketoglutarate to succinyl coenzyme A in Krebs cycle. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with OGDH.The function of OGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2014.

GAM337489 PSEN1 GGAGGAGGAGGCTGG A A TGCTGGT PSEN1 (Accession NM_007318.1) is another GAM337489 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337489 SLC6A4 GGAGGAGGAGGCTGG A A TGCTGGT Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM337489 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337489 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337489 is therefore inhibition of SLC6A4, a GAM337489 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337489 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM337490 ACT TTCAGGACTGTGGAC Activator of CAMP- responsive Element Modulator (CR (ACT, A A TGGGCTG Accession NM_020482.3) is a GAM337490 target gene. ACT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337490 is therefore inhibition of ACT, a GAM337490 target gene which a plasma protease inhibitor synthesized in the liver. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACT.The function of ACT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1484.

GAM337490 APBA2 TTCAGGACTGTGGAC Amyloid Beta (A4) Precursor Protein- binding, Family A, Member A A TGGGCTG 2 (X11- l (APBA2, Accession NM_005503.2) is another GAM337490 target gene. APBA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBA2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337490 is therefore inhibition of APBA2, a GAM337490 target gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. and therefore

is associated with Alzheimer. Accordingly, utilities of GAM337490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBA2.The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337490 APBB2 TTCAGGACTGTGGAC Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

TGGGCTG 2 (Fe65- (APBB2, Accession NM_173075.1) is another GAM337490 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337490 is therefore inhibition of APBB2, a GAM337490 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337490 PLCD1 TTCAGGACTGTGGAC Phospholipase C, Delta 1 (PLCD1, Accession NM_006225.1) is A A

TGGGCTG another GAM337490 target gene. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PLCD1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337490 is therefore inhibition of PLCD1, a GAM337490 target gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5-trisphosphate and therefore is associated with Alzheimer. Accordingly, utilities of GAM337490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PLCD1.The function of PLCD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.

GAM337490 TRPM2 TTCAGGACTGTGGAC TRPM2 (Accession NM_003307.1) is another GAM337490 target gene. A A

TGGGCTG TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337490 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337490 is therefore inhibition of TRPM2, a GAM337490 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337490 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337495 APBB2 GATTGCTTGAGCCCT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A
GGAGGTT 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337495 target gene. APBB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337495 is therefore inhibition of APBB2, a GAM337495 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337495 GFAP GATTGCTTGAGCCCT GFAP (Accession NM_002055.2) is another GAM337495 target gene. A A
GGAGGTT GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337495 is therefore inhibition of GFAP. Accordingly, utilities of GAM337495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337495 IGF1 GATTGCTTGAGCCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGAGGTT NM_000618.2) is another GAM337495 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337495 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337495 is therefore inhibition of IGF1, a GAM337495 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337495 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337496 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337496 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337496 is therefore inhibition of APPBP2, a GAM337496 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337496 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337496 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337496 is therefore inhibition of BACE2, a GAM337496 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337496 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337496 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337496 is therefore inhibition of FHL2, a GAM337496 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337496 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337496 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337496 is therefore inhibition of IGF1, a GAM337496 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337496 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337496 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337496 is therefore inhibition of MME, a GAM337496 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337496 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337496 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337496 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337496 is therefore inhibition of PRND, a GAM337496 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337496 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337497 APPBP2 GTGGCCTTTCTGGTC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGTGTAT Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337497 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337497 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337497 is therefore inhibition of APPBP2, a GAM337497 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM337497 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337497 FLNB GTGGCCTTTCTGGTC Filamin B, Beta (actin- binding protein- 278) (FLNB, Accession A A

TGTGTAT NM_001457.1) is another GAM337497 target gene. FLNB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FLNB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337497 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337497 is therefore inhibition of FLNB, a GAM337497 target gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337497 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FLNB.The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1193.

GAM337498 DSCR1 TGATTGTCCAAACGC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

AATTCTT NM_004414.3) is a GAM337498 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337498 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337498 is therefore inhibition of DSCR1, a GAM337498 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337498 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM337499 DSCR1 TGATTGTCCAAACGC Down Syndrome Critical Region Gene 1 (DSCR1, Accession A A

AATTCTT NM_004414.3) is a GAM337499 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337499 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337499 is therefore inhibition of DSCR1, a GAM337499 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337499 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM337500 DSCR1 TGATTGTCCAAACGC A A AATTCTT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM337500 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337500 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337500 is therefore inhibition of DSCR1, a GAM337500 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337500 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1332.

GAM337501 DSCR1 TGATTGTCCAAACGC A A AATTCTT Down Syndrome Critical Region Gene 1 (DSCR1, Accession NM_004414.3) is a GAM337501 target gene. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DSCR1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337501 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337501 is therefore inhibition of DSCR1, a GAM337501 target gene which inhibits calcineurin- dependent transcriptional responses. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337501 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DSCR1.The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM1332.

GAM337502 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337502 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337502 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337502 is therefore inhibition of APP. Accordingly, utilities of GAM337502 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337507 BAX CCTTGTGTTTTCCAG BCL2- associated X Protein (BAX, Accession NM_138764.1) is a A A

ATTCTGA GAM337507 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337507 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337507 is therefore inhibition of BAX, a GAM337507 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM337507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM337507 TNF CCTTGTGTTTTCCAG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

ATTCTGA Accession NM_000594.2) is another GAM337507 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337507 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337507 is therefore inhibition of TNF, a GAM337507 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337507 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM99.

GAM337508 BAX CCTTGTGTTTTCCAG BCL2- associated X Protein (BAX, Accession NM_138764.1) is a A A

ATTCTGA GAM337508 target gene. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BAX BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337508 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337508 is therefore inhibition of BAX, a GAM337508 target gene which accelerates programmed cell death and therefore is associated with Alzheimer. Accordingly, utilities of GAM337508 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BAX.The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1650.

GAM337508 TNF CCTTGTGTTTTCCAG Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, A A

ATTCTGA Accession NM_000594.2) is another GAM337508 target gene. TNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337508 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337508 is therefore inhibition of TNF, a GAM337508 target gene which mediates proinflammatory responses and apoptosis and therefore is associated with Alzheimer. Accordingly, utilities of GAM337508 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNF.The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337510 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337510 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337510 is therefore inhibition of APPBP2,

a GAM337510 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337510 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337510 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337510 is therefore inhibition of BACE2, a GAM337510 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337510 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337510 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337510 is therefore inhibition of FHL2, a GAM337510 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337510 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337510 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337510 is therefore inhibition of HD. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337510 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337510 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337510 is therefore inhibition of IGF1, a GAM337510 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337510 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337510 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337510 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337510 is therefore inhibition of PRND, a GAM337510 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337510 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM337511 RAGE AGAATGAAAGGCAGT Renal Tumor Antigen (RAGE, Accession NM_014226.1) is a A A TCCTAGC GAM337511 target gene. RAGE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAGE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of RAGE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337511 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337511 is therefore inhibition of RAGE, a GAM337511 target gene which is essential for the completion of the start, the controlling event, in the cell cycle and therefore is associated with Alzheimer. Accordingly, utilities of GAM337511 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with RAGE.The function of RAGE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1523.

GAM337512 FHL2 ACTGCACTCCTGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGTGAC a GAM337512 target gene. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337512 is therefore inhibition of FHL2, a GAM337512 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337512 IGF1 ACTGCACTCCTGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A GGGTGAC NM_000618.2) is another GAM337512 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337512 is therefore inhibition of

IGF1, a GAM337512 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337512 PRND ACTGCACTCCTGCCT GGGTGAC A A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337512 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337512 is therefore inhibition of PRND, a GAM337512 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337512 TNFRSF5 ACTGCACTCCTGCCT GGGTGAC A A TNFRSF5 (Accession NM_152854.1) is another GAM337512 target gene. TNFRSF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TNFRSF5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337512 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337512 is therefore inhibition of TNFRSF5. Accordingly, utilities of GAM337512 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TNFRSF5.

GAM337515 PSEN1 TGATGCTTGAGCACA GTACCTC A A PSEN1 (Accession NM_007318.1) is a GAM337515 target gene. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337515 RNA are set forth in Tables 6

and 7, hereby incorporated herein.

A function of GAM337515 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337515 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337516 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337516 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337516 is therefore inhibition of APPBP2, a GAM337516 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337516 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337516 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337516 is therefore inhibition of BACE2, a GAM337516 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337516 FHL2 ACTGCACTCCAGCCT GGGCAAC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337516 target gene. FHL2 BINDING SITE1 and FHL2 BINDING A A

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337516 is therefore inhibition of FHL2, a GAM337516 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337516 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337516 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337516 is therefore inhibition of IGF1, a GAM337516 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337516 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337516 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337516 is therefore inhibition of MME, a GAM337516 target gene which is thermolysin- like specificity.

and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337516 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337516 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337516 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337516 is therefore inhibition of PRND, a GAM337516 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337516 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337518 AVP GACCCCTTGCCCGTG AVP (Accession NM_000490.2) is a GAM337518 target gene. AVP A A

GCTCCCA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AVP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337518 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337518 is therefore inhibition of AVP. Accordingly, utilities of GAM337518 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AVP.

GAM337518 TGFB1 GACCCCTTGCCCGTG TGFB1 (Accession NM_000660.1) is another GAM337518 target gene. A A

GCTCCCA TGFB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337518 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337518 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337518 include diagnosis,

prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337520 MTNR1A TGTATGCTCTGTGAA A A GCTTACT Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is a GAM337520 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337520 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337520 is therefore inhibition of MTNR1A, a GAM337520 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337520 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337521 ACE TTGCAAGGAAGGGGA A A GGAGGCT Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 (ACE, Accession NM_152831.1) is a GAM337521 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337521 is therefore inhibition of ACE, a GAM337521 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337521 BACE2 TTGCAAGGAAGGGGA A A GGAGGCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337521 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337521 is therefore inhibition of BACE2, a GAM337521 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337521 CNTF TTGCAAGGAAGGGGA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A

GGAGGCT another GAM337521 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337521 is therefore inhibition of CNTF, a GAM337521 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337521 GLUL TTGCAAGGAAGGGGA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A

GGAGGCT NM_002065.3) is another GAM337521 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337521 is therefore inhibition of GLUL, a GAM337521 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337521 HD TTGCAAGGAAGGGGA HD (Accession NM_002111.3) is another GAM337521 target gene. HD A A

GGAGGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337521 is therefore inhibition of HD. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337521 IGF1 TTGCAAGGAAGGGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGAGGCT NM_000618.2) is another GAM337521 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337521 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337521 is therefore inhibition of IGF1, a GAM337521 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337521 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337522 ACE TTGCAAGGAAGGGGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GGAGGCT (ACE, Accession NM_152831.1) is a GAM337522 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337522 is therefore inhibition of ACE, a GAM337522 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM44.

GAM337522 BACE2 TTGCAAGGAAGGGGA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A GGAGGCT NM_138992.1) is another GAM337522 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337522 is therefore inhibition of BACE2, a GAM337522 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337522 CNTF TTGCAAGGAAGGGGA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A GGAGGCT another GAM337522 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337522 is therefore inhibition of CNTF, a GAM337522 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337522 GLUL TTGCAAGGAAGGGGA Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A GGAGGCT NM_002065.3) is another GAM337522 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337522 is therefore inhibition of GLUL, a GAM337522 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337522 HD TTGCAAGGAAGGGGA HD (Accession NM_002111.3) is another GAM337522 target gene. HD A A

GGAGGCT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337522 is therefore inhibition of HD. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337522 IGF1 TTGCAAGGAAGGGGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGAGGCT NM_000618.2) is another GAM337522 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337522 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337522 is therefore inhibition of IGF1, a GAM337522 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337522 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337523 ACE TTGCAAGGAAGGGGA Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GGAGGCT (ACE, Accession NM_152831.1) is a GAM337523 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence

of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337523 is therefore inhibition of ACE, a GAM337523 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337523 BACE2 TTGCAAGGAAGGGGA GGAGGCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337523 target gene. BACE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337523 is therefore inhibition of BACE2, a GAM337523 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337523 CNTF TTGCAAGGAAGGGGA GGAGGCT Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is another GAM337523 target gene. CNTF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337523 is therefore inhibition of CNTF, a GAM337523 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM175.

GAM337523 GLUL TTGCAAGGAAGGGGA A A GGAGGCT Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession NM_002065.3) is another GAM337523 target gene. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337523 is therefore inhibition of GLUL, a GAM337523 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337523 HD TTGCAAGGAAGGGGA A A GGAGGCT HD (Accession NM_002111.3) is another GAM337523 target gene. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337523 is therefore inhibition of HD. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337523 IGF1 TTGCAAGGAAGGGGA A A GGAGGCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337523 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337523 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337523 is therefore inhibition of IGF1, a GAM337523 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337523 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337524 ACE CGCTATGTTGGCCAG Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A

GCTGGTC (ACE, Accession NM_152831.1) is a GAM337524 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337524 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337524 is therefore inhibition of ACE, a GAM337524 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337524 ADAM17 CGCTATGTTGGCCAG A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis A A

GCTGGTC factor, (ADAM17, Accession NM_021832.1) is another GAM337524 target gene. ADAM17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAM17 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337524 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337524 is therefore inhibition of ADAM17, a GAM337524 target gene which is a member of ADAM family of zinc metalloproteases. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAM17.The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337524 HD CGCTATGTTGGCCAG HD (Accession NM_002111.3) is another GAM337524 target gene. HD A A

GCTGGTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337524

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337524 is therefore inhibition of HD. Accordingly, utilities of GAM337524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337524 IAPP CGCTATGTTGGCCAG Islet Amyloid Polypeptide (IAPP, Accession NM_000415.1) is A A
GCTGGTC another GAM337524 target gene. IAPP BINDING SITE1 and IAPP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IAPP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IAPP BINDING SITE1 and IAPP BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337524 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337524 is therefore inhibition of IAPP, a GAM337524 target gene which selectively inhibits insulin-stimulated glucose utilization and glycogen deposition and therefore is associated with Alzheimer. Accordingly, utilities of GAM337524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IAPP.The function of IAPP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.

GAM337524 TGFB1 CGCTATGTTGGCCAG TGFB1 (Accession NM_000660.1) is another GAM337524 target gene. A A
GCTGGTC TGFB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TGFB1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337524 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337524 is therefore inhibition of TGFB1. Accordingly, utilities of GAM337524 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TGFB1.

GAM337525 HD TTGCATATGCATGGG HD (Accession NM_002111.3) is a GAM337525 target gene. HD A A
TACACAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337525 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337525 is therefore inhibition of HD.

Accordingly, utilities of GAM337525 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337526 PRNP AGGCAGAGAGGTATT Prion Protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- A A
TAGGCAT Strausler- (PRNP, Accession NM_000311.1) is a GAM337526 target gene. PRNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRNP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337526 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337526 is therefore inhibition of PRNP, a GAM337526 target gene which the function of prp is not known. prp is encoded in the host genome and is expressed both in normal and infected cells. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337526 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRNP.The function of PRNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.

GAM337528 NPY GGCTAGAAAGCCAGA Neuropeptide Y (NPY, Accession NM_000905.2) is a GAM337528 A A
GAGACAG target gene. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NPY BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337528 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337528 is therefore inhibition of NPY, a GAM337528 target gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337528 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NPY.The function of NPY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.

GAM337529 APPBP2 TTTATTAGTTGTCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGTTTA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337529 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and

secondary structure complementarity to the nucleotide sequence of GAM337529 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337529 is therefore inhibition of APPBP2, a GAM337529 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337529 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337530 APBB2 TAAGAAGAGAAAGAA Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAGGCTG 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337530 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337530 is therefore inhibition of APBB2, a GAM337530 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337530 BACE TAAGAAGAGAAAGAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_138971.1) A A

GAGGCTG is another GAM337530 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337530 is therefore inhibition of BACE, a GAM337530 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with

BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337530 BCHE TAAGAAGAGAAAGAA BCHE (Accession NM_000055.1) is another GAM337530 target gene. A A

GAGGCTG BCHE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BCHE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337530 is therefore inhibition of BCHE. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BCHE.

GAM337530 FOS TAAGAAGAGAAAGAA V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

GAGGCTG Accession NM_005252.2) is another GAM337530 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337530 is therefore inhibition of FOS, a GAM337530 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337530 GYPA TAAGAAGAGAAAGAA Glycophorin A (includes MN blood group) (GYPA, Accession A A

GAGGCTG NM_002099.2) is another GAM337530 target gene. GYPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GYPA BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337530 is therefore inhibition of GYPA, a GAM337530 target gene which determines the M or N blood group. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with GYPA.The function of GYPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM317.

GAM337530 NGB A A TAAGAAGAGAAAGAA GAGGCTG Neuroglobin (NGB, Accession NM_021257.2) is another target gene. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NGB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337530 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337530 is therefore inhibition of NGB, a GAM337530 target gene which has function in oxygen transport and storage in humans. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337530 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NGB.The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337531 APP A A TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337531 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337531 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337531 is therefore inhibition of APP. Accordingly, utilities of GAM337531 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337533 APP A A TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337533 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337533 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337533 is therefore inhibition of APP. Accordingly, utilities of GAM337533 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337534 APP A A TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337534 target gene. APP

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337534 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337534 is therefore inhibition of APP. Accordingly, utilities of GAM337534 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337541 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337541 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337541 is therefore inhibition of APPBP2, a GAM337541 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337541 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337541 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337541 is therefore inhibition of BACE2, a GAM337541 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM189.

GAM337541 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337541 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337541 is therefore inhibition of FHL2, a GAM337541 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337541 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337541 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337541 is therefore inhibition of HD. Accordingly, utilities of GAM337541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337541 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337541 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337541 is therefore inhibition of IGF1, a GAM337541 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337541 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337541 PRND CATTGCACTCCAGCC TGGGCAA A A

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337541 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337541 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337541 is therefore inhibition of PRND, a GAM337541 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337541 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337542 APPBP2 CATTGCACTCCAGCC TGGGCAA A A

Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337542 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337542 is therefore inhibition of APPBP2, a GAM337542 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337542 BACE2 CATTGCACTCCAGCC TGGGCAA A A

Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337542 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337542 is therefore inhibition of BACE2, a GAM337542 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337542 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337542 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337542 is therefore inhibition of FHL2, a GAM337542 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337542 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337542 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337542 is therefore inhibition of HD. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337542 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337542 target gene. IGF1 BINDING SITE1

and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337542 is therefore inhibition of IGF1, a GAM337542 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337542 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM337542 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337542 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337542 is therefore inhibition of PRND, a GAM337542 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337542 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337543 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337543 target gene. APP A A GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337543 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337543 is therefore inhibition of APP. Accordingly, utilities of GAM337543 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337544 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337544 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337544 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337544 is therefore inhibition of APP. Accordingly, utilities of GAM337544 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337545 APPBP2 GCCATTGCACTCCAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

CCTGGAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337545 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337545 is therefore inhibition of APPBP2, a GAM337545 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337545 CTSB GCCATTGCACTCCAG CTSB (Accession NM_001908.2) is another GAM337545 target gene. A A

CCTGGAC CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CTSB BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337545 is therefore inhibition of CTSB. Accordingly, utilities of GAM337545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CTSB.

GAM337545 FHL2 GCCATTGCACTCCAG Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

CCTGGAC another GAM337545 target gene. FHL2 BINDING SITE is a target binding

site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337545 is therefore inhibition of FHL2, a GAM337545 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337545 IGF1 GCCATTGCACTCCAG A Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
CCTGGAC NM_000618.2) is another GAM337545 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337545 is therefore inhibition of IGF1, a GAM337545 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337545 PRND GCCATTGCACTCCAG A Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A
CCTGGAC another GAM337545 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337545 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337545 is therefore inhibition of PRND, a GAM337545 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM337545 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337547 IGF1 TCTTTCTTAAATGGA TGCATGA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is a GAM337547 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337547 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337547 is therefore inhibition of IGF1, a GAM337547 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337547 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337548 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337548 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337548 is therefore inhibition of APPBP2, a GAM337548 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337548 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337548 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a A A

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337548 is therefore inhibition of BACE2, a GAM337548 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337548 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337548 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337548 is therefore inhibition of FHL2, a GAM337548 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337548 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337548 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337548 is therefore inhibition of IGF1, a GAM337548 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337548 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337548 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337548 is therefore inhibition of MME, a GAM337548 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337548 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337548 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337548 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337548 is therefore inhibition of PRND, a GAM337548 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337548 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337549 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337549 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide

sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337549 is therefore inhibition of APPBP2, a GAM337549 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337549 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337549 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337549 is therefore inhibition of BACE2, a GAM337549 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337549 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337549 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337549 is therefore inhibition of FHL2, a GAM337549 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337549 IGF1 ACTGCACTCCAGCCT GGGCAAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337549 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337549 is therefore inhibition of IGF1, a GAM337549 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337549 MME ACTGCACTCCAGCCT GGGCAAC Membrane Metallo- endopeptidase (neutral endopeptidase, enkephalinase, (MME, Accession NM_000902.2) is another GAM337549 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337549 is therefore inhibition of MME, a GAM337549 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337549 PRND ACTGCACTCCAGCCT GGGCAAC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337549 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING A A

SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337549 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337549 is therefore inhibition of PRND, a GAM337549 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337549 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337552 APPBP2 ACTGCACTCCAGCCT GGGCAAC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337552 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337552 is therefore inhibition of APPBP2, a GAM337552 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337552 BACE2 ACTGCACTCCAGCCT GGGCAAC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_012105.3) is another GAM337552 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337552 is therefore inhibition of BACE2, a GAM337552 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The

function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337552 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337552 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337552 is therefore inhibition of FHL2, a GAM337552 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337552 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337552 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337552 is therefore inhibition of IGF1, a GAM337552 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337552 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337552 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences

of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337552 is therefore inhibition of MME, a GAM337552 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337552 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A GGGCAAC another GAM337552 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337552 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337552 is therefore inhibition of PRND, a GAM337552 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337552 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337553 FOS TGAAAGAGATGGGAC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A AGTGACT Accession NM_005252.2) is a GAM337553 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337553 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337553 is therefore inhibition of FOS, a GAM337553 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337553 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337554 FOS TGAAAGAGATGGGAC V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A

AGTGACT Accession NM_005252.2) is a GAM337554 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337554 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337554 is therefore inhibition of FOS, a GAM337554 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337554 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337555 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337555 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337555 is therefore inhibition of APPBP2, a GAM337555 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337555 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337555 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337555 is therefore inhibition of BACE2, a GAM337555 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337555 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337555 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337555 is therefore inhibition of FHL2, a GAM337555 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337555 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337555 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337555 is therefore inhibition of IGF1, a GAM337555 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337555 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337555 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337555 is therefore inhibition of MME, a GAM337555 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337555 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337555 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337555 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337555 is therefore inhibition of PRND, a GAM337555 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337555 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337556 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337556 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337556 is therefore inhibition of APPBP2, a GAM337556 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337556 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A GGGCAAC NM_012105.3) is another GAM337556 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337556 is therefore inhibition of BACE2, a GAM337556 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337556 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A GGGCAAC another GAM337556 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337556 is therefore inhibition of FHL2, a GAM337556 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337556 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337556 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337556 is therefore inhibition of IGF1, a GAM337556 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337556 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337556 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337556 is therefore inhibition of MME, a GAM337556 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337556 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337556 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337556 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337556 is therefore inhibition of PRND, a GAM337556 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337556 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337558 PRND ATGCCACAGCACTTC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is a A A
AGCCTGA GAM337558 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337558 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337558 is therefore inhibition of PRND, a GAM337558 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337558 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337566 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337566 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337566 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337566 is therefore inhibition of APP. Accordingly, utilities of GAM337566 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337567 APPBP2 TGTAAACATCCCCGA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
CTGGAAG Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337567 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337567 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337567 is therefore inhibition of APPBP2, a GAM337567 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated

with Alzheimer. Accordingly, utilities of GAM337567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337567 CASP3 TGTAAACATCCCCGA CTGGAAG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is another GAM337567 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337567 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337567 is therefore inhibition of CASP3, a GAM337567 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337567 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337568 APPBP2 TGTAAACATCCCCGA CTGGAAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337568 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337568 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337568 is therefore inhibition of APPBP2, a GAM337568 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337568 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337568 CASP3 TGTAAACATCCCCGA CTGGAAG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is another GAM337568 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, A A

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337568 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337568 is therefore inhibition of CASP3, a GAM337568 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337568 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337569 APPBP2 TGTAAACATCCCCGA CTGGAAG Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337569 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337569 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337569 is therefore inhibition of APPBP2, a GAM337569 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337569 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337569 CASP3 TGTAAACATCCCCGA CTGGAAG Caspase 3, Apoptosis- related Cysteine Protease (CASP3, Accession NM_032991.1) is another GAM337569 target gene. CASP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CASP3 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337569 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337569 is therefore inhibition of CASP3, a GAM337569 target gene which is one apoptosis- related cysteine protease and is important for the initiation of apoptotic cell death. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337569 include diagnosis, prevention and treatment

of Alzheimer, and of other diseases and clinical conditions associated with CASP3.The function of CASP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM801.

GAM337570 ACE TTGATGAATGGGTGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TCCAGGA (ACE, Accession NM_152831.1) is a GAM337570 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337570 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337570 is therefore inhibition of ACE, a GAM337570 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337570 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337570 IGF1 TTGATGAATGGGTGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCCAGGA NM_000618.2) is another GAM337570 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337570 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337570 is therefore inhibition of IGF1, a GAM337570 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337570 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337570 IL1A TTGATGAATGGGTGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TCCAGGA GAM337570 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the

nucleotide sequence of GAM337570 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337570 is therefore inhibition of IL1A, a GAM337570 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337570 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337571 ACE TTGATGAATGGGTGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A TCCAGGA (ACE, Accession NM_152831.1) is a GAM337571 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337571 is therefore inhibition of ACE, a GAM337571 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337571 IGF1 TTGATGAATGGGTGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A TCCAGGA NM_000618.2) is another GAM337571 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337571 is therefore inhibition of IGF1, a GAM337571 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337571 IL1A TTGATGAATGGGTGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TCCAGGA GAM337571 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337571 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337571 is therefore inhibition of IL1A, a GAM337571 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337571 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337572 ACE TTGATGAATGGGTGC Angiotensin I Converting Enzyme (peptidyl- dipeptidase A) 1 A A
TCCAGGA (ACE, Accession NM_152831.1) is a GAM337572 target gene. ACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337572 is therefore inhibition of ACE, a GAM337572 target gene which Angiotensin I- converting enzyme (dipeptidyl carboxypeptidase 1). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ACE.The function of ACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337572 IGF1 TTGATGAATGGGTGC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
TCCAGGA NM_000618.2) is another GAM337572 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337572 is therefore inhibition of IGF1, a GAM337572 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337572 IL1A TTGATGAATGGGTGC Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A

TCCAGGA GAM337572 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337572 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337572 is therefore inhibition of IL1A, a GAM337572 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337572 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337573 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337573 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337573 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337573 is therefore inhibition of APP. Accordingly, utilities of GAM337573 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337574 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337574 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337574 is therefore inhibition of APPBP2, a GAM337574 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337574 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337574 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337574 is therefore inhibition of BACE2, a GAM337574 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337574 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337574 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337574 is therefore inhibition of FHL2, a GAM337574 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical

conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337574 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337574 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337574 is therefore inhibition of HD. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337574 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337574 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337574 is therefore inhibition of IGF1, a GAM337574 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337574 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337574 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337574 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337574 is therefore inhibition of

PRND, a GAM337574 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337574 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337575 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337575 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337575 is therefore inhibition of APPBP2, a GAM337575 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337575 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337575 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337575 is therefore inhibition of BACE2, a GAM337575 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337575 FHL2 CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337575 target gene. FHL2 BINDING SITE1 and FHL2 BINDING A A

SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337575 is therefore inhibition of FHL2, a GAM337575 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337575 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337575 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337575 is therefore inhibition of HD. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337575 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337575 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337575 is therefore inhibition of IGF1, a GAM337575 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to GAM25.

GAM337575 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337575 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337575 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337575 is therefore inhibition of PRND, a GAM337575 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337575 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337576 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337576 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337576 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337576 is therefore inhibition of APP. Accordingly, utilities of GAM337576 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337578 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337578 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337578 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337578 is therefore inhibition of APP. Accordingly, utilities of GAM337578 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337579 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337579 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337579 is therefore inhibition of APPBP2, a GAM337579 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337579 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337579 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337579 is therefore inhibition of BACE2, a GAM337579 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337579 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337579 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337579 is therefore inhibition of FHL2, a GAM337579 target gene which Contains four LIM domains and an

additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337579 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337579 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337579 is therefore inhibition of IGF1, a GAM337579 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337579 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337579 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337579 is therefore inhibition of MME, a GAM337579 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337579 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337579 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337579 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337579 is therefore inhibition of PRND, a GAM337579 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337579 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337580 TRPM2 ACAGTCCTCTACTCC TRPM2 (Accession NM_003307.1) is a GAM337580 target gene. TRPM2 A A

AGCTCCC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337580 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337580 is therefore inhibition of TRPM2, a GAM337580 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of GAM337580 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337581 SLC17A7 GGCAGGATGGAGCAG SOLUTE CARRIER FAMILY 17, MEMBER 7 (SLC17A7, Accession A A

GGCTAAA NM_020309.1) is a GAM337581 target gene. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC17A7 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337581 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337581 is therefore inhibition of SLC17A7, a GAM337581 target gene which is a brain- specific Na-dependent inorganic phosphate cotransporter and therefore is associated with Alzheimer. Accordingly, utilities of GAM337581 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC17A7.The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as

described hereinabove with reference to GAM354.

GAM337584 AGER CCAGTACTGTCTTGA Advanced Glycosylation End Product- specific Receptor (AGER, A A TGCCTGC Accession NM_172197.1) is a GAM337584 target gene. AGER BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AGER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337584 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337584 is therefore inhibition of AGER, a GAM337584 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337584 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AGER.The function of AGER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2350.

GAM337585 AGER CCAGTACTGTCTTGA Advanced Glycosylation End Product- specific Receptor (AGER, A A TGCCTGC Accession NM_172197.1) is a GAM337585 target gene. AGER BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AGER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of AGER BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337585 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337585 is therefore inhibition of AGER, a GAM337585 target gene which Receptor for advanced glycosylation end products (receptor for AGE). and therefore is associated with Alzheimer. Accordingly, utilities of GAM337585 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with AGER.The function of AGER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2350.

GAM337586 MTNR1A GGCAACATGCTGAAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is a A A CCCCAGC GAM337586 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337586 is therefore inhibition of MTNR1A, a GAM337586 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337586 PRND GGCAACATGCTGAAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CCCCAGC another GAM337586 target gene. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337586 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337586 is therefore inhibition of PRND, a GAM337586 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337586 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337587 MTNR1A GGCAACATGCTGAAA Melatonin Receptor 1A (MTNR1A, Accession NM_005958.2) is a A A

CCCCAGC GAM337587 target gene. MTNR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTNR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MTNR1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337587 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337587 is therefore inhibition of MTNR1A, a GAM337587 target gene which likely mediates the reproductive and circadian actions of melatonin. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337587 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MTNR1A.The function of MTNR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.

GAM337587 PRND GGCAACATGCTGAAA Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

CCCCAGC another GAM337587 target gene. PRND BINDING SITE is a target binding

site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337587 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337587 is therefore inhibition of PRND, a GAM337587 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337587 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337588 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337588 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337588 is therefore inhibition of APPBP2, a GAM337588 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337588 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337588 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337588 is therefore inhibition of BACE2, a GAM337588 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337588

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337588 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337588 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337588 is therefore inhibition of FHL2, a GAM337588 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337588 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337588 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337588 is therefore inhibition of HD. Accordingly, utilities of GAM337588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337588 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337588 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337588 is therefore inhibition of

IGF1, a GAM337588 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337588 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337588 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337588 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337588 is therefore inhibition of PRND, a GAM337588 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337588 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337589 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337589 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337589 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337589 is therefore inhibition of APP. Accordingly, utilities of GAM337589 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337590 APPBP2 ATTGCACACCAACCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337590 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337590 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337590 is therefore inhibition of APPBP2, a GAM337590 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337590 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337590 PRND ATTGCACACCAACCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337590 target gene. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337590 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337590 is therefore inhibition of PRND, a GAM337590 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337590 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337591 CAV1 GAGATGACTGGTGGC Caveolin 1, Caveolae Protein, 22kD (CAV1, Accession A A

TGGGGGC NM_001753.3) is a GAM337591 target gene. CAV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CAV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CAV1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337591 is therefore inhibition of CAV1, a GAM337591 target gene which may act as a scaffolding protein within caveolar membranes, and interacts directly with g- protein alpha subunits and can functionally regulate their activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CAV1.The function of CAV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1087.

GAM337591 DHCR24 GAGATGACTGGTGGC 24- dehydrocholesterol Reductase (DHCR24, Accession A A

TGGGGGC NM_014762.1) is another GAM337591 target gene. DHCR24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of DHCR24 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337591 is therefore inhibition of DHCR24, a GAM337591 target gene which catalyzes the reduction of sterol intermediates. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with DHCR24.The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337591 SLC6A4 GAGATGACTGGTGGC Solute Carrier Family 6 (neurotransmitter transporter, A A
TGGGGGC serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM337591 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337591 is therefore inhibition of SLC6A4, a GAM337591 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM337591 TRPM2 GAGATGACTGGTGGC TRPM2 (Accession NM_003307.1) is another GAM337591 target gene. A A
TGGGGGC TRPM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of TRPM2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337591 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337591 is therefore inhibition of TRPM2, a GAM337591 target gene which may be a calcium channel and therefore is associated with Alzheimer. Accordingly, utilities of

GAM337591 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with TRPM2.The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.

GAM337592 HTR2A GAGATCCTTTCACAG TTGTGGT A A — 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession NM_000621.1) is a GAM337592 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337592 is therefore inhibition of HTR2A, a GAM337592 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337592 HTR2C GAGATCCTTTCACAG TTGTGGT A A — 5- hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868.1) is another GAM337592 target gene. HTR2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2C BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337592 is therefore inhibition of HTR2C, a GAM337592 target gene which activates phospholipase C and regulates intracellular calcium flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2C.The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.

GAM337592 SLC6A4 GAGATCCTTTCACAG TTGTGGT A A — Solute Carrier Family 6 (neurotransmitter transporter, serotonin), Mem (SLC6A4, Accession NM_001045.1) is another GAM337592 target gene. SLC6A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of SLC6A4 BINDING SITE, and secondary structure complementarity to the nucleotide

sequence of GAM337592 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337592 is therefore inhibition of SLC6A4, a GAM337592 target gene which terminates the action of serotonine by its high affinity sodium- dependent reuptake into presynaptic terminals. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337592 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with SLC6A4.The function of SLC6A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1294.

GAM337593 APP A A TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337593 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337593 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337593 is therefore inhibition of APP. Accordingly, utilities of GAM337593 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337594 APP A A TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337594 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337594 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337594 is therefore inhibition of APP. Accordingly, utilities of GAM337594 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337595 APP A A TGTGCACAACATGCA GGTTTGT APP (Accession NM_000484.1) is a GAM337595 target gene. APP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337595 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337595 is therefore inhibition of APP. Accordingly, utilities of GAM337595 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337597 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337597 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337597 is therefore inhibition of APPBP2, a GAM337597 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337597 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337597 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337597 is therefore inhibition of BACE2, a GAM337597 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337597 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337597 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence

of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337597 is therefore inhibition of FHL2, a GAM337597 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337597 HD A A TGGGCAA CATTGCACTCCAGCC

HD (Accession NM_002111.3) is another GAM337597 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337597 is therefore inhibition of HD. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337597 IGF1 A A TGGGCAA CATTGCACTCCAGCC

Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337597 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337597 is therefore inhibition of IGF1, a GAM337597 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337597 PRND A A TGGGCAA CATTGCACTCCAGCC

Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is another GAM337597 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions

of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337597 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337597 is therefore inhibition of PRND, a GAM337597 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337597 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337598 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337598 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337598 is therefore inhibition of APPBP2, a GAM337598 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337598 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337598 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337598 is therefore inhibition of BACE2, a GAM337598 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337598

include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337598 FHL2 A A CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337598 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337598 is therefore inhibition of FHL2, a GAM337598 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337598 HD HD A A CATTGCACTCCAGCC TGGGCAA HD (Accession NM_002111.3) is another GAM337598 target gene. BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337598 is therefore inhibition of HD. Accordingly, utilities of GAM337598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337598 IGF1 A A CATTGCACTCCAGCC TGGGCAA Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession NM_000618.2) is another GAM337598 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337598 is therefore inhibition of

IGF1, a GAM337598 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337598 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
TGGGCAA another GAM337598 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337598 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337598 is therefore inhibition of PRND, a GAM337598 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337598 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337599 FOS TGTGTAATGCTGAGA V- fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS, A A
TTTGGGC Accession NM_005252.2) is a GAM337599 target gene. FOS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FOS BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337599 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337599 is therefore inhibition of FOS, a GAM337599 target gene which Transcription factor, acting with JUN, may alter DNA methylation and therefore is associated with Alzheimer. Accordingly, utilities of GAM337599 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FOS.The function of FOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM846.

GAM337601 GFAP TCTCAGTTTCCTCTG GFAP (Accession NM_002055.2) is a GAM337601 target gene. GFAP A A
CAAACAG BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337601 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337601 is therefore inhibition of GFAP. Accordingly, utilities of GAM337601 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337602 GFAP TCTCAGTTTCCTCTG GFAP (Accession NM_002055.2) is a GAM337602 target gene. GFAP A A

CAAACAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GFAP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337602 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337602 is therefore inhibition of GFAP. Accordingly, utilities of GAM337602 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GFAP.

GAM337605 BACE2 TCCCCAGGTTCTAGT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

CCTGAGT NM_138992.1) is a GAM337605 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337605 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337605 is therefore inhibition of BACE2, a GAM337605 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337605 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337606 APP TTGCTTTGGTTCAAG APP (Accession NM_000484.1) is a GAM337606 target gene. APP A A

TTAGGCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337606

RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337606 is therefore inhibition of APP. Accordingly, utilities of GAM337606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337606 GLUL TTGCTTTGGTTCAAG Glutamate- ammonia Ligase (glutamine synthase) (GLUL, Accession A A
TTAGGCA NM_002065.3) is another GAM337606 target gene. GLUL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of GLUL BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337606 is therefore inhibition of GLUL, a GAM337606 target gene which catalyzes the condensation of glutamate and ammonia to form glutamine. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with GLUL.The function of GLUL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.

GAM337606 IL1A TTGCTTTGGTTCAAG Interleukin 1, Alpha (IL1A, Accession NM_000575.3) is another A A
TTAGGCA GAM337606 target gene. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IL1A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337606 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337606 is therefore inhibition of IL1A, a GAM337606 target gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337606 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IL1A.The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.

GAM337607 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337607 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337607 is therefore inhibition of APPBP2, a GAM337607 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337607 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
TGGGCAA NM_138992.1) is another GAM337607 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337607 is therefore inhibition of BACE2, a GAM337607 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337607 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
TGGGCAA another GAM337607 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337607 is therefore inhibition of FHL2, a GAM337607 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337607 include diagnosis, prevention

and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337607 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337607 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337607 is therefore inhibition of HD. Accordingly, utilities of GAM337607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337607 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337607 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337607 is therefore inhibition of IGF1, a GAM337607 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337607 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337607 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337607 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337607 is therefore inhibition of PRND, a GAM337607 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337607 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337608 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337608 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337608 is therefore inhibition of APPBP2, a GAM337608 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337608 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337608 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337608 is therefore inhibition of BACE2, a GAM337608 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337608 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337608 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337608 is therefore inhibition of FHL2, a GAM337608 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337608 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337608 target gene.
HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337608 is therefore inhibition of HD. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337608 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A

TGGGCAA NM_000618.2) is another GAM337608 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337608 is therefore inhibition of IGF1, a GAM337608 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been

established by previous studies, as described hereinabove with reference to GAM25.

GAM337608 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM337608 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337608 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337608 is therefore inhibition of PRND, a GAM337608 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337608 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337613 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337613 target gene. APP A A GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337613 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337613 is therefore inhibition of APP. Accordingly, utilities of GAM337613 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337614 IGF1 CACCCCCAGGACCAC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A CTTGCGA NM_000618.2) is a GAM337614 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337614 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337614 is therefore inhibition of IGF1, a GAM337614 target gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337614 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated

with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337615 ADAMTS5 GTCCTGAGAACTGCT A Disintegrin- like and Metalloprotease (reprolysin type) with A A

CCAGTTA Thrombos (ADAMTS5, Accession NM_007038.1) is a GAM337615 target gene. ADAMTS5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of ADAMTS5 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337615 is therefore inhibition of ADAMTS5, a GAM337615 target gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with ADAMTS5.The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1216.

GAM337615 MAPK10 GTCCTGAGAACTGCT Mitogen- activated Protein Kinase 10 (MAPK10, Accession A A

CCAGTTA NM_138980.1) is another GAM337615 target gene. MAPK10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MAPK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPK10 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337615 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337615 is therefore inhibition of MAPK10, a GAM337615 target gene which is a members of the mitogen-activated protein kinase (MAPK) family that activate the Jun (see 165160) transcription factor. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337615 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPK10.The function of MAPK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.

GAM337616 BACE TCAGTAGCTGTCAAA Beta- site APP- cleaving Enzyme (BACE, Accession NM_012104.2) A A

ACTGGAG is a GAM337616 target gene. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8.

Nucleotide sequences of BACE BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337616 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337616 is therefore inhibition of BACE, a GAM337616 target gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337616 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE.The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.

GAM337616 HTR2A TCAGTAGCTGTCAAA 5- hydroxytryptamine (serotonin) Receptor 2A (HTR2A, Accession A A
ACTGGAG NM_000621.1) is another GAM337616 target gene. HTR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HTR2A BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337616 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337616 is therefore inhibition of HTR2A, a GAM337616 target gene which modulates phosphatidylinositol production and intracellular Ca2 flux. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337616 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HTR2A.The function of HTR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM593.

GAM337617 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337617 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337617 is therefore inhibition of APPBP2, a GAM337617 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function

of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337617 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A
A
GGGCAAC NM_012105.3) is another GAM337617 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337617 is therefore inhibition of BACE2, a GAM337617 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337617 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is
A A
GGGCAAC another GAM337617 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337617 is therefore inhibition of FHL2, a GAM337617 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337617 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
GGGCAAC NM_000618.2) is another GAM337617 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure

complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337617 is therefore inhibition of IGF1, a GAM337617 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337617 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337617 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337617 is therefore inhibition of MME, a GAM337617 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337617 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337617 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337617 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337617 is therefore inhibition of PRND, a GAM337617 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337617 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.

GAM337619 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337619 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337619 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337619 is therefore inhibition of APP. Accordingly, utilities of GAM337619 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337620 APBB2 AATCATCATTATTTT Amyloid Beta (A4) Precursor Protein- binding, Family B, Member A A

GAAGTTTA 2 (Fe65- (APBB2, Accession NM_173075.1) is a GAM337620 target gene. APBB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APBB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APBB2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337620 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337620 is therefore inhibition of APBB2, a GAM337620 target gene which Interacts with beta- amyloid precursor protein and with APLP2. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337620 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APBB2.The function of APBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337620 MAPT AATCATCATTATTTT Microtubule- associated Protein Tau (MAPT, Accession A A

GAAGTTTA NM_005910.2) is another GAM337620 target gene. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MAPT BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337620 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337620 is therefore inhibition of MAPT, a GAM337620 target gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337620 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MAPT.The function of MAPT and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.

GAM337621 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337621 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337621 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337621 is therefore inhibition of APP. Accordingly, utilities of GAM337621 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337622 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337622 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337622 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337622 is therefore inhibition of APP. Accordingly, utilities of GAM337622 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337623 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337623 target gene. APP A A
GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337623 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337623 is therefore inhibition of APP. Accordingly, utilities of GAM337623 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337624 APPBP2 TCTAAGAGAAAGGAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GTTCAGA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337624 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

A function of GAM337624 is therefore inhibition of APPBP2, a GAM337624 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337624 CNTF TCTAAGAGAAAGGAA Ciliary Neurotrophic Factor (CNTF, Accession NM_000614.2) is A A GTTCAGA another GAM337624 target gene. CNTF BINDING SITE1 and CNTF BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CNTF, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CNTF BINDING SITE1 and CNTF BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337624 is therefore inhibition of CNTF, a GAM337624 target gene which is a survival factor for various neuronal cell types. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CNTF.The function of CNTF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.

GAM337624 CRH TCTAAGAGAAAGGAA Corticotropin Releasing Hormone (CRH, Accession NM_000756.1) is A A GTTCAGA another GAM337624 target gene. CRH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of CRH BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337624 is therefore inhibition of CRH, a GAM337624 target gene which regulates the release of corticotropin from pituitary gland. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with CRH.The function of CRH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1976.

GAM337624 HADH2 TCTAAGAGAAAGGAA Hydroxyacyl- Coenzyme A Dehydrogenase, Type II (HADH2,
A A
GTTCAGA Accession NM_004493.1) is another GAM337624 target gene. HADH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HADH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HADH2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337624 is therefore inhibition of HADH2, a GAM337624 target gene which catalyzes the reversible oxidation of L- 3- hydroxyacyl- CoAs to form 3- ketoacyl- CoAs and binds intracellular amyloid- beta. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HADH2.The function of HADH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1820.

GAM337624 NCSTN TCTAAGAGAAAGGAA NCSTN (Accession NM_015331.1) is another GAM337624 target gene. A A
GTTCAGA NCSTN BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCSTN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of NCSTN BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337624 is therefore inhibition of NCSTN, a GAM337624 target gene which has a central role in presenilin- mediated processing of beta- amyloid precursor protein (beta- APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with NCSTN.The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337624 PSEN1 TCTAAGAGAAAGGAA PSEN1 (Accession NM_007318.1) is another GAM337624 target gene. A A
GTTCAGA PSEN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PSEN1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337624 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337624 is therefore inhibition of PSEN1. Accordingly, utilities of GAM337624 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PSEN1.

GAM337625 APPBP2 CATTGCACTCCAGCC Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

TGGGCAA Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337625 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337625 is therefore inhibition of APPBP2, a GAM337625 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337625 BACE2 CATTGCACTCCAGCC Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

TGGGCAA NM_138992.1) is another GAM337625 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337625 is therefore inhibition of BACE2, a GAM337625 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337625 FHL2 CATTGCACTCCAGCC Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

TGGGCAA another GAM337625 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337625 is therefore inhibition of FHL2, a GAM337625 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337625 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337625 target gene. HD A A

TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337625 is therefore inhibition of HD. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337625 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

TGGGCAA NM_000618.2) is another GAM337625 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337625 is therefore inhibition of IGF1, a GAM337625 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337625 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

TGGGCAA another GAM337625 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337625 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337625 is therefore inhibition of PRND, a GAM337625 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337625 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337626 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337626 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337626 is therefore inhibition of APPBP2, a GAM337626 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337626 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337626 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337626 is therefore inhibition of

BACE2, a GAM337626 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337626 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337626 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337626 is therefore inhibition of FHL2, a GAM337626 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337626 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337626 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337626 is therefore inhibition of IGF1, a GAM337626 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337626 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337626 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337626 is therefore inhibition of MME, a GAM337626 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337626 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337626 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337626 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337626 is therefore inhibition of PRND, a GAM337626 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337626 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337627 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337627 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337627 is therefore inhibition of APPBP2, a GAM337627 target gene which interacts with the basolateral sorting

signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337627 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337627 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337627 is therefore inhibition of BACE2, a GAM337627 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337627 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
GGGCAAC another GAM337627 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337627 is therefore inhibition of FHL2, a GAM337627 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337627 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337627 target gene. IGF1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337627 is therefore inhibition of IGF1, a GAM337627 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337627 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337627 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337627 is therefore inhibition of MME, a GAM337627 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337627 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337627 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337627 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337627 is therefore inhibition of PRND, a GAM337627 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly,

utilities of GAM337627 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337628 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337628 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337628 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337628 is therefore inhibition of APP. Accordingly, utilities of GAM337628 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337629 APP TGTGCACAACATGCA APP (Accession NM_000484.1) is a GAM337629 target gene. APP A A

GGTTTGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APP BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337629 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337629 is therefore inhibition of APP. Accordingly, utilities of GAM337629 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APP.

GAM337630 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337630 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337630 is therefore inhibition of APPBP2, a GAM337630 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337630 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337630 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337630 is therefore inhibition of BACE2, a GAM337630 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337630 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337630 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337630 is therefore inhibition of FHL2, a GAM337630 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337630 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337630 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set

forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337630 is therefore inhibition of IGF1, a GAM337630 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337630 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337630 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337630 is therefore inhibition of MME, a GAM337630 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337630 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337630 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337630 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337630 is therefore inhibition of PRND, a GAM337630 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337630 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337631 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337631 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337631 is therefore inhibition of APPBP2, a GAM337631 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337631 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337631 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337631 is therefore inhibition of BACE2, a GAM337631 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337631 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337631 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby

incorporated herein.

Another function of GAM337631 is therefore inhibition of FHL2, a GAM337631 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337631 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A
GGGCAAC NM_000618.2) is another GAM337631 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337631 is therefore inhibition of IGF1, a GAM337631 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337631 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337631 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337631 is therefore inhibition of MME, a GAM337631 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337631 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337631 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337631 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337631 is therefore inhibition of PRND, a GAM337631 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337631 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337632 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A

GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337632 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337632 is therefore inhibition of APPBP2, a GAM337632 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337632 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A

GGGCAAC NM_012105.3) is another GAM337632 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337632 is therefore inhibition of BACE2, a GAM337632 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337632 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A

GGGCAAC another GAM337632 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337632 is therefore inhibition of FHL2, a GAM337632 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337632 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

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Another function of GAM337632 is therefore inhibition of IGF1, a GAM337632 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337632 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A
GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337632 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337632 is therefore inhibition of MME, a GAM337632 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337632 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A
GGGCAAC another GAM337632 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337632 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337632 is therefore inhibition of PRND, a GAM337632 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337632 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337633 APPBP2 ACTGCACTCCAGCCT Amyloid Beta Precursor Protein (cytoplasmic tail)- binding A A
GGGCAAC Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337633 target gene. APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APPBP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE1 and APPBP2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

A function of GAM337633 is therefore inhibition of APPBP2, a GAM337633 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337633 BACE2 ACTGCACTCCAGCCT Beta- site APP- cleaving Enzyme 2 (BACE2, Accession A A
GGGCAAC NM_012105.3) is another GAM337633 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337633 is therefore inhibition of BACE2, a GAM337633 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337633 FHL2 ACTGCACTCCAGCCT Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is A A
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Another function of GAM337633 is therefore inhibition of FHL2, a GAM337633 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337633 IGF1 ACTGCACTCCAGCCT Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A A

GGGCAAC NM_000618.2) is another GAM337633 target gene. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337633 is therefore inhibition of IGF1, a GAM337633 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337633 MME ACTGCACTCCAGCCT Membrane Metallo- endopeptidase (neutral endopeptidase, A A

GGGCAAC enkephalinase, (MME, Accession NM_000902.2) is another GAM337633 target gene. MME BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of MME BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337633 is therefore inhibition of MME, a GAM337633 target gene which is thermolysin- like specificity. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with MME.The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337633 PRND ACTGCACTCCAGCCT Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A

GGGCAAC another GAM337633 target gene. PRND BINDING SITE1 through PRND BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE3, and secondary structure complementarity to the nucleotide sequence of GAM337633 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337633 is therefore inhibition of PRND, a GAM337633 target gene which is similar to prion protein

PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337633 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337634 APPBP2 CATTGCACTCCAGCC TGGGCAA Amyloid Beta Precursor Protein (cytoplasmic tail)- binding Protein 2 (APPBP2, Accession NM_006380.2) is a GAM337634 target gene. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of APPBP2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

A function of GAM337634 is therefore inhibition of APPBP2, a GAM337634 target gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with APPBP2.The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM337634 BACE2 CATTGCACTCCAGCC TGGGCAA Beta- site APP- cleaving Enzyme 2 (BACE2, Accession NM_138992.1) is another GAM337634 target gene. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of BACE2 BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein. A A

Another function of GAM337634 is therefore inhibition of BACE2, a GAM337634 target gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore is associated with Alzheimer. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with BACE2.The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337634 FHL2 CATTGCACTCCAGCC TGGGCAA Four and A Half LIM Domains 2 (FHL2, Accession NM_001450.2) is another GAM337634 target gene. FHL2 BINDING SITE1 and FHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA A A

encoded by FHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of FHL2 BINDING SITE1 and FHL2 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337634 is therefore inhibition of FHL2, a GAM337634 target gene which Contains four LIM domains and an additional zinc finger. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with FHL2.The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.

GAM337634 HD CATTGCACTCCAGCC HD (Accession NM_002111.3) is another GAM337634 target gene.
HD A A
TGGGCAA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of HD BINDING SITE, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337634 is therefore inhibition of HD. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with HD.

GAM337634 IGF1 CATTGCACTCCAGCC Insulin- like Growth Factor 1 (somatomedin C) (IGF1, Accession A
A
TGGGCAA NM_000618.2) is another GAM337634 target gene. IGF1 BINDING SITE1 and IGF1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IGF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of IGF1 BINDING SITE1 and IGF1 BINDING SITE2, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337634 is therefore inhibition of IGF1, a GAM337634 target gene which are structurally and functionally related to insulin but have a much higher growth-promoting activity and therefore is associated with Alzheimer. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with IGF1.The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM25.

GAM337634 PRND CATTGCACTCCAGCC Prion Protein 2 (dublet) (PRND, Accession NM_012409.1) is A A TGGGCAA another GAM337634 target gene. PRND BINDING SITE1 through PRND BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Nucleotide sequences of PRND BINDING SITE1 through PRND BINDING SITE4, and secondary structure complementarity to the nucleotide sequence of GAM337634 RNA are set forth in Tables 6 and 7, hereby incorporated herein.

Another function of GAM337634 is therefore inhibition of PRND, a GAM337634 target gene which is similar to prion protein PRNP. and therefore is associated with Alzheimer. Accordingly, utilities of GAM337634 include diagnosis, prevention and treatment of Alzheimer, and of other diseases and clinical conditions associated with PRND.The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.

GAM NAME	GAM RNA SEQUENCE	TARGET	REFERENCES	GAM POS
GAM25	AATTGCTTGAACCC AGGAAGTG	IGF1	Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin - like growth factor - I and cognitive function inhealthy older men. J. Clin. Endocr. Metab. 84: 471 - 475, 1999.	A
GAM25	AATTGCTTGAACCC AGGAAGTG	IGF1	Baker, J.; Liu, J. - P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin - like growth factors in embryonic and postnatal growth. Cell 75:73 - 82, 1993.	A
GAM25	AATTGCTTGAACCC AGGAAGTG	IGF1	Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and absence of association with stature among African Pygmies. Hum.Genet. 85: 349 - 354, 1990.	A
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GAM25	AATTGCTTGAACCC AGGAAGTG	IGF1	Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of genes for insulin - like growth factors I and II and epidermalgrowth factor. Nature 310: 781 - 784, 1984.	A
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